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(19) World Intellectual Property Organization
International Bureau



(43) International Publication Date
9 August 2001 (09.08.2001)

PCT

(10) International Publication Number
WO 01/57278 A2

(51) International Patent Classification⁷: **C12Q 1/68,**
G06F 19/00, C07K 14/47

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(21) International Application Number: PCT/US01/00670

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(22) International Filing Date: 30 January 2001 (30.01.2001)

(25) Filing Language: English

(81) Designated States (*national*): AE, AG, AL, AM, AT, AU,
AZ, BA, BB, BG, ~~BR, BY, BZ~~, CA, CH, CN, CR, CU, CZ,
DE, DK, DM, ~~DZ~~, EE, ES, FI, GB, GD, GE, GH, GM, HR,
HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR,
LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ,
NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM,
TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.

(26) Publication Language: English

(30) Priority Data:
60/180,312 4 February 2000 (04.02.2000) US
60/207,456 26 May 2000 (26.05.2000) US
09/608,408 30 June 2000 (30.06.2000) US
09/632,366 3 August 2000 (03.08.2000) US
60/234,687 21 September 2000 (21.09.2000) US
60/236,359 27 September 2000 (27.09.2000) US
0024263.6 4 October 2000 (04.10.2000) GB

(84) Designated States (*regional*): ARIPO patent (GH, GM,
KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian
patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European
patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE,
IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF,
CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

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Published:

- without international search report and to be republished
upon receipt of that report
- entirely in electronic form (except for this front page) and
available upon request from the International Bureau

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*For two-letter codes and other abbreviations, refer to the "Guid-
ance Notes on Codes and Abbreviations" appearing at the begin-
ning of each regular issue of the PCT Gazette.*

(54) Title: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ANALYSIS OF GENE
EXPRESSION IN HUMAN HELA CELLS OR OTHER HUMAN CERVICAL EPITHELIAL CELLS

(57) Abstract: A single exon nucleic acid microarray comprising a plurality of single exon nucleic acid probes for measuring gene
expression in a sample derived from human HeLa cells is described. Also described are single exon nucleic acid probes expressed
in the HeLa cells and their use in methods for detecting gene expression.

WO 01/57278 A2

HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
FOR ANALYSIS OF GENE EXPRESSION IN HUMAN HELA CELLS OR
OTHER HUMAN CERVICAL EPITHELIAL CELLS

5 CROSS REFERENCE TO RELATED APPLICATIONS

The present application is a continuation-in-part of U.S.
patent application serial nos. 09/632,366, filed August 3,
2000 and 09/608,408, filed June 30, 2000; claims the
10 benefit under 35 U.S.C. s 119(e) of U.S. provisional patent
application serial nos. 60/236,359, filed September 27,
2000, 60/234,687, filed September 21, 2000, 60/207,456,
filed May 26, 2000, and 60/180,312, filed February 4, 2000;
and further claims the benefit under 35 U.S.C. s 119(a) of
15 UK patent application no. 0024263.6, filed October 4, 2000,
the disclosures of which are incorporated herein by
reference in their entireties.

REFERENCE TO SEQUENCE LISTING AND INCORPORATION BY
20 REFERENCE THEREOF

The present application includes a Sequence Listing in
electronic format, filed pursuant to PCT Administrative
Instructions 801 - 806 on a single CD-R disc, in
25 triplicate, containing a file named pto_HELA.txt, created
24 January 2001, having 18,781,468 bytes. The Sequence
Listing contained in said file on said disc is incorporated
herein by reference in its entirety.

30 Field of the Invention

The present invention relates to genome-derived
single exon microarrays useful for verifying the expression
of regions of genomic DNA predicted to encode protein. In
35 particular, the present invention relates to unique genome-

derived single exon nucleic acid probes expressed in human HeLa cells and single exon nucleic acid microarrays that include such probes.

5 Background of the Invention

For almost two decades following the invention of general techniques for nucleic acid sequencing, Sanger et al., *Proc. Natl. Acad. Sci. USA* 70(4):1209-13 (1973); Gilbert et al., *Proc. Natl. Acad. Sci. USA* 70(12):3581-4
10 (1973), these techniques were used principally as tools to further the understanding of proteins - known or suspected - about which a basic foundation of biological knowledge had already been built. In many cases, the cloning effort that preceded sequence identification had
15 been both informed and directed by that antecedent biological understanding.

For example, the cloning of the T cell receptor for antigen was predicated upon its known or suspected cell type-specific expression, by its suspected membrane
20 association, and by the predicted assembly of its gene via T cell-specific somatic recombination. Subsequent sequencing efforts at once confirmed and extended understanding of this family of proteins. Hedrick et al., *Nature* 308(5955):153-8 (1984).

25 More recently, however, the development of high throughput sequencing methods and devices, in concert with large public and private undertakings to sequence the human and other genomes, has altered this investigational paradigm: today, sequence information often precedes
30 understanding of the basic biology of the encoded protein product.

One of the approaches to large-scale sequencing is predicated upon the proposition that expressed sequences - that is, those accessible through isolation of
35 mRNA - are of greatest initial interest. This "expressed

sequence tag" ("EST") approach has already yielded vast amounts of sequence data (see for example Adams et al., *Science* 252:1651 (1991); Williamson, *Drug Discov. Today* 4:115 (1999)). For nucleic acids sequenced by this approach, often the only biological information that is known *a priori* with any certainty is the likelihood of biologic expression itself. By virtue of the species and tissue from which the mRNA had originally been obtained, most such sequences are also annotated with the identity of the species and at least one tissue in which expression appears likely.

More recently, the pace of genomic sequencing has accelerated dramatically. When genomic DNA serves as the initial substrate for sequencing efforts, expression cannot be presumed; often the only *a priori* biological information about the sequence includes the species and chromosome (and perhaps chromosomal map location) of origin.

With the ever-accelerating pace of sequence accumulation by directed, EST, and genomic sequencing approaches – and in particular, with the accumulation of sequence information from multiple genera, from multiple species within genera, and from multiple individuals within a species – there is an increasing need for methods that rapidly and effectively permit the functions of nucleic sequences to be elucidated. And as such functional information accumulates, there is a further need for methods of storing such functional information in meaningful and useful relationship to the sequence itself; that is, there is an increasing need for means and apparatus for annotating raw sequence data with known or predicted functional information.

Although the increase in the pace of genomic sequencing is due in large part to technological changes in sequencing strategies and instrumentation, Service, *Science* 280:995 (1998); Pennisi, *Science* 283: 1822-1823 (1999),

there is an important functional motivation as well.

While it was understood that the EST approach would rarely be able to yield sequence information about the noncoding portions of the genome, it now also appears
5 the EST approach is capable of capturing only a fraction of a genome's actual expression complexity.

For example, when the *C. elegans* genome was fully sequenced, gene prediction algorithms identified over 19,000 potential genes, of which only 7,000 had been found
10 by EST sequencing. *C. elegans* Sequencing Consortium, *Science* 282:2012 (1998). Analogously, the recently completed sequence of chromosome 2 of *Arabidopsis* predicts over 4000 genes, Lin et al., *Nature*, 402:761 (1999), of which only about 6% had previously been identified via EST
15 sequencing efforts. Although the human genome has the greatest depth of EST coverage, it is still woefully short of surrendering all of its genes. One recent estimate suggests that the human genome contains more than 146,000 genes, which would at this point leave greater than half of
20 the genes undiscovered. It is now predicted that many genes, perhaps 20 to 50%, will only be found by genomic sequencing.

There is, therefore, a need for methods that permit the functional regions of genomic sequence - and
25 most importantly, but not exclusively, regions that function to encode genes - to be identified.

Much of the coding sequence of the human genome is not homologous to known genes, making detection of open reading frames ("ORFs") and predictions of gene function
30 difficult. Computational methods exist for predicting coding regions in eukaryotic genomes. Gene prediction programs such as GRAIL and GRAIL II, Uberbacher et al., *Proc. Natl. Acad. Sci. USA* 88(24):11261-5 (1991); Xu et al., *Genet. Eng.* 16:241-53 (1994); Uberbacher et al.,
35 *Methods Enzymol.* 266:259-81 (1996); GENEFINDER, Solovyev et

al., *Nucl. Acids. Res.* 22:5156-63 (1994); Solovyev et al.,
Ismb 5:294-302 (1997); and GENESCAN, Burge et al., *J. Mol.*
Biol. 268:78-94 (1997), predict many putative genes without
known homology or function. Such programs are known,
5 however, to give high false positive rates. Burset et al.,
Genomics 34:353-367 (1996). Using a consensus obtained by
a plurality of such programs is known to increase the
reliability of calling exons from genomic sequence.
Ansari-Lari et al., *Genome Res.* 8(1):29-40 (1998)

10 Identification of functional genes from genomic
data remains, however, an imperfect art. For example, in
reporting the full sequence of human chromosome 21, the
Chromosome 21 Mapping and Sequencing Consortium reports
that prior bioinformatic estimates of human gene number may
15 need to be revised substantially downwards. *Nature*
405:311-199 (2000); Reeves, *Nature* 405:283-284 (2000).

Thus, there is a need for methods and apparatus
that permit the functions of the regions identified
bioinformatically - and specifically, that permit the
20 expression of regions predicted to encode protein - readily
to be confirmed experimentally.

Recently, the development of nucleic acid
microarrays has made possible the automated and highly
parallel measurement of gene expression. Reviewed in
25 Schena (ed.), DNA Microarrays : A Practical Approach
(Practical Approach Series), Oxford University Press (1999)
(ISBN: 0199637768); *Nature Genet.* 21(1)(suppl):1 - 60
(1999); Schena (ed.), Microarray Biochip: Tools and
Technology, Eaton Publishing Company/BioTechniques Books
30 Division (2000) (ISBN: 1881299376).

It is common for microarrays to be derived from
cDNA/EST libraries, either from those previously described
in the literature, such as those from the I.M.A.G.E.
consortium, Lennon et al., *Genomics* 33(1):151-2 (1996), or
35 from the construction of "problem specific" libraries

targeted at a particular biological question, R.S. Thomas et al., *Cancer Res.* (in press). Such microarrays by definition can measure expression only of those genes found in EST libraries, and thus have not been useful as probes
5 for genes discovered solely by genomic sequencing.

The utility of using whole genome nucleic acid microarrays to answer certain biological questions has been demonstrated for the yeast *Saccharomyces cerevisiae*. De Risi et al., *Science* 278:680 (1997). The vast majority of
10 yeast nuclear genes, approximately 95% however, are single exon genes, i.e., lack introns, Lopez et al., *RNA* 5:1135-1137 (1999); Goffeau et al., *Science* 274:563-67 (1996), permitting coding regions more readily to be identified. Whole genome nucleic acid microarrays have not generally
15 been used to probe gene expression from more complex eukaryotic genomes, and in particular from those averaging more than one intron per gene.

Summary of the Invention

20

The present invention solves these and other problems in the art by providing methods and apparatus for predicting, confirming, and displaying functional information derived from genomic sequence. The present
25 invention also provides apparatus for verifying the expression of putative genes identified within genomic sequence.

In particular, the invention provides novel genome-derived single exon nucleic acid microarrays useful
30 for verifying the expression of putative genes identified within genomic sequence.

The present invention also provides compositions and kits for the ready production of nucleic acids identical in sequence to, or substantially identical in
35 sequence to, probes on the genome-derived single exon

microarrays of the present invention.

Accordingly, in a first aspect of the invention, there is provided a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human HeLa cells or other human cervical epithelial cells, comprising a plurality of single exon nucleic acid probes according to any one of the nucleotide sequences set out in SEQ ID NOS: 1 - 9,290 or a complementary sequence, or a portion of such a sequence.

By plurality is meant at least two, suitably at least 20, most suitably at least 100, preferably at least 1000 and, most preferably, upto 5000.

In one embodiment of the first aspect, each of said plurality of probes is separately and addressably amplifiable.

In an alternative embodiment, each of said plurality of probes is separately and addressably isolatable from said plurality.

In a preferred embodiment, each of said plurality of probes is amplifiable using at least one common primer. Preferably, each of said plurality of probes is amplifiable using a first and a second common primer.

In yet another embodiment, said set of single exon nucleic acid probes comprises between 50 - 20,000 probes, for example, 50 - 5000.

Suitably, said set of single exon nucleic acid probes comprises at least 50 - 1000 discrete single exon nucleic acid probes having a sequence as set out in any of SEQ ID NOS.: 1 - 18,392 or a complimentary sequence, or a portion of such a sequence.

Preferably, the average length of the single exon nucleic acid probes is between 200 and 500 bp. It is preferred that the average length should be at least 200bp, suitably at least 250bp, most suitably at least 300bp, preferably at least 400bp and, most preferably, 500 bp.

In another embodiment, the single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence. It is preferred that at least 50%, suitably at least 60%, most suitably at least 70%, preferably at least 5 75%, more preferably at least 80, 85, 90, 95 or 99% of said single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence.

In another preferred embodiment, said single exon nucleic acid lack homopolymeric stretches of A or T. It is 10 preferred that at least 50%, suitably at least 60%, most suitably at least 70%, preferably at least 75%, more preferably at least 80, 85, 90, 95 or 99% of said single exon nucleic acid probes lack homopolymeric stretches of A or T.

15 Preferably, a spatially-addressable set of single exon nucleic acid probes in accordance with the first aspect of the invention is addressably disposed upon a substrate.

Suitable substrates include a filter membrane 20 which may, preferably, be nitrocellulose or nylon. The nylon may preferably, be positively-charged. Other suitable substrates include glass, amorphous silicon, crystalline silicon, and plastic. Further suitable materials include polymethylacrylic, polyethylene, polypropylene, 25 polyacrylate, polymethylmethacrylate, polyvinylchloride, polytetrafluoroethylene, polystyrene, polycarbonate, polyacetal, polysulfone, celluloseacetate, cellulosenitrate, nitrocellulose, and mixtures thereof.

In a second aspect of the invention, there is 30 provided a microarray comprising a spatially addressable set of single exon nucleic acid probes in accordance with the first aspect of the invention.

In one embodiment, a genome-derived single-exon microarray is packaged together with such an ordered set of 35 amplifiable probes corresponding to the probes, or one or

more subsets of probes, thereon. In alternative embodiments, the ordered set of amplifiable probes is packaged separately from the genome-derived single exon microarray.

5 In another aspect, the invention provides genome-derived single exon nucleic acid probes useful for gene expression analysis, and particularly for gene expression analysis by microarray. In particular embodiments of this aspect, the present invention provides human single-exon
10 probes that include specifically-hybridizable fragments of SEQ ID Nos. 9,291 - 18,392, wherein the fragment hybridizes at high stringency to an expressed human gene. In particular embodiments, the invention provides single exon probes comprising SEQ ID Nos. 1 - 9,290.

15 Accordingly, in a third aspect of the invention, there is provided a single exon nucleic acid probe for measuring human gene expression in a sample derived from human HeLa cells or other human cervical epithelial cells which is a nucleic acid molecule comprising a nucleotide
20 sequence as set out in any of SEQ ID NOS.: 1 - 9,290 or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid expressed in the human HeLa cells or other human cervical epithelial cells.

25 In one embodiment, a single exon nucleic acid probe in accordance with the third aspect comprises a nucleotide sequence as set out in any of SEQ ID NOS.: 9,291 - 18,392 or a complementary sequence or a fragment thereof.

In a fourth aspect of the invention, there is
30 provided a single exon nucleic acid probe for measuring human gene expression in a sample derived from human HeLa cells or other human cervical epithelial cells which is a nucleic acid molecule having a sequence encoding a peptide comprising a peptide sequence as set out in any of SEQ ID
35 NOS.: 18,393 - 26,941 or a complementary sequence or a

fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid expressed in the human HeLa cells or other human cervical epithelial cells.

Preferably, a single exon nucleic acid probe in accordance with the third or fourth aspects of the invention comprises between at least 15 and 50 contiguous nucleotides of said SEQ ID NO:. It is preferred that the single exon nucleic acid probe comprises at least 15, suitably at least 20, more suitably at least 25 or preferably at least 50 contiguous nucleotides of said SEQ ID NO:.

In another preferred embodiment, a single exon nucleic acid probe in accordance with the third or fourth aspects of the invention is between 3kb and 25kb in length. It is preferred that said probe is no more than 3kb, suitably no more than 5kb, more suitably no more than 10kb, preferably 15kb, more preferably 20kb or, most preferably, no more than 20kb in length.

Preferably, a single exon nucleic acid probe in accordance with either the fifth or sixth aspect of the invention is DNA, preferably single-stranded DNA, RNA or PNA.

In another embodiment of either the third or fourth aspect of the invention, a single exon nucleic acid probe is detectably labeled. Suitable detectable labels include a radionuclide, a fluorescent label or a first member of a specific binding pair. Suitable fluorescent labels include dyes such as cyanine dyes, preferably Cy3 and Cy5 although other suitable dyes will be known to those skilled in the art.

In a particularly preferred embodiment, a single exon nucleic acid probe in accordance with either the third or fourth aspect of the invention lacks prokaryotic and bacteriophage vector sequence. In yet another embodiment, a single exon nucleic acid probe in accordance with either

the third or fourth aspect of the invention lacks homopolymeric stretches of A or T.

In a fifth aspect of the invention, there is provided an amplifiable nucleic acid composition,
5 comprising:

the single exon nucleic acid probe in accordance with either of the third or fourth aspects of the invention; and at least one nucleic acid primer;

wherein said at least one primer is sufficient to
10 prime enzymatic amplification of said probe.

In an sixth aspect of the invention, there is provided a method of measuring gene expression in a sample derived from human HeLa cells or other human cervical epithelial cells, comprising:

15 contacting the single exon microarray in accordance with the second aspect of the invention, with a first collection of detectably labeled nucleic acids, said first collection of nucleic acids derived from mRNA of human HeLa cells or other human cervical epithelial cells;
20 and then

measuring the label detectably bound to each probe of said microarray.

In a seventh aspect of the invention, there is provided a method of identifying exons in a eukaryotic
25 genome, comprising:

algorithmically predicting at least one exon from genomic sequence of said eukaryote; and then

detecting specific hybridization of detectably labeled nucleic acids to a single exon probe,

30 wherein said detectably labeled nucleic acids are derived from mRNA from the HeLa cells or other human cervical epithelial cells of said eukaryote, said probe is a single exon probe having a fragment identical in sequence to, or complementary in sequence to, said predicted exon,
35 said probe is included within a single exon microarray in

accordance with the first aspect of the invention, and said fragment is selectively hybridizable at high stringency.

In a eighth aspect of the invention, there is provided a method of assigning exons to a single gene,
5 comprising:

identifying a plurality of exons from genomic sequence in accordance with the seventh aspect of the invention; and then

measuring the expression of each of said exons in
10 a plurality of tissues and/or cell types using hybridization to single exon microarrays having a probe with said exon,

wherein a common pattern of expression of said exons in said plurality of tissues and/or cell types
15 indicates that the exons should be assigned to a single gene.

In an ninth aspect of the invention, there is provided a nucleic acid sequence as set out in any of SEQ ID NOS: 1 - 18,392 wherein said sequence encodes a peptide.

20 In a tenth aspect of the invention, there is provided a peptide encoded by a sequence comprising a sequence as set out in any of SEQ ID NOS: 9,291 - 18,392, or a complementary sequence or coding portion thereof.

In a preferred embodiment, a peptide may be
25 encoded by a sequence comprising a sequence set out in any of SEQ ID NOS.: 1 -9,290.

In a further aspect, the invention provides peptides comprising an amino acid sequence translated from the DNA fragments, said amino acid sequences comprising SEQ
30 ID NOS.: 18,393 - 26,941.

Accordingly in a eleventh aspect of the invention there is provided a peptide comprising a sequence as set out in any of SEQ ID NOS: 18,393 - 26,941, or fragment thereof.

35 In another aspect, the invention provides means

for displaying annotated sequence, and in particular, for displaying sequence annotated according to the methods and apparatus of the present invention. Further, such display can be used as a preferred graphical user interface for electronic search, query, and analysis of such annotated sequence.

Detailed Description of the Invention

Definitions

As used herein, the term "microarray" and phrase "nucleic acid microarray" refer to a substrate-bound collection of plural nucleic acids, hybridization to each of the plurality of bound nucleic acids being separately detectable. The substrate can be solid or porous, planar or non-planar, unitary or distributed.

As so defined, the term "microarray" and phrase "nucleic acid microarray" include all the devices so called in Schena (ed.), DNA Microarrays: A Practical Approach (Practical Approach Series), Oxford University Press (1999) (ISBN: 0199637768); *Nature Genet.* 21(1)(suppl):1 - 60 (1999); and Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376). As so defined, the term "microarray" and phrase "nucleic acid microarray" further include substrate-bound collections of plural nucleic acids in which the nucleic acids are distributably disposed on a plurality of beads, rather than on a unitary planar substrate, as is described, *inter alia*, in Brenner et al., *Proc. Natl. Acad. Sci. USA* 97(4):166501670 (2000); in such case, the term "microarray" and phrase "nucleic acid microarray" refer to the plurality of beads in aggregate.

As used herein with respect to a nucleic acid

microarray, the term "probe" refers to the nucleic acid that is, or is intended to be, bound to the substrate; in such context, the term "target" thus refers to nucleic acid intended to be bound thereto by Watson-Crick

5 complementarity. As used herein with respect to solution phase hybridization, the term "probe" refers to the nucleic acid of known sequence that is detectably labeled.

As used herein, the expression "probe comprising SEQ ID NO.", and variants thereof, intends a nucleic acid
10 probe, at least a portion of which probe has either (i) the sequence directly as given in the referenced SEQ ID NO., or (ii) a sequence complementary to the sequence as given in the referenced SEQ ID NO., the choice as between sequence directly as given and complement thereof dictated by the
15 requirement that the probe hybridize to mRNA.

As used herein, the term "open reading frame" and the equivalent acronym "ORF" refer to that portion of an exon that can be translated in its entirety into a sequence of contiguous amino acids i.e. a nucleic acid sequence
20 that, in at least one reading frame, does not possess stop codons; the term does not require that the ORF encode the entirety of a natural protein.

As used herein, the term "amplicon" refers to a PCR product amplified from human genomic DNA, containing
25 the predicted exon.

As used herein the term "exon" refers to the consensus prediction of the various exon and gene predicting algorithms i.e. a nucleic acid sequence bioinformatically predicted to encode a portion of a
30 natural protein.

As used herein, the term "peptide" refers to a sequence of amino acids. The sequences referred to as PEPTIDE SEQ ID NOS.: are the predicted peptide sequences that would be translated from one of the exons, or a
35 portion thereof set out in exon SEQ ID NOS.: The codons

encoding the peptide are wholly contained within the exon.

As used herein, a "portions" of a defined nucleotide sequence or sequences can be and, preferably, are fragments unique to that sequence or to one or a
5 combination of those sequences. A fragment unique to a nucleic acid molecule is one that is a signature for the larger nucleic acid molecule.

As used herein, the phrase "expression of a probe" and its linguistic variants means that the ORF
10 present within the probe, or its complement, is present within a target mRNA.

As used herein, "stringent conditions" refers to parameters well known to those skilled in the art. When a nucleic acid molecule is said to be hybridisable to another
15 of a given sequence under "stringent conditions" it is meant that it is homologous to the given sequence.

As used herein, the phrase "specific binding pair" intends a pair of molecules that bind to one another with high specificity. Binding pairs are said to exhibit
20 specific binding when they exhibit avidity of at least 10^7 , preferably at least 10^8 , more preferably at least 10^9 liters/mole. Nonlimiting examples of specific binding pairs are: antibody and antigen; biotin and avidin; and biotin and streptavidin.

As used herein with respect to the visual display of annotated genomic sequence, the term "rectangle" means any geometric shape that has at least a first and a second border, wherein the first and second borders each are capable of mapping uniquely to a point of another visual
30 object of the display.

As used herein, a "Mondrian" means a visual display in which a single genomic sequence is annotated with predicted and experimentally confirmed functional information.

Brief Description of the Drawings

The present invention is further illustrated with
5 reference to the following non-limiting figures and
examples in which:

FIG. 1 illustrates a process for predicting
functional regions from genomic sequence, confirming the
functional activity of such regions experimentally, and
10 associating and displaying the data so obtained in
meaningful and useful relationship to the original sequence
data;

FIG. 2 further elaborates that portion of the
process schematized in FIG. 1 for predicting functional
15 regions from genomic sequence;

FIG. 3 illustrates a Mondrian visual display;

FIG. 4 presents a Mondrian showing a hypothetical
annotated genomic sequence;

FIG. 5 is a histogram showing the distribution of
20 ORF length and PCR products as obtained, with ORF length
shown in black and PCR product length shown in dotted
lines;

FIG. 6 is a histogram showing the distribution,
among exons predicted according to the methods described,
25 of expression as measured using simultaneous two color
hybridization to a genome-derived single exon microarray.
The graph shows the number of sequence-verified products
that were either not expressed ("0"), expressed in one or
more but not all tested tissues ("1" - "9"), or expressed
30 in all tissues tested ("10");

FIG. 7 is a pictorial representation of the
expression of verified sequences that showed expression
with signal intensity greater than 3 in at least one
tissue, with: FIG. 7A showing the expression as measured by
35 microarray hybridization in each of the 10 measured

tissues, and the expression as measured "bioinformatically" by query of EST, NR and SwissProt databases; with FIG. 7B showing the legend for display of physical expression (ratio) in FIG. 7A; and with FIG. 7C showing the legend for scoring EST hits as depicted in FIG. 7A;

FIG. 8 shows a comparison of normalized CY3 signal intensity for arrayed sequences that were identical to sequences in existing EST, NR and SwissProt databases or that were dissimilar (unknown), where black denotes the signal intensity for all sequence-verified products with a BLAST Expect ("E") value of greater than $1e-30$ (1×10^{-30}) ("unknown") and a dotted line denotes sequence-verified spots with a BLAST expect ("E") value of less than $1e-30$ (1×10^{-30}) ("known");

FIG. 9 presents a Mondrian of BAC AC008172 (bases 25,000 to 130,000), containing the carbamyl phosphate synthetase gene (AF154830.1); and

FIG. 10 is a Mondrian of BAC A049839.

Methods and Apparatus for Predicting, Confirming, Annotating, and Displaying Functional Regions From Genomic Sequence Data

FIG. 1 is a flow chart illustrating in broad outline a process for predicting functional regions from genomic sequence, confirming and characterizing the functional activity of such regions experimentally, and then associating and displaying the information so obtained in meaningful and useful relationship to the original sequence data.

The initial input into process 10 of the present invention is drawn from one or more databases containing genomic sequence data. Because genomic sequence is usually obtained from subgenomic fragments, the sequence

data typically will be stored in a series of records corresponding to these subgenomic sequenced fragments. Some fragments will have been catenated to form larger contiguous sequences ("contigs"); others will not. A
5 finite percentage of sequence data in the database will typically be erroneous, consisting *inter alia* of vector sequence, sequence created from aberrant cloning events, sequence of artificial polylinkers, and sequence that was erroneously read.

10 Each sequence record in database 100 will minimally contain as annotation a unique sequence identifier (accession number), and will typically be annotated further to identify the date of accession, species of origin, and depositor. Because database 100 can
15 contain nongenomic sequence, each sequence will typically be annotated further to permit query for genomic sequence. Chromosomal origin, optionally with map location, can also be present. Data can be, and over time increasingly will be, further annotated with additional information, in part
20 through use of the present invention, as described below. Annotation can be present within the data records, in information external to database 100 and linked to the records thereto, or through a combination of the two.

Databases useful as genomic sequence database 100
25 in the present invention include GenBank, and particularly include several divisions thereof, including the htgs(draft), NT (nucleotide, command line), and NR (nonredundant) divisions. GenBank is produced by the National Institutes of Health and is maintained by the
30 National Center for Biotechnology Information (NCBI). Databases of genomic sequence from species other than human, such as mouse, rat, *Arabidopsis*, *C. elegans*, *C. brigssii*, *Drosophila*, zebra fish, and other higher eukaryotic organisms will also prove useful as genomic
35 sequence database 100.

Genomic sequence obtained by query of genomic sequence database 100 is then input into one or more processes 200 for identification of regions therein that are predicted to have a biological function as specified by the user. Such functions include, but are not limited to, encoding protein, regulating transcription, regulating message transport after transcription into mRNA, regulating message splicing after transcription into mRNA, of regulating message degradation after transcription into mRNA, and the like. Other functions include directing somatic recombination events, contributing to chromosomal stability or movement, contributing to allelic exclusion or X chromosome inactivation, and the like.

The particular genomic sequence to be input into process 200 will depend upon the function for which relevant sequence is to be identified as well as upon the approach chosen for such identification. Process step 200 can be iterated to identify different functions within a given genomic region. In such case, the input often will be different for the several iterations.

Sequences predicted to have the requisite function by process 200 are then input into process 300, where a subset of the input sequences suitable for experimental confirmation is identified. Experimental confirmation can involve physical and/or bioinformatic assay. Where the subsequent experimental assay is bioinformatic, rather than physical, there are fewer constraints on the sequences that can be tested, and in this latter case therefore process 300 can output the entirety of the input sequence.

The subset of sequences output from process 300 is then used in process 400 for experimental verification and characterization of the function predicted in process 200, which experimental verification can, and often will, include both physical and bioinformatic assay.

Process 500 annotates the sequence data with the functional information obtained in the physical and/or bioinformatic assays of process 400. Such annotation can be done using any technique that usefully relates the functional information to the sequence, as, for example, by incorporating the functional data into the sequence data record itself, by linking records in a hierarchical or relational database, by linking to external databases, by a combination thereof, or by other means well known within the database arts. The data can even be submitted for incorporation into databases maintained by others, such as GenBank, which is maintained by NCBI.

As further noted in FIG. 1, additional annotation can be input into process 500 from external sources 600.

The annotated data is then displayed in process 800, either before, concomitantly with, or after optional storage 700 on nontransient media, such as magnetic disk, optical disc, magnetooptical disk, flash memory, or the like.

FIG. 1 shows that the experimental data output from process 400 can be used in each preceding step of process 10: e.g., facilitating identification of functional sequences in process 200, facilitating identification of an experimentally suitable subset thereof in process 300, and facilitating creation of physical and/or informational substrates for, and performance of subsequent assay, of functional sequences in process 400.

Information from each step can be passed directly to the succeeding process, or stored in permanent or interim form prior to passage to the succeeding process. Often, data will be stored after each, or at least a plurality, of such process steps. Any or all process steps can be automated.

FIG. 2 further elaborates the prediction of functional sequence within genomic sequence according to

process 200.

Genomic sequence database 100 is first queried 20 for genomic sequence.

The sequence required to be returned by query 20 will depend, in the first instance, upon the function to be identified.

For example, genomic sequences that function to encode protein can be identified *inter alia* using gene prediction approaches, comparative sequence analysis approaches, or combinations of the two. In gene prediction analysis, sequence from one genome is input into process 200 where at least one, preferably a plurality, of algorithmic methods are applied to identify putative coding regions. In comparative sequence analysis, by contrast, corresponding, e.g., syntenic, sequence from a plurality of sources, typically a plurality of species, is input into process 200, where at least one, possibly a plurality, of algorithmic methods are applied to compare the sequences and identify regions of least variability.

The exact content of query 20 will also depend upon the database queried. For example, if the database contains both genomic and nongenomic sequence, perhaps derived from multiple species, and the function to be determined is protein coding regions in human genomic sequence, the query will accordingly require that the sequence returned be genomic and derived from humans.

Query 20 can also incorporate criteria that compel return of sequence that meets operative requirements of the subsequent analytical method. Alternatively, or in addition, such operative criteria can be enforced in subsequent preprocess step 24.

For example, if the function sought to be identified is protein coding, query 20 can incorporate criteria that return from genomic sequence database 100 only those sequences present within contigs sufficiently

long as to have obviated substantial fragmentation of any given exon among a plurality of separate sequence fragments.

Such criteria can, for example, consist of a
5 required minimal individual genomic sequence fragment length, such as 10 kb, more typically 20 kb, 30 kb, 40kb, and preferably 50 kb or more, as well as an optional further or alternative requirement that sequence from any given clone, such as a bacterial artificial chromosome
10 ("BAC"), be presented in no more than a finite maximal number of fragments, such as no more than 20 separate pieces, more typically no more than 15 fragments, even more typically no more than about 10 - 12 fragments.

Results using the present invention have shown
15 that genomic sequence from bacterial artificial chromosomes (BACs) is sufficient for gene prediction analysis according to the present invention if the sequence is at least 50 kb in length, and if additionally the sequence from any given BAC is presented in fewer than 15, and preferably fewer
20 than 10, fragments. Accordingly, query 20 can incorporate a requirement that data accessioned from BAC sequencing be in fewer than 15, preferably fewer than 10, fragments.

An additional criterion that can be incorporated into the query can be the date, or range of dates, of
25 sequence accession. Although the process has been described above as if genomic sequence database 100 were static, it is of course understood that the genomic sequence databases need not be static, and indeed are typically updated on a frequent, even hourly, basis. Thus,
30 as further described in Examples 1 and 2, *infra*, it is possible to query the database for newly added sequence, either newly added after an absolute date, or newly added relative to a prior analysis performed using the methods and apparatus of the present invention. In this way, the
35 process herein described can incorporate a dynamic,

temporal component.

One utility of such temporal limitation is to identify, from newly accessioned genomic sequence, the presence of novel genes, particularly those not previously identified by EST sequencing (or other sequencing efforts that are similarly based upon gene expression). As further described in Example 1, such an approach has shown that newly accessioned human genomic sequence, when analyzed for sequences that function to encode protein, readily identifies genes that are novel over those in existing EST and other expression databases. This makes the methods of the present invention extremely powerful gene discovery tools. And as would be appreciated, such gene discovery can be performed using genomic sequence from species other than human.

If query 20 incorporates multiple criteria, such as above-described, the multiple criteria can be performed as a series of separate queries or as a single query, depending in part upon the query language, the complexity of the query, and other considerations well known in the database arts.

If query 20 returns no genomic sequence meeting the query criteria, the negative result can be reported by process 22, and process 200 (and indeed, entire process 10) ended 23, as shown. Alternatively, or in addition to report and termination of the initial inquiry, a new query 20 can be generated that takes into account the initial negative result.

When query 20 returns sequence meeting the query criteria, the returned sequence is then passed to optional preprocessing 24, suitable and specific for the desired analytical approach and the particular analytical methods thereof to be used in process 25.

Preprocessing 24 can include processes suitable for many approaches and methods thereof, as well as

processes specifically suited for the intended subsequent analysis.

Preprocessing 24 suitable for most approaches and methods will include elimination of sequence irrelevant to, or that would interfere with, the subsequent analysis. Such sequence includes repetitive sequence, such as Alu repeats and LINE elements, vector sequence, artificial sequence, such as artificial polylinkers, and the like. Such removal can readily be performed by identification and subsequent masking of the undesired sequence.

Identification can be effected by comparing the genomic sequence returned by query 20 with public or private databases containing known repetitive sequence, vector sequence, artificial sequence, and other artifactual sequence. Such comparison can readily be done using programs well known in the art, such as CROSS_MATCH, or by proprietary sequence comparison programs the engineering of which is well within the skill in the art.

Alternatively, or in addition, undesirable, including artifactual, sequence can be identified algorithmically without comparison to external databases and thereafter removed. For example, synthetic polylinker sequence can be identified by an algorithm that identifies a significantly higher than average density of known restriction sites. As another example, vector sequence can be identified by algorithms that identify nucleotide or codon usage at variance with that of the bulk of the genomic sequence.

Once identified, undesired sequence can be removed. Removal can usefully be done by masking the undesired sequence as, for example, by converting the specific nucleotide references to one that is unrecognized by the subsequent bioinformatic algorithms, such as "X". Alternatively, but at present less preferred, the undesired sequence can be excised from the returned genomic sequence,

leaving gaps.

Preprocessing 24 can further include selection from among duplicative sequences of that one sequence of highest quality. Higher quality can be measured as a lower percentage of, fewest number of, or least densely clustered occurrence of ambiguous nucleotides, defined as those nucleotides that are identified in the genomic sequence using symbols indicating ambiguity. Higher quality can also or alternatively be valued by presence in the longest contig.

Preprocessing 24 can, and often will, also include formatting of the data as specifically appropriate for passage to the analytical algorithms of process 25. Such formatting can and typically will include, *inter alia*, addition of a unique sequence identifier, either derived from the original accession number in genomic sequence database 100, or newly applied, and can further include additional annotation. Formatting can include conversion from one to another sequence listing standard, such as conversion to or from FASTA or the like, depending upon the input expected by the subsequent process.

Preprocessing, which can be optional depending upon the function desired to be identified and the informational requirements of the methods for effecting such identification, is followed by sequence processing 25, where sequences with the desired function are identified within the genomic sequence.

As mentioned above, such functions can include, but are not limited to, encoding protein, regulating transcription, regulating message transport after transcription into mRNA, regulating message splicing after transcription, of regulating message degradation, and the like. Other functions include directing somatic recombination events, contributing to chromosomal stability or movement, contributing to allelic exclusion or X

chromosome inactivation, or the like.

The methods of the present invention are particularly useful for gene discovery, that is, for identifying, from genomic sequence, regions that function to encode genes, and in a particularly useful embodiment, for identifying regions that function to encode genes not hitherto identified by expression-based or directed cloning and sequencing. In conjunction with verification using the novel single exon microarrays of the present invention, as further described below, the methods herein described become powerful gene discovery tools.

Accordingly, in a preferred embodiment of the present invention, process 25 is used to identify putative coding regions. Two preferred approaches in process 25 for identifying sequence that encodes putative genes are gene prediction and comparative sequence analysis.

Gene prediction can be performed using any of a number of algorithmic methods, embodied in one or more software programs, that identify open reading frames (ORFs) using a variety of heuristics, such as GRAIL, DICTION, and GENEFINDER. Comparative sequence analysis similarly can be performed using any of a variety of known programs that identify regions with lower sequence variability.

As further described in Example 1, below, gene finding software programs yield a range of results. For the newly accessioned human genomic sequence input in Example 1, for example, GRAIL identified the greatest percentage of genomic sequence as putative coding region, 2% of the data analyzed; GENEFINDER was second, calling 1%; and DICTION yielded the least putative coding region, with 0.8% of genomic sequence called as coding region.

Increased reliability can be obtained when consensus is required among several such methods. Although discussed herein particularly with respect to exon calling, consensus among methods will in general increase

reliability of predicting other functions as well.

Thus, as indicated by query 26, sequence processing 25, optionally with preprocessing 24, can be repeated with a different method, with consensus among such
5 iterations determined and reported in process 27.

Process 27 compares the several outputs for a given input genomic sequence and identifies consensus among the separately reported results. The consensus itself, as well as the sequence meeting that consensus, is then stored
10 in process 29a, displayed in process 29b, and/or output to process 300 for subsequent identification of a subset thereof suitable for assay.

Multiple levels of consensus can be calculated and reported by process 27. For example, as further
15 described in Example 1, *infra*, process 27 can report consensus as between all specific pairs of methods of gene prediction, as consensus among any one or more of the pairs of methods of gene prediction, or as among all of the gene prediction algorithms used. Thus, in Example 1, process 27
20 reported that GRAIL and GENEFINDER programs agreed on 0.7% of genomic sequence, that GRAIL and DICTION agreed on 0.5% of genomic sequence, and that the three programs together agreed on 0.25% of the data analyzed. Put another way, 0.25% of the genomic sequence was identified by all three
25 of the programs as containing putative coding region.

Furthermore, consensus can be required among different approaches to identifying a chosen function.

For example, if the function desired to be identified is coding of protein sequence, and a first used
30 approach to exon calling is gene prediction, the process can be repeated on the same input sequence, or subset thereof, with another approach, such as comparative sequence analysis. In such a case, where comparative sequence analysis follows gene prediction, the comparison
35 can be performed not only on genomic nucleic acid sequence,

but additionally or alternatively can be performed on the predicted amino acid sequence translated from the ORFs prior identified by the gene prediction approach.

Although shown as an iterative process, the
5 multiple analyses required to achieve consensus can be done in series, in parallel, or some combination thereof.

Predicted functional sequence, optionally representing a consensus among a plurality of methods and approaches for determination thereof, is passed to process
10 300 for identification of a subset thereof for functional assay.

In the preferred embodiment of the methods of the present invention, wherein the function sought to be identified is protein coding, process 300 is used to
15 identify a subset thereof suitable for experimental verification by physical and/or bioinformatic approaches.

For example, putative ORFs identified in process 200 can be classified, or binned, bioinformatically into putative genes. This binning can be based *inter alia* upon
20 consideration of the average number of exons/gene in the species chosen for analysis, upon density of exons that have been called on the genomic sequence, and other empirical rules. Thereafter, one or more among the gene-specific ORFs can be chosen for subsequent use in gene
25 expression assay.

Where such subsequent gene expression assay uses amplified nucleic acid, considerations such as desired amplicon length, primer synthesis requirements, putative exon length, sequence GC content, existence of possible
30 secondary structure, and the like can be used to identify and select those ORFs that appear most likely successfully to amplify. Where subsequent gene expression assay relies upon nucleic acid hybridization, whether or not using amplified product, further considerations involving
35 hybridization stringency can be applied to identify that

subset of sequences that will most readily permit sequence-specific discrimination at a chosen hybridization and wash stringency. One particular such consideration is avoidance of putative exons that span repetitive sequence; such
5 sequence can hybridize spuriously to nonspecific message, reducing specific signal in the hybridization.

For bioinformatic assay, there are fewer constraints on the sequences that can be tested experimentally, and in this latter case therefore process
10 300 can output the entirety of the input sequence.

The subset of sequences identified by process 300 as suitable for use in assay is then used in process 400 to create the physical and/or informational substrate for experimental verification of the predictions made in
15 process 200, and thereafter to assay those substrates.

As mentioned, the methods of the present invention are particularly useful for identifying potential coding regions within genomic sequence. In a preferred embodiment of process 400, therefore, the expression of the
20 sequences predicted to encode protein is verified. The combination of the predictive and experimental methods provides a powerful gene discovery engine.

Thus, in another aspect, the present invention provides methods and apparatus for verifying the expression
25 of putative genes identified within genomic sequence. In particular, the invention provides a novel method of verifying gene expression in which expression of predicted ORFs is measured and confirmed using a novel type of nucleic acid microarray, the genome-derived single exon
30 nucleic acid microarrays of the present invention.

Putative ORFs as predicted by a consensus of gene calling, particularly gene prediction, algorithms in process 200, and as further identified as suitable by process 300, are amplified from genomic DNA using the
35 polymerase chain reaction (PCR). Although PCR is

conveniently used, other amplification approaches can also be used.

Amplification schemes can be designed to capture the entirety of each predicted ORF in an amplicon with
5 minimal additional (that is, intronic or intergenic) sequence. Because ORFs predicted from human genomic sequence using the methods of the present invention differ in length, such an approach results in amplicons of varying length.

10 However, most predicted ORFs are shorter than 500 bp in length, and although amplicons of at least about 100 or 200 base pairs can be immobilized as probes on nucleic acid microarrays, early experimental results using the methods of the present invention have suggested that longer
15 amplicons, at least about 400 or 500 base pairs, are more effective. Furthermore, certain advantages derive from application to the microarray of amplicons of defined size.

Therefore, amplification schemes can alternatively, and preferably, be designed to amplify
20 regions of defined size, preferably at least about 300, 400 or 500 bp, centered about each predicted ORF. Such an approach results in a population of amplicons of limited size diversity, but that typically contain intronic and/or intergenic nucleic acid in addition to putative ORF.

25 Conversely, somewhat fewer than 10% of ORFs predicted from human genomic sequence according to the methods of the present invention exceed 500 bp in length. Portions of such extended ORFs, preferably at least about 300, 400 or 500 bp in length, can be amplified. However, it
30 has been discovered that the percentage success at amplifying pieces of such ORFs is low, and that such putative exons are more effectively amplified when larger fragments, at least about 1000 or 1500 bp, and even as large as 2000 bp are amplified.

35 The putative ORFs selected in process 300 are

thus input into one or more primer design programs, such as
PRIMER3 (available online for use at
<http://www-genome.wi.mit.edu/cgi-bin/primer/>), with a goal
of amplifying at least about 500 base pairs of genomic
5 sequence centered within or about ORFs predicted to be no
more than about 500 bp, or at least about 1000 - 1500 bp of
genomic sequence for ORFs predicted to exceed 500 bp in
length, and the primers synthesized by standard techniques.
Primers with the requisite sequences can be purchased
10 commercially or synthesized by standard techniques.

Conveniently, a first predetermined sequence can
be added commonly to the ORF-specific 5' primer and a
second, typically different, predetermined sequence
commonly added to each 3' ORF-unique primer. This serves
15 to immortalize the amplicon, that is, serves to permit
further amplification of any amplicon using a single set of
primers complementary respectively to the common 5' and
common 3' sequence elements. The presence of these
"universal" priming sequences further facilitates later
20 sequence verification, providing a sequence common to all
amplicons at which to prime sequencing reactions. The
common 5' and 3' sequences further serve to add a cloning
site should any of the ORFs warrant further study.

Such predetermined sequence is usefully at least
25 about 10, 12 or 15 nt in length, and usually does not
exceed about 25 nt in length. The "universal" priming
sequences used in the examples presented *infra* were each 16
nt long.

The genomic DNA to be used as substrate for
30 amplification will come from the eukaryotic species from
which the genomic sequence data had originally been
obtained, or a closely related species, and can
conveniently be prepared by well known techniques from
somatic or germline tissue or cultured cells of the
35 organism. See, e.g., Short Protocols in Molecular Biology

: A Compendium of Methods from Current Protocols in Molecular Biology, Ausubel et al. (eds.), 4th edition (April 1999), John Wiley & Sons (ISBN: 047132938X) and Maniatis et al., Molecular Cloning : A Laboratory Manual, 2nd edition (December 1989), Cold Spring Harbor Laboratory Press (ISBN: 0879693096). Many such prepared genomic DNAs are available commercially, with the human genomic DNAs additionally having certification of donor informed consent.

Although the intronic and intergenic material flanking putative coding regions in the amplicons could potentially interfere with hybridizations during microarray experiments, we have found, surprisingly, that differential expression ratios are not significantly affected. Rather, the predominant effect of exon size is to alter the absolute signal intensity, rather than its ratio. Equally surprising, the art had suggested that single exon probes would not provide sufficient signal intensity for high stringency hybridization analyses; we find that such probes not only provide adequate signal, but have substantial advantages, as herein described.

After partial purification, as by size exclusion spin column, with or without confirmation as to amplicon quality as by gel electrophoresis, each amplicon (single exon probe) is disposed in an array upon a support substrate.

Methods for creating microarrays by deposition and fixation of nucleic acids onto support substrates are well known in the art (Reviewed by Schena et al., see above).

Typically, the support substrate will be glass, although other materials, such as amorphous or crystalline silicon or plastics. Such plastics include polymethylacrylic, polyethylene, polypropylene, polyacrylate, polymethylmethacrylate, polyvinylchloride,

polytetrafluoroethylene, polystyrene, polycarbonate, polyacetal, polysulfone, celluloseacetate, cellulosenitrate, nitrocellulose, or mixtures thereof, can also be used. Typically, the support will be rectangular, 5 although other shapes, particularly circular disks and even spheres, present certain advantages. Particularly advantageous alternatives to glass slides as support substrates for array of nucleic acids are optical discs, as described in WO 98/12559.

10 The amplified nucleic acids can be attached covalently to a surface of the support substrate or, more typically, applied to a derivatized surface in a chaotropic agent that facilitates denaturation and adherence by presumed noncovalent interactions, or some combination 15 thereof.

 Robotic spotting devices useful for arraying nucleic acids on support substrates can be constructed using public domain specifications (The MGuide, version 2.0, <http://cmgm.stanford.edu/pbrown/mguide/index.html>), or 20 can conveniently be purchased from commercial sources (MicroArray GenII Spotter and MicroArray GenIII Spotter, Molecular Dynamics, Inc., Sunnyvale, CA). Spotting can also be effected by printing methods, including those using ink jet technology.

25 As is well known in the art, microarrays typically also contain immobilized control nucleic acids. For controls useful in providing measurements of background signal for the genome-derived single exon microarrays of the present invention, a plurality of *E. coli* genes can 30 readily be used. As further described in Example 1, 16 or 32 *E. coli* genes suffice to provide a robust measure of background noise in such microarrays.

 As is well known in the art, the amplified product disposed in arrays on a support substrate to create 35 a nucleic acid microarray can consist entirely of natural

nucleotides linked by phosphodiester bonds, or alternatively can include either nonnative nucleotides, alternative internucleotide linkages, or both, so long as complementary binding can be obtained in the hybridization.

- 5 If enzymatic amplification is used to produce the immobilized probes, the amplifying enzyme will impose certain further constraints upon the types of nucleic acid analogs that can be generated.

Although particularly described herein as using
10 high density microarrays constructed on planar substrates, the methods of the present invention for confirming the expression of ORFs predicted from genomic sequence can use any of the known types of microarrays, as herein defined, including lower density planar arrays, and microarrays on
15 nonplanar, nonunitary, distributed substrates.

- For example, gene expression can be confirmed using hybridization to lower density arrays, such as those constructed on membranes, such as nitrocellulose, nylon, and positively-charged derivatized nylon membranes.
- 20 Further, gene expression can also be confirmed using nonplanar, bead-based microarrays such as are described in Brenner et al., *Proc. Natl. Acad. Sci. USA* 97(4):166501670 (2000); U.S. Patent No. 6,057,107; and U.S. Patent No. 5,736,330. In theory, a packed collection of such beads
25 provides in aggregate a higher density of nucleic acid probe than can be achieved with spotting or lithography techniques on a single planar substrate.

Planar microarrays on solid substrates, however, provide certain useful advantages, including high
30 throughput and compatibility with existing readers. For example, each standard microscope slide can include at least 1000, typically at least 2000, preferably 5000 and upto 10,000 - 50,000 or more nucleic acid probes of discrete sequence. The number of sequences deposited will
35 depend on their required application.

Each putative gene can be represented in the array by a single predicted ORF. Alternatively, genes can be represented by more than one predicted ORF. For purposes of measuring differential splicing, more than one
5 predicted ORF will be provided for a putative gene. And as is well known in the art, each probe of defined sequence, representing a single predicted ORF, can be deposited in a plurality of locations on a single microarray to provide redundancy of signal.

10 The genome-derived single exon microarrays described above differ in several fundamental and advantageous ways from microarrays presently used in the gene expression art, including (1) those created by deposition of mRNA-derived nucleic acids, (2) those created
15 by *in situ* synthesis of oligonucleotide probes, and (3) those constructed from yeast genomic DNA.

Most nucleic acid microarrays that are in use for study of eukaryotic gene expression have as immobilized probes nucleic acids that are derived - either directly or
20 indirectly - from expressed message. As discussed above, it is common, for example, for such microarrays to be derived from cDNA/EST libraries, either from those previously described in the literature, see Lennon et al.,
25 libraries targeted at a particular biological question, R.S. Thomas et al., *Cancer Res.* (in press). Such microarrays are herein collectively denominated "EST microarrays".

Such EST microarrays by definition can measure
30 expression only of those genes found in EST libraries, shown herein to represent only a fraction of expressed genes. Furthermore, such libraries - and thus microarrays based thereupon - are biased by the tissue or cell type of message origin, by the expression levels of the respective
35 genes within the tissues, and by the ability of the message

successfully to have been reverse-transcribed and cloned.

Thus, as further discussed in Example 1, the methods of the present invention enable sequences that do not appear in EST or other expression databases to be
5 determined - subsequently arrayed for expression measurements could not, therefore, have been represented as probes on an EST microarray. And as further demonstrated in the examples, *infra*, the remaining population of genes identified from genomic sequence by the methods of the
10 present invention - that is, the one third of sequences that had previously been accessioned in EST or other expression databases - are biased toward genes with higher expression levels.

Representation of a message in an EST and/or cDNA
15 library depends upon the successful reverse transcription, optionally but typically with subsequent successful cloning, of the message. This introduces substantial bias into the population of probes available for arraying in EST microarrays.

20 In contrast, neither reverse transcription nor cloning is required to produce the probes arrayed on the genome-derived single exon microarrays of the present invention. And although the ultimate deposition of a probe on the genome-derived single exon microarray of the present
25 invention depends upon a successful amplification from genomic material, a priori knowledge of the sequence of the desired amplicon affords greater opportunity to recover any given probe sequence recalcitrant to amplification than is afforded by the requirement for successful reverse
30 transcription and cloning of unknown message in EST approaches.

Thus, the genome-derived single exon microarrays of the present invention present a far greater diversity of probes for measuring gene expression, with far less bias,
35 than do EST microarrays presently used in the art.

As a further consequence of their ultimate origin from expressed message, the probes in EST microarrays often contain poly-A (or complementary poly-T) stretches derived from the poly-A tail of mature mRNA. These homopolymeric stretches contribute to cross-hybridization, that is, to a spurious signal occasioned by hybridization to the homopolymeric tail of a labeled cDNA that lacks sequence homology to the gene-specific portion of the probe.

In contrast, the probes arrayed in the genome-derived single exon microarrays of the present invention lack homopolymeric stretches derived from message polyadenylation, and thus can provide more specific signal. Typically, at least about 50, 60 or 75% of the probes on the genome-derived single exon microarrays of the present invention lack homopolymeric regions consisting of A or T, where a homopolymeric region is defined for purposes herein as stretches of 25 or more, typically 30 or more, identical nucleotides.

A further distinction, which also affects the specificity of hybridization, is occasioned by the typical derivation of EST microarray probes from cloned material. Because much of the probe material disposed as probes on EST microarrays is excised or amplified from plasmid, phage, or phagemid vectors, EST microarrays typically include a fair amount of vector sequence, more so when the probes are amplified, rather than excised, from the vector.

In contrast, the vast majority of probes in the genome-derived single exon microarrays of the present invention contain no prokaryotic or bacteriophage vector sequence, having been amplified directly or indirectly from genomic DNA. Typically, therefore, at least about 50, 60, 70 or 80% or more of individual exon-including probes disposed on a genome-derived single exon microarray of the present invention lack vector sequence, and particularly lack sequences drawn from plasmids and bacteriophage.

Preferably, at least about 85, 90 or more than 90% of exon-including probes in the genome-derived single exon microarray of the present invention lack vector sequence. With attention to removal of vector sequences through
5 preprocessing 24, percentages of vector-free exon-including probes can be as high as 95 - 99%. The substantial absence of vector sequence from the genome-derived single exon microarrays of the present invention results in greater specificity during hybridization, since spurious cross-
10 hybridization to a probe vector sequence is reduced.

As a further consequence of excision or amplification of probes from vectors in construction of EST microarrays, the probes arrayed thereon often contain artificial sequence, derived from vector polylinker
15 multiple cloning sites, at both 5' and 3' ends. The probes disposed upon the genome-derived single exon microarrays need have no such artificial sequence appended thereto.

As mentioned above, however, the ORF-specific primers used to amplify putative ORFs can include
20 artificial sequences, typically 5' to the ORF-specific primer sequence, useful for "universal" (that is, independent of ORF sequence) priming of subsequent amplification or sequencing reactions. When such "universal" 5' and/or 3' priming sequences are appended to
25 the amplification primers, the probes disposed upon the genome-derived single exon microarray will include artificial sequence similar to that found in EST microarrays. However, the genome-derived single exon microarray of the present invention can be made without
30 such sequences, and if so constructed, presents an even smaller amount of nonspecific sequence that would contribute to nonspecific hybridization.

Yet another consequence of typical use of cloned material as probes in EST microarrays is that such
35 microarrays contain probes that result from cloning

artifacts, such as chimeric molecules containing coding region of two separate genes. Derived from genomic material, typically not thereafter cloned, the probes of the genome-derived single exon microarrays of the present invention lack such cloning artifacts, and thus provide greater specificity of signal in gene expression measurements.

A further consequence of the cloned origin of probes on many EST microarrays is that the individual probes often have disparate sizes, which can cause the optimal hybridization stringency to vary among probes on a single microarray. In contrast, as discussed above, the probes arrayed on the genome-derived single exon microarrays of the present invention can readily be designed to have a narrow distribution in sizes, with the range of probe sizes no greater than about 10% of the average size, typically no greater than about 5% of the average probe size.

Because of their origin from fully- or partially-spliced message, probes disposed upon EST arrays will often include multiple exons. The percentage of such exon-spanning probes in an EST microarray can be calculated, on average, based upon the predicted number of exons/gene for the given species and the average length of the immobilized probes. For human genes, the near-complete sequence of human chromosome 22, Dunham et al., *Nature* 402(6761):489-95 (1999), predicts that human genes average 5.5 exons/gene. Even with probes of 200 - 500 bp, the vast majority of human EST microarray probes include more than one exon.

In contrast, by virtue of their origin from algorithmically identified ORFs in genomic sequence, the probes in the genome-derived single exon microarrays of the present invention can consist of individual exons. Thus, in contrast to EST microarrays, at least about 50, 60, 70, 75, 80, 85, 95 or 99% of probes deposited in the genome-

derived microarray of the present invention consist of, or include, no more than one predicted ORF.

This provides the ability, not readily achieved using EST microarrays, to use the genome-derived single
5 exon microarrays of the present invention to measure tissue-specific expression of individual exons, which in turn allows differential splicing events to be detected and characterized, and in particular, allows the correlation of differential splicing to tissue-specific expression
10 patterns.

Furthermore, the exons that are represented in EST microarrays are often biased toward the 3' or 5' end of their respective genes, since sequencing strategies used for EST identification are so biased. In contrast, no such
15 3' or 5' bias necessarily inheres in the selection of exons for disposition on the genome-derived single exon microarrays of the present invention.

Conversely, the probes provided on the genome-derived single exon microarrays of the present invention
20 typically, but need not necessarily, include intronic and/or intergenic sequence that is absent from EST microarrays, which are derived from mature mRNA. Typically, at least about 50, 60, 70, 80 or 90% of the exon-including probes on the genome-derived single exon
25 microarrays of the present invention include sequence drawn from noncoding regions. As discussed above, the additional presence of noncoding region does not significantly interfere with measurement of gene expression, and provides the additional opportunity to assay prespliced RNA, and
30 thus measure such phenomena such as nuclear export control.

The genome-derived single exon microarrays of the present invention are also quite different from *in situ* synthesis microarrays, where probe size is severely constrained by inadequacies in the photolithographic
35 synthesis process.

Typically, probes arrayed on *in situ* synthesis microarrays are limited to a maximum of about 25 bp. As a well known consequence, hybridization to such chips must be performed at low stringency. In order, therefore, to
5 achieve unambiguous sequence-specific hybridization results, the *in situ* synthesis microarray requires substantial redundancy, with concomitant programmed arraying for each probe of probe analogues with altered (*i.e.*, mismatched) sequence.

10 In contrast, the longer probe length of the genome-derived single exon microarrays of the present invention allows much higher stringency hybridization and wash. Typically, therefore, exon-including probes on the genome-derived single exon microarrays of the present
15 invention average at least about 100, 200, 300, 400 or 500 bp in length. By obviating the need for substantial probe redundancy, this approach permits a higher density of probes for discrete exons or genes to be arrayed on the microarrays of the present invention than can be achieved
20 for *in situ* synthesis microarrays.

A further distinction is that the probes in *in situ* synthesis microarrays typically are covalently linked to the substrate surface. In contrast, the probes disposed on the genome-derived microarray of the present invention
25 typically are, but need not necessarily be, bound noncovalently to the substrate.

Furthermore, the short probe size on *in situ* microarrays causes large percentage differences in the melting temperature of probes hybridized to their
30 complementary target sequence, and thus causes large percentage differences in the theoretically optimum stringency across the array as a whole.

In contrast, the larger probe size in the microarrays of the present invention create lower
35 percentage differences in melting temperature across the

range of arrayed probes.

A further significant advantage of the microarrays of the present invention over *in situ* synthesized arrays is that the quality of each individual probe can be confirmed before deposition. In contrast, the quality of probes cannot be assessed on a probe-by-probe basis for the *in situ* synthesized microarrays presently being used.

The genome-derived single exon microarrays of the present invention are also distinguished over, and present substantial benefits over, the genome-derived microarrays from lower eukaryotes such as yeast. Lashkari et al., *Proc. Natl. Acad. Sci. USA* 94:13057-13062 (1997).

Only about 220 - 250 of the 6100 or so nuclear genes in *Saccharomyces cerevisiae* - that is, only about 4 - 5% - have standard, spliceosomal, introns, Lopez et al., *Nucl. Acids Res.* 28:85-86 (2000); Spingola et al., *RNA* 5(2):221-34 (1999). Furthermore, the entire yeast genome has already been sequenced. These two facts permit the ready amplification and disposition of single-ORF amplicons on such microarray without the requirement for antecedent use of gene prediction and/or comparative sequence analyses.

Thus, a significant aspect of the present invention is the ability to identify and to confirm expression of predicted coding regions in genomic sequence drawn from eukaryotic organisms that have a higher percentage of genes having introns than do yeast such as *Saccharomyces cerevisiae*, particularly in genomic sequence drawn from eukaryotes in which at least about 10, 20 or 50% of protein-encoding genes have introns. In preferred embodiments, the methods and apparatus of the present invention are used to identify and confirm expression of novel genes from genomic sequence of eukaryotes in which the average number of introns per gene is at least about

one, two or three or more.

After the physical substrate is prepared, experimental verification of predicted function is performed.

5 In a preferred embodiment of the present invention, where the function sought to be identified in genomic sequence is protein coding, experimental verification is performed by measuring expression of the putative ORFs, typically through nucleic acid hybridization
10 experiments, and in particularly preferred embodiments, through hybridization to genome-derived single exon microarrays prepared as above- described.

Expression is conveniently measured and expressed for each probe in the microarray as a ratio of the
15 expression measured concurrently in a plurality of mRNA sources, according to techniques well known in the microarray art, Reviewed in Schena et al., and as further described in Example 2, below. The mRNA source for the reference against which specific expression is measured can
20 be drawn from a homogeneous mRNA source, such as a single cultured cell-type, or alternatively can be heterogeneous, as from a pool of mRNA derived from multiple tissues and/or cell types, as further described in Example 2, *infra*.

mRNA can be prepared by standard techniques, see
25 Ausubel et al. and Maniatis et al., or purchased commercially. The mRNA is then typically reverse-transcribed in the presence of labeled nucleotides: the index source (that in which expression is desired to be measured) is reverse transcribed in the presence of
30 nucleotides labeled with a first label, typically a fluorophore (fluorochrome; fluor; fluorescent dye); the reference source is reverse transcribed in the presence of a second label, typically a fluorophore, typically fluorometrically-distinguishable from the first label. As
35 further described in Example 2, *infra*, Cy3 and Cy5 dyes

prove particularly useful in these methods. After partial purification of the index and reference targets, hybridization to the probe array is conducted according to standard techniques, typically under a coverslip.

5 After wash, microarrays are conveniently scanned using a commercial microarray scanning device, such as a Gen3 Scanner (Molecular Dynamics, Sunnyvale, CA). Data on expression is then passed, with or without interim storage, to process 500, where the results for each probe are
10 related to the original sequence.

Often, hybridization of target material to the genome-derived single exon microarray will identify certain of the probes thereon as of particular interest. Thus, it is often desirable that the user be able readily to obtain
15 sufficient quantities of an individual probe, either for subsequent arrayed deposition upon an additional support substrate, often as part of a microarray having a plurality of probes so identified, or alternatively or additionally as a solitary solid-phase or solution-phase probe, for
20 further use.

Thus, in another aspect, the present invention provides compositions and kits for the ready production of nucleic acids identical in sequence to, or substantially identical in sequence to, probes on the genome-derived
25 single exon microarrays of the present invention.

In this aspect, a small quantity of each probe is disposed, typically without attachment to substrate, in a spatially-addressable ordered set, typically one per well of a microtiter dish. Although a 96 well microtiter plate
30 can be used, greater efficiency is obtained using higher density arrays, such as are provided by microtiter plates having 384, 864, 1536, 3456, 6144, or 9600 wells, and although microtiter plates having physical depressions (wells) are conveniently used, any device that permits
35 addressable withdrawal of reagent from fluidly-

noncommunicating areas can be used.

In this aspect of the invention, therefore, a fluidly noncommunicating addressable ordered set of individual probes, corresponding to those on a genome-derived single exon microarray, is provided, with each probe in sufficient quantity to permit amplification, such as by PCR. As earlier mentioned, the ORF-specific 5' primers used for genomic amplification can have a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification can have a second, different, common sequence added thereto, thus permitting, in this preferred embodiment, the use of a single set of 5' and 3' primers to amplify any one of the probes from the amplifiable ordered set.

Each discrete amplifiable probe can also be packaged with amplification primers, solutes, buffers, etc., and can be provided in dry (e.g., lyophilized) form or wet, in the latter case typically with addition of agents that retard evaporation.

In another aspect of the present invention, a genome-derived single-exon microarray is packaged together with such an ordered set of amplifiable probes corresponding to the probes, or one or more subsets of probes, thereon. In alternative embodiments, the ordered set of amplifiable probes is packaged separately from the genome-derived single exon microarray.

In some embodiments, the microarray and/or ordered probe set are further packaged with recordable media that provide probe identification and addressing information, and that can additionally contain annotation information, such as gene expression data. Such recordable media can be packaged with the microarray, with the ordered probe set, or with both.

If the microarray is constructed on a substrate that incorporates recordable media, such as is described in

international patent application no. WO 98/12559, then separate packaging of the genome-derived single exon microarray and the bioinformatic information is not required.

5 The amount of amplifiable probe material should be sufficient to permit at least one amplification sufficient for subsequent hybridization assay.

 Although the use of high density genome-derived microarrays on solid planar substrates is presently a
10 preferred approach for the physical confirmation and characterization of the expression of sequences predicted to encode protein, other types of microarrays (as herein defined) can also be used.

 Furthermore, as earlier mentioned, experimental
15 verification of the function predicted from genomic sequence in process 200 can be bioinformatic, rather than, or additional to, physical verification.

 For example, where the function desired to be identified is protein coding, the predicted ORFs can be
20 compared bioinformatically to sequences known or suspected of being expressed.

 Thus, the sequences output from process 300 (or process 200), can be used to query expression databases, such as EST databases, SNP ("single nucleotide
25 polymorphism") databases, known cDNA and mRNA sequences, SAGE ("serial analysis of gene expression") databases, and more generalized sequence databases that allow query for expressed sequences. Such query can be done by any sequence query algorithm, such as BLAST ("basic local
30 alignment search tool"). The results of such query - including information on identical sequences and information on nonidentical sequences that have diffuse or focal regions of sequence homology to the query sequence - can then be passed directly to process 500, or used to
35 inform analyses subsequently undertaken in process 200,

process 300, or process 400.

Experimental data, whether obtained by physical or bioinformatic assay in process 400, is passed to process 500 where it is usefully related to the sequence data itself, a process colloquially termed "annotation". Such annotation can be done using any technique that usefully relates the functional information to the sequence, as, for example, by incorporating the functional data into the record itself; by linking records in a hierarchical or relational database, by linking to external databases, or by a combination thereof. Such database techniques are well within the skill in the art.

The annotated sequence data can be stored locally, uploaded to genomic sequence database 100, and/or displayed 800.

The methods and apparatus of the present invention rapidly produce functional information from genomic sequence. Coupled with the escalating pace at which sequence now accumulates, the rapid pace of sequence annotation produces a need for methods of displaying the information in meaningful ways.

FIG. 3 shows visual display 80 presenting a single genomic sequence annotated according to the present invention. Because of its nominal resemblance to artistic works of Piet Mondrian, visual display 80 is alternatively described herein as a "Mondrian".

Each of the visual elements of display 80 is aligned with respect to the genomic sequence being annotated (hereinafter, the "annotated sequence"). Given the number of nucleotides typically represented in an annotated sequence, representation of individual nucleotides would rarely be readable in hard copy output of display 80. Typically, therefore, the annotated sequence is schematized as rectangle 89, extending from the left border of display 80 to its right border. By convention

herein, the left border of rectangle 89 represents the first nucleotide of the sequence and the right border of rectangle 89 represents the last nucleotide of the sequence.

5 As further discussed below, however, the Mondrian visual display of annotated sequence can serve as a convenient graphical user interface for computerized representation, analysis, and query of information stored electronically. For such use, the individual nucleotides
10 can conveniently be linked to the X axis coordinate of rectangle 89. This permits the annotated sequence at any point within rectangle 89 readily to be viewed, either automatically - for example, by time-delayed appearance of a small overlaid window upon movement of a cursor or other
15 pointer over rectangle 89 - or through user intervention, as by clicking a mouse or other pointing device at a point in rectangle 89.

Visual display 80 is generated after user specification of the genomic sequence to be displayed.
20 Such specification can consist of or include an accession number for a single clone (e.g., a single BAC accessioned into GenBank), wherein the starting and stopping nucleotides are thus absolutely identified, or alternatively can consist of or include an anchor or
25 fulcrum point about which a chosen range of sequence is anchored, thus providing relative endpoints for the sequence to be displayed. For example, the user can anchor such a range about a given chromosomal map location, gene name, or even a sequence returned by query for similarity
30 or identity to an input query sequence. When visual display 80 is used as a graphical user interface to computerized data, additional control over the first and last displayed nucleotide will typically be dynamically selectable, as by use of standard zooming and/or selection
35 tools.

Field 81 of visual display 80 is used to present the output from process 200, that is, to present the bioinformatic prediction of those sequences having the desired function within the genomic sequence. Functional sequences are typically indicated by at least one rectangle 83 (83a, 83b, 83c), the left and right borders of which respectively indicate, by their X-axis coordinates, the starting and ending nucleotides of the region predicted to have function.

Where a single bioinformatic method or approach identifies a plurality of regions having the desired function, a plurality of rectangles 83 is disposed horizontally in field 81. Where multiple methods and/or approaches are used to identify function, each such method and/or approach can be represented by its own series of horizontally disposed rectangles 83, each such horizontally disposed series of rectangles offset vertically from those representing the results of the other methods and approaches.

Thus, rectangles 83a in FIG. 3 represent the functional predictions of a first method of a first approach for predicting function, rectangles 83b represent the functional predictions of a second method and/or second approach for predicting that function, and rectangles 83c represent the predictions of a third method and/or approach.

Where the function desired to be identified is protein coding, field 81 is used to present the bioinformatic prediction of sequences encoding protein. For example, rectangles 83a can represent the results from GRAIL or GRAIL II, rectangles 83b can represent the results from GENEFINDER, and rectangles 83c can represent the results from DICTION.

Optionally, and preferably, rectangles 83 collectively representing predictions of a single method

and/or approach are identically colored and/or textured, and are distinguishable from the color and/or texture used for a different method and/or approach.

Alternatively, or in addition, the color, hue, density, or texture of rectangles 83 can be used further to report a measure of the bioinformatic reliability of the prediction. For example, many gene prediction programs will report a measure of the reliability of prediction. Thus, increasing degrees of such reliability can be indicated, e.g., by increasing density of shading. Where display 80 is used as a graphical user interface, such measures of reliability, and indeed all other results output by the program, can additionally or alternatively be made accessible through linkage from individual rectangles 83, as by time-delayed window ("tool tip" window), or by pointer (e.g., mouse)-activated link.

As earlier described, increased predictive reliability can be achieved by requiring consensus among methods and/or approaches to determining function. Thus, field 81 can include a horizontal series of rectangles 83 that indicate one or more degrees of consensus in predictions of function.

Although FIG. 3 shows three series of horizontally disposed rectangles in field 81, display 80 can include as few as one such series of rectangles and as many as can discriminably be displayed, depending upon the number of methods and/or approaches used to predict a given function.

Furthermore, field 81 can be used to show predictions of a plurality of different functions. However, the increased visual complexity occasioned by such display makes more useful the ability of the user to select a single function for display. When display 80 is used as a graphical user interface for computer query and analysis, such function can usefully be indicated and user-

selectable, as by a series of graphical buttons or tabs (not shown in FIG. 3).

Rectangle 89 is shown in FIG. 3 as including interposed rectangle 84. Rectangle 84 represents the
5 portion of annotated sequence for which predicted functional information has been assayed physically, with the starting and ending nucleotides of the assayed material indicated by the X axis coordinates of the left and right borders of rectangle 84. Rectangle 85, with optional
10 inclusive circles 86 (86a, 86b, and 86c) displays the results of such physical assay.

Although a single rectangle 84 is shown in FIG. 3, physical assay is not limited to just one region of annotated genomic sequence. It is expected that an
15 increasing percentage of regions predicted to have function by process 200 will be assayed physically, and that display 80 will accordingly, for any given genomic sequence, have an increasing number of rectangles 84 and 85, representing an increased density of sequence annotation.

20 Where the function desired to be identified is protein coding, rectangle 84 identifies the sequence of the probe used to measure expression. In embodiments of the present invention where expression is measured using genome-derived single exon microarrays, rectangle 84
25 identifies the sequence included within the probe immobilized on the support surface of the microarray. As noted supra, such probe will often include a small amount of additional, synthetic, material incorporated during amplification and designed to permit reamplification of the
30 probe, which sequence is typically not shown in display 80.

Rectangle 87 is used to present the results of bioinformatic assay of the genomic sequence. For example, where the function desired to be identified is protein coding, process 400 can include bioinformatic query of
35 expression databases with the sequences predicted in

process 200 to encode exons. And as earlier discussed, because bioinformatic assay presents fewer constraints than does physical assay, often the entire output of process 200 can be used for such assay, without further subsetting thereof by process 300. Therefore, rectangle 87 typically need not have separate indicators therein of regions submitted for bioinformatic assay; that is, rectangle 87 typically need not have regions therein analogous to rectangles 84 within rectangle 89.

10 Rectangle 87 as shown in FIG. 3 includes smaller rectangles 880 and 88. Rectangles 880 indicate regions that returned a positive result in the bioinformatic assay, with rectangles 88 representing regions that did not return such positive results. Where the function desired to be
15 predicted and displayed is protein coding, rectangles 880 indicate regions of the predicted exons that identify sequence with significant similarity in expression databases, such as EST, SNP, SAGE databases, with rectangles 88 indicating genes novel over those identified
20 in existing expression data bases.

 Rectangles 880 can further indicate, through color, shading, texture, or the like, additional information obtained from bioinformatic assay.

 For example, where the function assayed and
25 displayed is protein coding, the degree of shading of rectangles 880 can be used to represent the degree of sequence similarity found upon query of expression databases. The number of levels of discrimination can be as few as two (identity, and similarity, where similarity
30 has a user-selectable lower threshold). Alternatively, as many different levels of discrimination can be indicated as can visually be discriminated.

 Where display 80 is used as a graphical user interface, rectangles 880 can additionally provide links
35 directly to the sequences identified by the query of

expression databases, and/or statistical summaries thereof. As with each of the precedingly-discussed uses of display 80 as a graphical user interface, it should be understood that the information accessed via display 80 need not be resident on the computer presenting such display, which often will be serving as a client, with the linked information resident on one or more remotely located servers.

Rectangle 85 displays the results of physical assay of the sequence delimited by its left and right borders.

Rectangle 85 can consist of a single rectangle, thus indicating a single assay, or alternatively, and increasingly typically, will consist of a series of rectangles (85a, 85b, 85c) indicating separate physical assays of the same sequence.

Where the function assayed is gene expression, and where gene expression is assayed as herein described using simultaneous two-color fluorescent detection of hybridization to genome-derived single exon microarrays, individual rectangles 85 can be colored to indicate the degree of expression relative to control. Conveniently, shades of green can be used to depict expression in the sample over control values, and shades of red used to depict expression less than control, corresponding to the spectra of the Cy3 and Cy5 dyes conventionally used for respective labeling thereof. Additional functional information can be provided in the form of circles 86 (86a, 86b, 86c), where the diameter of the circle can be used to indicate expression intensity. As discussed infra, such relative expression (expression ratios) and absolute expression (signal intensity) can be expressed using normalized values.

Where display 80 is used as a graphical user interface, rectangle 85 can be used as a link to further

expression of message specifically containing that ORF.

It should be appreciated, however, that the probes of the present invention, for which expression in the HeLa cells has been demonstrated are useful for both measurement in the HeLa cells or other human cervical epithelial cells and for survey of expression in other tissues.

Significant among such advantages is the presence of probes for novel genes.

As mentioned above and further detailed in Examples 1 and 2, the methods described enable ORFs which are not present in existing expression databases to be identified. And the fewer the number of tissues in which the ORF can be shown to be expressed, the more likely the ORF will prove to be part of a novel gene: as further discussed in Example 2, ORFs whose expression was measurable in only a single of the tested tissues were represented in existing expression databases at a rate of only 11%, whereas 36% of ORFs whose expression was measurable in 9 tissues were present in existing expression databases, and fully 45% of those ORFs expressed in all ten tested tissues were present in existing expressed sequence databases.

Either as tools for measuring gene expression or tools for surveying gene expression, the genome-derived single exon probes of the present invention have significant advantages over the cDNA or EST-based probes that are currently available for achieving these utilities.

The genome-derived single exon probes of the present invention are useful in constructing genome-derived single exon microarrays; the genome-derived single exon microarrays, in turn, are useful devices for measuring and for surveying gene expression in the human.

Gene expression analysis using microarrays – conventionally using microarrays having probes derived from

expressed message - is well-established as useful in the biological research arts (see Lockhart et al. *Nature* 405, 827-836).

Microarrays have been used to determine gene
5 expression profiles in cells in response to drug treatment
(see, for example, Kaminski et al., "Global Analysis of
Gene Expression in Pulmonary Fibrosis Reveals Distinct
Programs Regulating Lung Inflammation and Fibrosis," *Proc.
Natl. Acad. Sci. USA* 97(4):1778-83 (2000); Bartosiewicz et
10 al., "Development of a Toxicological Gene Array and
Quantitative Assessment of This Technology," *Arch. Biochem.
Biophys.* 376(1):66-73 (2000)), viral infection (see for
example, Geiss et al., "Large-scale Monitoring of Host Cell
Gene Expression During HIV-1 Infection Using cDNA
15 Microarrays," *Virology* 266(1):8-16 (2000)) and during cell
processes such as differentiation, senescence and apoptosis
(see, for example, Shelton et al., "Microarray Analysis of
Replicative Senescence," *Curr. Biol.* 9(17):939-45 (1999);
Voehringer et al., "Gene Microarray Identification of Redox
20 and Mitochondrial Elements That Control Resistance or
Sensitivity to Apoptosis," *Proc. Natl. Acad. Sci. USA*
97(6):2680-5 (2000)).

Microarrays have also been used to determine
abnormal gene expression in diseased tissues (see, for
25 example, Alon et al., "Broad Patterns of Gene Expression
Revealed by Clustering Analysis of Tumor and Normal Colon
Tissues Probed by Oligonucleotide Arrays," *Proc. Natl.
Acad. Sci. USA* 96(12):6745-50 (1999); Perou et al.,
"Distinctive Gene Expression Patterns in Human Mammary
30 Epithelial Cells and Breast Cancers," *Proc. Natl. Acad. Sci.
USA* 96(16):9212-7 (1999); Wang et al., "Identification of
Genes Differentially Over-expressed in Lung Squamous Cell
Carcinoma Using Combination of cDNA Subtraction and
Microarray Analysis," *Oncogene* 19(12):1519-28 (2000);
35 Whitney et al., "Analysis of Gene Expression in Multiple

Sclerosis Lesions Using cDNA Microarrays," *Ann. Neurol.* 46(3):425-8 (1999)), in drug discovery screens (see, for example, Scherf et al., "A Gene Expression Database for the Molecular Pharmacology of Cancer," *Nat. Genet.* 24(3):236-44 (2000)) and in diagnosis to determine appropriate treatment strategies (see, for example, Sgroi et al., "In vivo Gene Expression Profile Analysis of Human Breast Cancer Progression," *Cancer Res.* 59(22):5656-61 (1999)).

In microarray-based gene expression screens of pharmacological drug candidates upon cells, each probe provides specific useful data. In particular, it should be appreciated that even those probes that show no change in expression are as informative as those that do change, serving, in essence, as negative controls.

For example, where gene expression analysis is used to assess toxicity of chemical agents on cells, the failure of the agent to change a gene's expression level is evidence that the drug likely does not affect the pathway of which the gene's expressed protein is a part. Analogously, where gene expression analysis is used to assess side effects of pharmacological agents - whether in lead compound discovery or in subsequent screening of lead compound derivatives - the inability of the agent to alter a gene's expression level is evidence that the drug does not affect the pathway of which the gene's expressed protein is a part.

WO 99/58720 provides methods for quantifying the relatedness of a first and second gene expression profile and for ordering the relatedness of a plurality of gene expression profiles. The methods so described permit useful information to be extracted from a greater percentage of the individual gene expression measurements from a microarray than methods previously used in the art.

Other uses of microarrays are described in Gerhold et al., *Trends Biochem. Sci.* 24(5):168-173 (1999)

and Zweiger, *Trends Biotechnol.* 17(11):429-436 (1999);
Schena et al.

The invention particularly provides genome-
derived single-exon probes known to be expressed in HeLa
5 cells.

The individual single exon probes can be provided
in the form of substantially isolated and purified nucleic
acid, typically, but not necessarily, in a quantity
sufficient to perform a hybridization reaction.

10 Such nucleic acid can be in any form directly
hybridizable to the message that contains the probe's ORF,
such as double stranded DNA, single-stranded DNA
complementary to the message, single-stranded RNA
complementary to the message, or chimeric DNA/RNA molecules
15 so hybridizable. The nucleic acid can alternatively or
additionally include either nonnative nucleotides,
alternative internucleotide linkages, or both, so long as
complementary binding can be obtained. For example, probes
can include phosphorothioates, methylphosphonates,
20 morpholino analogs, and peptide nucleic acids (PNA), as are
described, for example, in U.S. Patent Nos. 5,142,047;
5,235,033; 5,166,315; 5,217,866; 5,184,444; 5,861,250.

Usefully, however, such probes are provided in a
form and quantity suitable for amplification, where the
25 amplified product is thereafter to be used in the
hybridization reactions that probe gene expression.
Typically, such probes are provided in a form and quantity
suitable for amplification by PCR or by other well known
amplification technique. One such technique additional to
30 PCR is rolling circle amplification, as is described, *inter*
alia, in U.S. Patent Nos. 5,854,033 and 5,714,320 and
international patent publications WO 97/19193 and
WO 00/15779. As is well understood, where the probes are
to be provided in a form suitable for amplification, the
35 range of nucleic acid analogues and/or internucleotide

linkages will be constrained by the requirements and nature of the amplification enzyme.

Where the probe is to be provided in form suitable for amplification, the quantity need not be
5 sufficient for direct hybridization for gene expression analysis, and need be sufficient only to function as an amplification template, typically at least about 1, 10 or 100 pg or more.

Each discrete amplifiable probe can also be
10 packaged with amplification primers, either in a single composition that comprises probe template and primers, or in a kit that comprises such primers separately packaged therefrom. As earlier mentioned, the ORF-specific
15 5' primers used for genomic amplification can have a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification can have a second, different, common sequence added thereto, thus permitting, in this embodiment, the use of a single set of 5' and 3' primers to amplify any one of the probes. The probe
20 composition and/or kit can also include buffers, enzyme, etc., required to effect amplification.

As mentioned earlier, when intended for use on a genome-derived single exon microarray of the present invention, the genome-derived single exon probes of the
25 present invention will typically average at least about 100, 200, 300, 400 or 500 bp in length, including (and typically, but not necessarily centered about) the ORF. Furthermore, when intended for use on a genome-derived single exon microarray of the present invention, the
30 genome-derived single exon probes of the present invention will typically not contain a detectable label.

When intended for use in solution phase hybridization, however - that is, for use in a hybridization reaction in which the probe is not first
35 bound to a support substrate (although the target may

indeed be so bound) - length constraints that are imposed in microarray-based hybridization approaches will be relaxed, and such probes will typically be labeled.

In such case, the only functional constraint that
5 dictates the minimum size of such probe is that each such probe must be capable of specifically identifying in a hybridization reaction the exon from which it is drawn. In theory, a probe of as little as 17 nucleotides is capable of uniquely identifying its cognate sequence in the human
10 genome. For hybridization to expressed message - a subset of target sequence that is much reduced in complexity as compared to genomic sequence - even fewer nucleotides are required for specificity.

Therefore, the probes of the present invention
15 can include as few as 20, 25 or 50 bp or ORF, or more. In particular embodiments, the ORF sequences are given in SEQ ID NOS. 9,291 - 18,392, respectively, for probe SEQ ID NOS. 1 - 9,290. The minimum amount of ORF required to be included in the probe of the present invention in order to
20 provide specific signal in either solution phase or microarray-based hybridizations can readily be determined for each of ORF SEQ ID NOS. 9,291 - 18,392 individually by routine experimentation using standard high stringency conditions.

25 Such high stringency conditions are described, *inter alia*, in Ausubel et al. and Maniatis et al. For microarray-based hybridization, standard high stringency conditions can usefully be 50% formamide, 5X SSC, 0.2 µg/µl poly(dA), 0.2 µg/µl human c₀t1 DNA, and 0.5 % SDS, in a
30 humid oven at 42°C overnight, followed by successive washes of the microarray in 1X SSC, 0.2% SDS at 55°C for 5 minutes, and then 0.1X SSC, 0.2% SDS, at 55°C for 20 minutes. For solution phase hybridization, standard high stringency conditions can usefully be aqueous hybridization
35 at 65°C in 6X SSC. Lower stringency conditions, suitable

for cross-hybridization to mRNA encoding structurally- and functionally-related proteins, can usefully be the same as the high stringency conditions but with reduction in temperature for hybridization and washing to room
5 temperature (approximately 25°C).

When intended for use in solution phase hybridization, the maximum size of the single exon probes of the present invention is dictated by the proximity of other expressed exons in genomic DNA: although each single
10 exon probe can include intergenic and/or intronic material contiguous to the ORF in the human genome, each probe of the present invention will include portions of only one expressed exon.

Thus, each single exon probe will include no more
15 than about 25 kb of contiguous genomic sequence, more typically no more than about 20 kb of contiguous genomic sequence, more usually no more than about 15 kb, even more usually no more than about 10 kb. Usually, probes that are maximally about 5 kb will be used, more typically no more
20 than about 3 kb.

It will be appreciated that the Sequence Listing appended hereto presents, by convention, only that strand of the probe and ORF sequence that can be directly translated reading from 5' to 3' end. As would be well
25 understood by one of skill in the art, single stranded probes must be complementary in sequence to the ORF as present in an mRNA; it is well within the skill in the art to determine such complementary sequence. It will further be understood that double stranded probes can be used in
30 both solution-phase hybridization and microarray-based hybridization if suitably denatured.

Thus, it is an aspect of the present invention to provide single-stranded nucleic acid probes that have sequence complementary to those described herein above and
35 below, and double-stranded probes one strand of which has

sequence complementary to the probes described herein.

The probes can, but need not, contain intergenic and/or intronic material that flanks the ORF, on one or both sides, in the same linear relationship to the ORF that the intergenic and/or intronic material bears to the ORF in genomic DNA. The probes do not, however, contain nucleic acid derived from more than one expressed ORF.

And when intended for use in solution hybridization, the probes of the present invention can usefully have detectable labels. Nucleic acid labels are well known in the art, and include, *inter alia*, radioactive labels, such as ^3H , ^{32}P , ^{33}P , ^{35}S , ^{125}I , ^{131}I ; fluorescent labels, such as Cy3, Cy5, Cy5.5, Cy7, SYBR[®]

Green and other labels described in Haugland, *Handbook of Fluorescent Probes and Research Chemicals*, 7th ed., Molecular Probes Inc., Eugene, OR (2000), or fluorescence resonance energy transfer tandem conjugates thereof; labels suitable for chemiluminescent and/or enhanced chemiluminescent detection; labels suitable for ESR and NMR detection; and labels that include one member of a specific binding pair, such as biotin, digoxigenin, or the like.

The probes, either in quantity sufficient for hybridization or sufficient for amplification, can be provided in individual vials or containers.

Alternatively, such probes can usefully be packaged as a plurality of such individual genome-derived single exon probes.

When provided as a collection of plural individual probes, the probes are typically made available in amplifiable form in a spatially-addressable ordered set, typically one per well of a microtiter dish. Although a 96 well microtiter plate can be used, greater efficiency is obtained using higher density arrays.

If, as earlier mentioned, the ORF-specific

5' primers used for genomic amplification had a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification had a second, different, common sequence added thereto, a single set of 5' and 3' primers can be used to amplify all of the probes from the amplifiable ordered set.

Such collections of genome-derived single exon probes can usefully include a plurality of probes chosen for the common attribute of expression in the human HeLa cells.

In such defined subsets, typically at least 50, 60, 75, 80, 85, 90 or 95% or more of the probes will be chosen by their expression in the defined tissue or cell type.

The single exon probes of the present invention, as well as fragments of the single exon probes comprising selectively hybridizable portions of the probe ORF, can be used to obtain the full length cDNA that includes the ORF by (i) screening of cDNA libraries; (ii) rapid amplification of cDNA ends ("RACE"); or (iii) other conventional means, as are described, *inter alia*, in Ausubel et al. and Maniatis et al.

It is another aspect of the present invention to provide genome-derived single exon nucleic acid microarrays useful for gene expression analysis, where the term "microarray" has the meaning given in the definitional section of this description, *supra*.

The invention particularly provides genome-derived single-exon nucleic acid microarrays comprising a plurality of probes known to be expressed in human HeLa cells. In preferred embodiments, the present invention provides human genome-derived single exon microarrays comprising a plurality of probes drawn from the group consisting of SEQ ID NOS.: 1 - 9,290.

When used for gene expression analysis, the

genome-derived single exon microarrays provide greater physical informational density than do the genome-derived single exon microarrays that have lower percentages of probes known to be expressed commonly in the tested tissue.

5 At a fixed probe density, for example, a given microarray surface area of the defined subset genome-derived single exon microarray can yield a greater number of expression measurements. Alternatively, at a given probe density, the same number of expression measurements can be obtained from

10 a smaller substrate surface area. Alternatively, at a fixed probe density and fixed surface area, probes can be provided redundantly, providing greater reliability in signal measurement for any given probe. Furthermore, with a higher percentage of probes known to be expressed in the

15 assayed tissue, the dynamic range of the detection means can be adjusted to reveal finer levels discrimination among the levels of expression.

Although particularly described with respect to their utility as probes of gene expression, particularly as

20 probes to be included on a genome-derived single exon microarray, each of the nucleic acids having SEQ ID NOS.: 1 - 9,290 contains an open-reading frame, set forth respectively in SEQ ID NOS.: 9,291 - 18,392, that encodes a protein domain. Thus, each of SEQ ID NOS. 1 - 9,290 can be

25 used, or that portion thereof in SEQ ID NOS. 9,291 - 18,392 used, to express a protein domain by standard *in vitro* recombinant techniques. See Ausubel et al. and Maniatis et al.

Additionally, kits are available commercially

30 that readily permit such nucleic acids to be expressed as protein in bacterial cells, insect cells, or mammalian cells, as desired (e.g., HAT[™] Protein Expression & Purification System, ClonTech Laboratories, Palo Alto, CA; Adeno-X[™] Expression System, ClonTech Laboratories, Palo

35 Alto, CA; Protein Fusion & Purification (pMAL[™]) System, New

England Biolabs, Beverley, MA)

Furthermore, shorter peptides can be chemically synthesized using commercial peptide synthesizing equipment and well known techniques. Procedures are described, *inter alia*, in Chan et al. (eds.), Fmoc Solid Phase Peptide Synthesis: A Practical Approach (Practical Approach Series, (Paper)), Oxford Univ. Press (March 2000) (ISBN: 0199637245); Jones, Amino Acid and Peptide Synthesis (Oxford Chemistry Primers, No 7) , Oxford Univ. Press (August 1992) (ISBN: 0198556683); and Bodanszky, Principles of Peptide Synthesis (Springer Laboratory), Springer Verlag (December 1993) (ISBN: 0387564314).

It is, therefore, another aspect of the invention to provide peptides comprising an amino acid sequence translated from SEQ ID NOS.: 9,291 - 18,392. Such amino acid sequences are set out in SEQ ID NOS: 18,393 - 26,941. Any such recombinantly-expressed or synthesized peptide of at least 8, and preferably at least about 15, amino acids, can be conjugated to a carrier protein and used to generate antibody that recognizes the peptide. Thus, it is a further aspect of the invention to provide peptides that have at least 8, preferably at least 15, consecutive amino acids.

The following examples are offered by way of illustration and not by way of limitation.

EXAMPLE 1

Preparation of Single Exon Microarrays from ORFs Predicted in Human Genomic Sequence

Bioinformatics Results

All human BAC sequences in fewer than 10 pieces that had been accessioned in a five month period immediately preceding this study were downloaded from

GenBank. This corresponds to ~2200 clones, totaling ~350 MB of sequence, or approximately 10% of the human genome.

After masking repetitive elements using the program CROSS_MATCH, the sequence was analyzed for open
5 reading frames using three separate gene finding programs. The three programs predict genes using independent algorithmic methods developed on independent training sets: GRAIL uses a neural network, GENEFINDER uses a hidden Markoff model, and DICTION, a program proprietary to
10 Genetics Institute, operates according to a different heuristic. The results of all three programs were used to create a prediction matrix across the segment of genomic DNA.

The three gene finding programs yielded a range
15 of results. GRAIL identified the greatest percentage of genomic sequence as putative coding region, 2% of the data analyzed. GENEFINDER was second, calling 1%, and DICTION yielded the least putative coding region, with 0.8% of genomic sequence called as coding region.

20 The consensus data were as follows. GRAIL and GENEFINDER agreed on 0.7% of genomic sequence, GRAIL and DICTION agreed on 0.5% of genomic sequence, and the three programs together agreed on 0.25% of the data analyzed. That is, 0.25% of the genomic sequence was identified by
25 all three of the programs as containing putative coding region.

ORFs predicted by any two of the three programs ("consensus ORFs") were assorted into "gene bins" using two criteria: (1) any 7 consecutive exons within a 25 kb window
30 were placed together in a bin as likely contributing to a single gene, and (2) all ORFs within a 25 kb window were placed together in a bin as likely contributing to a single gene if fewer than 7 exons were found within the 25 kb window.

35

PCR

The largest ORF from each gene bin that did not span repetitive sequence was then chosen for amplification, as were all consensus ORFs longer than 500 bp. This method approximated one exon per gene; however, a number of genes were found to be represented by multiple elements.

Previously, we had determined that DNA fragments fewer than 250 bp in length do not bind well to the amino-modified glass surface of the slides used as support substrate for construction of microarrays; therefore, amplicons were designed in the present experiments to approximate 500 bp in length.

Accordingly, after selecting the largest ORF per gene bin, a 500 bp fragment of sequence centered on the ORF was passed to the primer picking software, PRIMER3 (available online for use at <http://www-genome.wi.mit.edu/cgi-bin/primer/>). A first additional sequence was commonly added to each ORF-unique 5' primer, and a second, different, additional sequence was commonly added to each ORF-unique 3' primer, to permit subsequent reamplification of the amplicon using a single set of "universal" 5' and 3' primers, thus immortalizing the amplicon. The addition of universal priming sequences also facilitates sequence verification, and can be used to add a cloning site should some ORFs be found to warrant further study.

The ORFs were then PCR amplified from genomic DNA, verified on agarose gels, and sequenced using the universal primers to validate the identity of the amplicon to be spotted in the microarray.

Primers were supplied by Operon Technologies (Alameda, CA). PCR amplification was performed by standard techniques using human genomic DNA (Clontech, Palo Alto, CA) as template. Each PCR product was verified by SYBR® green (Molecular Probes, Inc., Eugene, OR) staining of

agarose gels, with subsequent imaging by Fluorimager (Molecular Dynamics, Inc., Sunnyvale, CA). PCR amplification was classified as successful if a single band appeared.

5 The success rate for amplifying ORFs of interest directly from genomic DNA using PCR was approximately 75%. FIG. 5 graphs the distribution of predicted ORF (exon) length and distribution of amplified PCR products, with ORF length shown in red and PCR product length shown in blue
10 (which may appear black in the figure). Although the range of ORF sizes is readily seen to extend to beyond 900 bp, the mean predicted exon size was only 229 bp, with a median size of 150 bp (n=9498). With an average amplicon size of 475 ± 25 bp, approximately 50% of the average PCR
15 amplification product contained predicted coding region, with the remaining 50% of the amplicon containing either intron, intergenic sequence, or both.

 Using a strategy predicated on amplifying about 500 bp, it was found that long exons had a higher PCR
20 failure rate. To address this, the bioinformatics process was adjusted to amplify 1000, 1500 or 2000 bp fragments from exons larger than 500 bp. This improved the rate of successful amplification of exons exceeding 500 bp, constituting about 9.2% of the exons predicted by the gene
25 finding algorithms.

 Approximately 75% of the probes disposed on the array (90% of those that successfully PCR amplified) were sequence-verified by sequencing in both the forward and reverse direction using MegaBACE sequencer (Molecular
30 , Dynamics, Inc., Sunnyvale, CA), universal primers, and standard protocols.

 Some genomic clones (BACs) yielded very poor PCR and sequencing results. The reasons for this are unclear, but may be related to the quality of early draft sequence
35 or the inclusion of vector and host contamination in some

submitted sequence data.

Although the intronic and intergenic material flanking coding regions could theoretically interfere with hybridization during microarray experiments, subsequent
5 empirical results demonstrated that differential expression ratios were not significantly affected by the presence of noncoding sequence. The variation in exon size was similarly found not to affect differential expression ratios significantly; however, variation in exon size was
10 observed to affect the absolute signal intensity (data not shown).

The 350 MB of genomic DNA was, by the above-described process, reduced to 9750 discrete probes, which were spotted in duplicate onto glass slides using
15 commercially available instrumentation (MicroArray GenII Spotter and/or MicroArray GenIII Spotter, Molecular Dynamics, Inc., Sunnyvale, CA). Each slide additionally included either 16 or 32 *E. coli* genes, the average hybridization signal of which was used as a measure of
20 background biological noise.

Each of the probe sequences was BLASTed against the human EST data set, the NR data set, and SwissProt GenBank (May 7, 1999 release 2.0.9).

One third of the probe sequences (as amplified)
25 produced an exact match (BLAST Expect ("E") values less than 1×10^{-100}) to either an EST (20% of sequences) or a known mRNA (13% of sequences). A further 22% of the probe sequences showed some homology to a known EST or mRNA (BLAST E values from 1×10^{-5} to 1×10^{-99}). The remaining 45% of
30 the probe sequences showed no significant sequence homology to any expressed, or potentially expressed, sequences present in public databases.

All of the probe sequences (as amplified) were then analyzed for protein similarities with the SwissProt
35 database using BLASTX, Gish et al., *Nature Genet.* 3:266

(1993). The predicted functional breakdowns of the 2/3 of probes identical or homologous to known sequences are presented in Table 1.

5

Table 1

Function of Predicted ORFs As Deduced From Comparative Sequence Analysis			
Total	V6 chip	V7 chip	Function Predicted from Comparative Sequence Analysis
211	96	115	Receptor
120	43	77	Zinc Finger
30	11	19	Homeobox
25	9	16	Transcription Factor
17	11	7	Transcription
118	57	61	Structural
95	39	56	Kinase
36	18	18	Phosphatase
83	31	52	Ribosomal
45	19	26	Transport
21	17	14	Growth Factor
17	12	5	Cytochrome
50	33	17	Channel

As can be seen, the two most common types of genes were transcription factors and receptors, making up 2.2% and 1.8% of the arrayed elements, respectively.

10

EXAMPLE 2

Gene Expression Measurements From Genome-Derived Single Exon Microarrays

15

The two genome-derived single exon microarrays prepared according to Example 1 were hybridized in a series of simultaneous two-color fluorescence experiments to (1) 5 Cy3-labeled cDNA synthesized from message drawn individually from each of brain, heart, liver, fetal liver, placenta, lung, bone marrow, HeLa, BT 474, or HBL 100 cells, and (2) Cy5-labeled cDNA prepared from message pooled from all ten tissues and cell types, as a control in 10 each of the measurements. Hybridization and scanning were carried out using standard protocols and Molecular Dynamics equipment.

Briefly, mRNA samples were bought from commercial sources (Clontech, Palo Alto, CA and Amersham Pharmacia 15 Biotech (APB)). Cy3-dCTP and Cy5-dCTP (both from APB) were incorporated during separate reverse transcriptions of 1 µg of polyA⁺ mRNA performed using 1 µg oligo(dT)12-18 primer and 2 µg random 9mer primers as follows. After heating to 70°C, the RNA:primer mixture was snap cooled on ice. After 20 snap cooling on ice, added to the RNA to the stated final concentration was: 1X Superscript II buffer, 0.01 M DTT, 100µM dATP, 100 µM dGTP, 100 µM dTTP, 50 µM dCTP, 50 µM Cy3-dCTP or Cy5-dCTP 50 µM, and 200 U Superscript II enzyme. The reaction was incubated for 2 hours at 42°C. 25 After 2 hours, the first strand cDNA was isolated by adding 1 U Ribonuclease H, and incubating for 30 minutes at 37°C. The reaction was then purified using a Qiagen PCR cleanup column, increasing the number of ethanol washes to 5. Probe was eluted using 10 mM Tris pH 8.5.

30 Using a spectrophotometer, probes were measured for dye incorporation. Volumes of both Cy3 and Cy5 cDNA corresponding to 50 pmoles of each dye were then dried in a Speedvac, resuspended in 30 µl hybridization solution containing 50% formamide, 5X SSC, 0.2 µg/µl poly(dA), 0.2 35 µg/µl human c₀t1 DNA, and 0.5 % SDS.

Hybridizations were carried out under a coverslip, with the array placed in a humid oven at 42°C overnight. Before scanning, slides were washed in 1X SSC, 0.2% SDS at 55°C for 5 minutes, followed by 0.1X SSC, 0.2% SDS, at 55°C for 20 minutes. Slides were briefly dipped in water and dried thoroughly under a gentle stream of nitrogen.

Slides were scanned using a Molecular Dynamics Gen3 scanner, as described. Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376).

Although the use of pooled cDNA as a reference permitted the survey of a large number of tissues, it attenuates the measurement of relative gene expression, since every highly expressed gene in the tissue/cell type-specific fluorescence channel will be present to a level of at least 10% in the control channel. Because of this fact, both signal and expression ratios (the latter hereinafter, "expression" or "relative expression") for each probe were normalized using the average ratio or average signal, respectively, as measured across the whole slide.

Data were accepted for further analysis only when signal was at least three times greater than biological noise, the latter defined by the average signal produced by the *E. coli* control genes.

The relative expression signal for these probes was then plotted as function of tissue or cell type, and is presented in FIG. 6.

FIG. 6 shows the distribution of expression across a panel of ten tissues. The graph shows the number of sequence-verified products that were either not expressed ("0"), expressed in one or more but not all tested tissues ("1" - "9"), and expressed in all tissues tested ("10").

Of 9999 arrayed elements on the two microarrays (including positive and negative controls and "failed" products), 2353 (51%) were expressed in at least one tissue or cell type. Of the gene elements showing significant
5 signal - where expression was scored as "significant" if the normalized Cy3 signal was greater than 1, representing signal 5-fold over biological noise (0.2) - 39% (991) were expressed in all 10 tissues. The next most common class (15%) consisted of gene elements expressed in only a single
10 tissue.

The genes expressed in a single tissue were further analyzed, and the results of the analyses are compiled in FIG. 7.

FIG. 7A is a matrix presenting the expression of
15 all verified sequences that showed expression greater than 3 in at least one tissue. Each clone is represented by a column in the matrix. Each of the 10 tissues assayed is represented by a separate row in the matrix, and relative expression of a clone in that tissue is indicated at the
20 respective node by intensity of green shading, with the intensity legend shown in panel B. The top row of the matrix ("EST Hit") contains "bioinformatic" rather than "physical" expression data - that is, presents the results returned by query of EST, NR and SwissProt databases using
25 the probe sequence. The legend for "bioinformatic expression" (i.e., degree of homology returned) is presented in panel C. Briefly, white is known, black is novel, with gray depicting nonidentical with significant homology (white: E values < 1e-100; gray: E values from 1e-
30 05 to 1e-99; black: E values > 1e-05).

As FIG. 7 readily shows, heart and brain were demonstrated to have the greatest numbers of genes that were shown to be uniquely expressed in the respective tissue. In brain, 200 uniquely expressed genes were
35 identified; in heart, 150. The remaining tissues gave the

following figures for uniquely expressed genes: liver, 100; lung, 70; fetal liver, 150; bone marrow, 75; placenta, 100; HeLa, 50; HBL, 100; and BT474, 50.

It was further observed that there were many more
5 "novel" genes among those that were up-regulated in only one tissue, as compared with those that were down-regulated in only one tissue. In fact, it was found that ORFs whose expression was measurable in only a single of the tested tissues were represented in sequencing databases at a rate
10 of only 11%, whereas 36% of the ORFs whose expression was measurable in 9 of the tissues were present in public databases. As for those ORFs expressed in all ten tissues, fully 45% were present in existing expressed sequence databases. These results are not unexpected, since genes
15 expressed in a greater number of tissues have a higher likelihood of being, and thus of having been, discovered by EST approaches.

Comparison of Signal from Known and Unknown Genes

20 The normalized signal of the genes found to have high homology to genes present in the GenBank human EST database were compared to the normalized signal of those genes not found in the GenBank human EST database. The data are shown in FIG. 8.

25 FIG. 8 shows the normalized Cy3 signal intensity for all sequence-verified products with a BLAST Expect ("E") value of greater than $1e-30$ (designated "unknown") upon query of existing EST, NR and SwissProt databases, and shows in blue the normalized Cy3 signal intensity for all
30 sequence-verified products with a BLAST Expect value of less than $1e-30$ ("known"). Note that biological background noise has an averaged normalized Cy3 signal intensity of 0.2.

As expected, the most highly expressed of the
35 ORFs were "known" genes. This is not surprising, since

very high signal intensity correlates with very commonly-expressed genes, which have a higher likelihood of being found by EST sequence.

However, a significant point is that a large
5 number of even the high expressers were "unknown". Since the genomic approach used to identify genes and to confirm their expression does not bias exons toward either the 3' or 5' end of a gene, many of these high expression genes will not have been detected in an end-sequenced cDNA
10 library.

The significant point is that presence of the gene in an EST database is not a prerequisite for incorporation into a genome-derived microarray, and further, that arraying such "unknown" exons can help to
15 assign function to as-yet undiscovered genes.

Verification of Gene Expression

To ascertain the validity of the approach described above to identify genes from raw genomic
20 sequence, expression of two of the probes was assayed using reverse transcriptase polymerase chain reaction (RT PCR) and northern blot analysis.

Two microarray probes were selected on the basis of exon size, prior sequencing success, and tissue-specific
25 gene expression patterns as measured by the microarray experiments. The primers originally used to amplify the two respective ORFs from genomic DNA were used in RT PCR against a panel of tissue-specific cDNAs (Rapid-Scan gene expression panel 24 human cDNAs) (OriGene Technologies,
30 Inc., Rockville, MD).

Sequence AL079300_1 was shown by microarray hybridization to be present in cardiac tissue, and sequence AL031734_1 was shown by microarray experiment to be present in placental tissue (data not shown). RT-PCR on these two
35 sequences confirmed the tissue-specific gene expression as

measured by microarrays, as ascertained by the presence of a correctly sized PCR product from the respective tissue type cDNAs.

Clearly, all microarray results cannot, and indeed should not, be confirmed by independent assay methods, or the high throughput, highly parallel advantages of microarray hybridization assays will be lost. However, in addition to the two RT-PCR results presented above, the observation that 1/3 of the arrayed genes exist in expression databases provides powerful confirmation of the power of our methodology - which combines bioinformatic prediction with expression confirmation using genome-derived single exon microarrays - to identify novel genes from raw genomic data.

To verify that the approach further provides correct characterization of the expression patterns of the identified genes, a detailed analysis was performed of the microarrayed sequences that showed high signal in brain.

For this latter analysis, sequences that showed high (normalized) signal in brain, but which showed very low (normalized) signal (less than 0.5, determined to be biological noise) in all other tissues, were further studied. There were 82 sequences that fit these criteria, approximately 2% of the arrayed elements. The 10 sequences showing the highest signal in brain in microarray hybridizations are detailed in Table 2, along with assigned function, if known or reasonably predicted.

Table 2

Function of the Most Highly Expressed Genes Expressed Only in Brain

Microarray Sequence Name	Normal ized Signal	Expressi on Ratio	Homology to EST present in GenBank	Gene Function as described by GenBank
AP000217-1	5.2	+7.7	High	S-100 protein, b-chain, Ca^{2+} binding protein expressed in central nervous system
AP000047-1	2.3		High	Unknown Function
AC006548-9	1.7		High	Similar to mouse membrane glyco-protein M6, expressed in central nervous system
AC007245-5	1.5		High	Similar to amphiphysin, a synaptic vesicle- associated protein. Ref 21
L44140-4	1.2	+2.0	High	Endothelial actin-binding protein found in nonmuscle filamin

AC004689-9	1.2	+3.5	High	Protein Phosphatase PP2A, neuronal/ downregulates activated protein kinases
AL031657-1	1.2	+3.0	High	Unknown function/ Contains the anhyrin motif, a common protein sequence motif
AC009266-2	1.1	+3.7	Low	Low homology to the Synaptotagmin I protein in rat/present at low levels throughout rat brain
AP000086-1	1.0	+2.7	Low	Unknown, very poor homology to collagen
AC004689-3	1.0		High	Protein Phosphatase PP2A, neuronal/ downregulates activated protein kinases

Of the ten sequences studied by these latter confirmatory approaches, eight were previously known. Of these eight, six had previously been reported to be
5 important in the central nervous system or brain. The exon

giving the highest signal (AP00217-1) was found to be the gene encoding an S100B Ca^{2+} binding protein, reported in the literature to be highly and uniquely expressed in the central nervous system. Heizmann, *Neurochem. Res.* 9:1097
5 (1997).

A number of the brain-specific probe sequences (including AC006548-9, AC009266-2) did not have homology to any known human cDNAs in GenBank but did show homology to rat and mouse cDNAs. Sequences AC004689-9 and AC004689-3
10 were both found to be phosphatases present in neurons (Millward et al., *Trends Biochem. Sci.* 24(5):186-191 (1999)). Two microarray sequences, AP000047-1 and AP000086-1 have unknown function, with AP000086-1 being absent from GenBank. Functionality can now be narrowed
15 down to a role in the central nervous system for both of these genes, showing the power of designing microarrays in this fashion.

Next, the function of the chip sequences with the highest (normalized) signal intensity in brain, regardless
20 of expression in other tissues, was assessed. In this latter analysis, we found expression of many more common genes, since the sequences were not limited to those expressed only in brain. For example, looking at the 20 highest signal intensity spots in brain, 4 were similar to
25 tubulin (AC00807905; AF146191-2; AC007664-4; AF14191-2), 2 were similar to actin (AL035701-2; AL034402-1), and 6 were found to be homologous to glyceraldehyde-3-phosphate dehydrogenase (GAPDH) (AL035604-1; Z86090-1; AC006064-L, AC006064-K; AC035604-3; AC006064-L). These genes are often
30 used as controls or housekeeping genes in microarray experiments of all types.

Other interesting genes highly expressed in brain were a ferritin heavy chain protein, which is reported in the literature to be found in brain and liver (Joshi et
35 al., *J. Neurol. Sci.* 134(Suppl):52-56 (1995)), a result

duplicated with the array. Other highly expressed chip
 sequences included a translation elongation factor 1 α
 (AC007564-4), a DEAD-box homolog (AL023804-4), and a Y-
 chromosome RNA-binding motif (Chai et al., *Genomics*
 5 49(2):283-89 (1998)) (AC007320-3). A low homology analog
 (AP00123-1/2) to a gene, DSCR1, thought to be involved in
 trisomy 21 (Down's syndrome), showed high expression in
 both brain and heart, in agreement with the literature
 (Fuentes et al., *Mol. Genet.* 4(10):1935-44 (1995)).

10 As a further validation of the approach, we
 selected the BAC AC006064 to be included on the array.
 This BAC was known to contain the GAPDH gene, and thus
 could be used as a control for the ORF selection process.
 The gene finding and exon selection algorithms resulted in
 15 choosing 25 exons from BAC AC006064 for spotting onto the
 array, of which four were drawn from the GAPDH gene. Table
 3 shows the comparison of the average expression ratio for
 the 4 exons from BAC006064 compared with the average
 expression ratio for 5 different dilutions of a
 20 commercially available GAPDH cDNA (Clontech).

Table 3

Comparison of Expression Ratio, for each tissue, of GAPDH		
	AC006064 (n = 4)	Control (n = 5)
Bone Marrow	-1.81 \pm 0.11	-1.85 \pm 0.08
Brain	-1.41 \pm 0.11	-1.17 \pm 0.05
BT474	1.85 \pm 0.09	1.66 \pm 0.12
Fetal Liver	-1.62 \pm 0.07	-1.41 \pm 0.05
HBL100	1.32 \pm 0.05	2.64 \pm 0.12
Heart	1.16 \pm 0.09	1.56 \pm 0.10
HeLa	1.11 \pm 0.06	1.30 \pm 0.15
Liver	-1.62 \pm 0.22	-2.07 \pm

Lung	-4.95 ± 0.93	-3.75 ± 0.21
Placenta	-3.56 ± 0.25	-3.52 ± 0.43

Each tissue shows excellent agreement between the experimentally chosen exons and the control, again demonstrating the validity of the present exon mining approach. In addition, the data also show the variability of expression of GAPDH within tissues, calling into question its classification as a housekeeping gene and utility as a housekeeping control in microarray experiments.

EXAMPLE 3

Representation of Sequence and Expression Data as a "Mondrian"

For each genomic clone processed for microarray as above-described, a plethora of information was accumulated, including full clone sequence, probe sequence within the clone, results of each of the three gene finding programs, EST information associated with the probe sequences, and microarray signal and expression for multiple tissues, challenging our ability to display the information.

Accordingly, we devised a new tool for visual display of the sequence with its attendant annotation which, in deference to its visual similarity to the paintings of Piet Mondrian, is hereinafter termed a "Mondrian". FIGS. 3 and 4 present the key to the information presented on a Mondrian.

FIG. 9 presents a Mondrian of BAC AC008172 (bases 25,000 to 130,000 shown), containing the carbamyl phosphate synthetase gene (AF154830.1). Purple background within the region shown as field 81 in FIG. 3 indicates all 37 known

exons for this gene.

As can be seen, GRAIL II successfully identified 27 of the known exons (73%), GENEFINDER successfully identified 37 of the known exons (100%), while DICTION 5 identified 7 of the known exons (19%).

Seven of the predicted exons were selected for physical assay, of which 5 successfully amplified by PCR and were sequenced. These five exons were all found to be from the same gene, the carbamyl phosphate synthetase gene 10 (AF154830.1).

The five exons were arrayed, and gene expression measured across 10 tissues. As is readily seen in the Mondrian, the five chip sequences on the array show identical expression patterns, elegantly demonstrating the 15 reproducibility of the system.

FIG. 10 is a Mondrian of BAC AL049839. We selected 12 exons from this BAC, of which 10 successfully sequenced, which were found to form between 5 and 6 genes. Interestingly, 4 of the genes on this BAC are protease 20 inhibitors. Again, these data elegantly show that exons selected from the same gene show the same expression patterns, depicted below the red line. From this figure, it is clear that our ability to find known genes is very good. A novel gene is also found from 86.6 kb to 88.6 kb, 25 upon which all the exon finding programs agree. We are confident we have two exons from a single gene since they show the same expression patterns and the exons are proximal to each other. Backgrounds in the following colors indicate a known gene (top to bottom): 30 red = kallistatin protease inhibitor (P29622); purple = plasma serine protease inhibitor (P05154); turquoise = α 1 anti-chymotrypsin (P01011); mauve = 40S ribosomal protein (P08865). Note that chip sequence 8 and 12 did not sequence verify.

35

EXAMPLE 4Genome-Derived Single Exon Probes Useful For Measuring
Human Gene Expression

5

The protocols set forth in Examples 1 and 2, *supra*, were applied to additional human genomic sequence as it became newly available in GenBank to identify unique exons in the human genome that could be shown to be
10 expressed at significant levels in HeLa cell line.

These unique exons are within longer probe sequences. Each probe was completely sequenced on both strands prior to its use on a genome-derived single exon microarray; sequencing confirms the exact chemical
15 structure of each probe. An added benefit of sequencing is that it placed us in possession of a set of single base-incremented fragments of the sequenced nucleic acid, starting from the sequencing primer 3' OH. (Since the single exon probes were first obtained by PCR amplification
20 from genomic DNA, we were of course additionally in possession of an even larger set of single base incremented fragments of each of the 9,290 single exon probes, each fragment corresponding to an extension product from one of the two amplification primers.)

25 The structures of the 9,290 unique single exon probes are clearly presented in the Sequence Listing as SEQ ID Nos.: 1 - 9,290. The 16 nt 5' primer sequence and 16 nt 3' primer sequence present on the amplicon are not included in the sequence listing. The sequences of the exons
30 present within each of these probes is presented in the Sequence Listing as SEQ ID Nos.: 9,291 - 18,392, respectively. It will be noted that some amplicons have more than one exon, some exons are contained in more than one amplicon.

35 As detailed in Example 2, expression was

demonstrated by disposing the amplicons as single exon probes on nucleic acid microarrays and then performing two-color fluorescent hybridization analysis; significant expression is based on a statistical confidence that the
5 signal is significantly greater than negative biological control spots. The negative biological control is formed from spotted DNA sequences from a different species. Here, 32 sequences from E.Coli were spotted in duplicate to give a total of 64 spots.

10 For each hybridisation (each slide, each colour) the median value of the signal from all of the spots is determined. The normalised signal value is the arithmetic mean of the signal from duplicate spots divided by the population median.

15 Control spots are eliminated if there is more than a five-fold difference between each one of the duplicate spots raw signals.

The median of the signal from the remaining control spots is calculated and all subsequent calculations
20 are done with normalised signals.

Control spots having a signal of greater than median + 2.4 (the value 2.4 is roughly 12 times the observed standard deviation of control spot populations) are eliminated. Spots with such high signals are considered
25 to be "outliers".

The mean and standard deviation of the modified control spot populations are calculated.

The mean + 3x the standard deviation (mean + (3*SD)) is used as the signal threshold qualifier for that
30 particular hybridisation. Thus, individual thresholds are determined for each channel and each hybridisation.

This means that, assuming that the data is distributed normally, there is a 99% confidence that any signal exceeding the threshold is significant.

35 The probes and their expression data are

presented in Table 4, set forth respectively in Example 5. Example 5 presents the subset of probes that is significantly expressed in the human HeLa cells and thus presents the subset of probes that was recognized to be useful for measuring expression of their cognate genes in human HeLa cells.

The sequence of each of the exon probes identified by SEQ ID NOS.: 9,291 - 18,392 was individually used as a BLAST (or, for SWISSPROT, BLASTX) query to identify the most similar sequence in each of dbEST, SwissProt (BLASTX), and NR divisions of GenBank. Because the query sequences are themselves derived from genomic sequence in GenBank, only nongenic hits from NR were scored.

The smallest in value of the BLAST (or BLASTX) expect ("E") scores for each query sequence across the three database divisions was used as a measure of the "expression novelty" of the probe's ORF. Table 4 is sorted in descending order based on this measure, reported as "Most Similar (top) Hit BLAST E Value". Those sequences for which no "Hit E Value" is listed are those exons which were found to have no similar sequences.

As sorted, Table 4 thus lists its respective probes (by "AMPLICON SEQ ID NO.:" and additionally by the SEQ ID NO.: of the exon contained within the probe:"EXON SEQ ID NO.:") from least similar to sequences known to be expressed (i.e., highest BLAST E value), at the beginning of the table, to most similar to sequences known to be expressed (i.e., lowest BLAST E value), at the bottom of the table.

Table 4 further provides, for each listed probe, the accession number of the database sequence that yielded the "Most Similar (top) Hit BLAST E Value", along with the name of the database in which the database sequence is found ("Top Hit Database Source").

Table 4 further provides SEQ ID NOS.

corresponding to the predicted amino acid sequences where they have been determined for the probe and exon nucleotide sequences. These are set out as PEPTIDE SEQ ID NOS... The peptide sequences for a given exon are predicted as follows: Since each chip exon is a consensus sequence drawn from predictions from various exon finding programs (i.e. Grail, GeneFinder and GenScan), the multiple initial ORFs are first determined in a uniform way according to each prediction. In particular, the reading frame for predicting the first amino acid in the peptide sequence always starts with the first base of any codon and ends with the last base of non-termination codon. Next, for each strand of the exon, initial ORFs are merged into one or more final ORFs in an exhaustive process based on the following criteria: 1) the merging ORFs must be overlapping, and 2) the merging ORFs must be in the same frame.

The Sequence Listing, which is a superset of all of the data presented in Table 4, further includes, for each probe, the most similar hit, with accession number and BLAST E value, from the each of the three queried databases.

Table 4 further lists, for each probe, a portion of the descriptor for the top hit ("Top Hit Descriptor") as provided in the sequence database. For those ORFs that are similar in sequence, but nonidentical to known sequences (e.g., those with BLAST E values between about $1e-05$ and $1e-100$), the descriptor reveals the likely function of the protein encoded by the probe's ORF.

Using BLAST E value cutoffs of $1e-05$ (i.e., 1×10^{-5}) and $1e-100$ (i.e., 1×10^{-100}) as evidence of similarity to sequences known to be expressed is of course arbitrary: in Example 2, *supra*, a BLAST E value of $1e-30$ was used as the boundary when only two classes were to be defined for analysis (unknown, $>1e-30$; known $<1e-30$) (see also FIG. 8).

Furthermore, even when the "Most Similar (Top) Hit BLAST E Value" is low, e.g., less than about $1e-100$ - which is probative evidence that the query sequence has previously been shown to be expressed - the top hit is highly unlikely
5 exactly to match the probe sequence.

First, such expression entries typically will not have the intronic and/or intergenic sequence present within the single exon probes listed in the Table. Second, even the ORF itself is unlikely in such cases to be present
10 identically in the databases, since most of the EST and mRNA clones in existing databases include multiple exons, without any indication of the location of exon boundaries.

As noted, the data presented in Table 4 represent a proper subset of the data present within the attached
15 sequence listing. For each amplicon probe (SEQ ID NOs.: 1 - 9,290) and probe exon (SEQ ID NOs.: 9,291 - 18,392, respectively), the sequence listing further provides, through iterated annotation fields <220> and <223>:

(a) the accession number of the BAC from which
20 the sequence was derived ("MAP TO"), thus providing a link to the chromosomal map location and other information about the genomic milieu of the probe sequence;

(b) the most similar sequence provided by BLAST query of the EST database, with accession number and BLAST
25 E value for the "hit";

(c) the most similar sequence provided by BLAST query of the GenBank NR database, with accession number and BLAST E value for the "hit"; and

(d) the most similar sequence provided by BLASTX
30 query of the SWISSPROT database, with accession number and BLAST E value for the "hit".

EXAMPLE 5

35 Genome-Derived Single Exon Probes Useful For Measuring

Expression of Genes in Human HeLa cells

Table 4 (382 pages) presents expression, homology, and functional information for the genome-derived single exon
5 probes that are expressed significantly in human HeLa cell line.

CLAIMS

1. A spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived
5 from human HeLa cells or other human cervical epithelial cells comprising a plurality single exon nucleic probes, said probes comprising any one of the nucleotide sequences set out in SEQ ID NOS: 1 - 9,290 or a complementary sequence, or a portion of such a sequence.
10
2. A spatially-addressable set of single exon nucleic acid probes as claimed in claim 1 wherein each of said plurality of probes is separately and addressably amplifiable.
- 15 3. A spatially-addressable set of single exon nucleic acid probes as claimed in claim 1 wherein each of said plurality of probes is separately and addressably isolatable from said plurality.
- 20 4. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 3 wherein said probes comprise any one of the nucleotide sequences set out in SEQ ID NOS.: 9,291 - 18,392.
- 25 5. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 4, wherein each of said plurality of probes is amplifiable using at least one common primer.
- 30 6. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 5 wherein the set comprises between 50 - 20,000 single exon nucleic acid probes.
- 35 7. A spatially-addressable set of single exon nucleic acid

probes as claimed in any of claims 1 to 6, wherein the average length of the single exon nucleic acid probes is between 200 and 500 bp.

- 5 8. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 7, wherein at least 50% of said single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence.
- 10 9. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 8, wherein at least 50% of said single exon nucleic acid probes lack homopolymeric stretches of A or T.
- 15 10. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 - 9 characterised in that said set of probes is addressably disposed upon a substrate.
- 20 11. A spatially-addressable set of single exon nucleic acid probes as claimed in claim 10 wherein said substrate is selected from glass, amorphous silicon, crystalline silicon and plastic.
- 25 12. A microarray comprising a spatially addressable set of single exon nucleic acid probes as claimed in any of claims 1 - 11.
- 30 13. A single exon nucleic acid probe for measuring human gene expression in a sample derived from human HeLa cells or other human cervical epithelial cells comprising a nucleotide sequence as set out in any of SEQ ID NOS.: 1 - 9,290 or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a
- 35 nucleic acid molecule expressed in the human HeLa cells or

other human cervical epithelial cells.

14. A single exon nucleic acid probe as claimed in claim 13 comprising a nucleotide sequence as set out in any of SEQ ID NOs.: 9,291 - 18,392 or a complementary sequence or a fragment thereof.
15. A single exon nucleic acid probe for measuring human gene expression in a sample derived from human HeLa cells or other human cervical epithelial cells which is a nucleic acid molecule having a sequence encoding a peptide comprising a peptide sequence as set out in any of SEQ ID NOs.: 18,393 - 26,941, or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid expressed in the human HeLa cells or other human cervical epithelial cells.
16. A single exon nucleic acid probe as claimed in any one of claims 13 to 15 wherein said single exon nucleic acid probe comprises between 15 and 25 contiguous nucleotides of said SEQ ID NO.
17. A single exon nucleic acid probe as claimed in any one of claims 13 to 15, wherein said probe is between 3 - 25 kb in length.
18. A single exon nucleic acid probe as claimed in any one of claims 13 - 17, wherein said probe is DNA, RNA or PNA.
19. A single exon nucleic acid probe as claimed in any one of claims 13 - 18, wherein said probe is detectably labeled.
20. A single exon nucleic acid probe as claimed in any one of claims 13 - 19, wherein said probe lacks prokaryotic and

bacteriophage vector sequence.

21. A single exon nucleic acid probe as claimed in any one of claims 13 - 20, wherein said probe lacks homopolymeric stretches of A or T.

22. A method of measuring gene expression in a sample derived from human HeLa cells or other human cervical epithelial cells, comprising:

10 contacting the microarray of claim 12, with a first collection of detectably labeled nucleic acids, said first collection of nucleic acids derived from mRNA of human HeLa cells or other human cervical epithelial cells; and then
15 measuring the label detectably bound to each probe of said microarray.

23. A method of identifying exons in a eukaryotic genome, comprising:

20 algorithmically predicting at least one exon from genomic sequence of said eukaryote; and then detecting specific hybridization of detectably labeled nucleic acids to a single exon probe,
wherein said detectably labeled nucleic acids are derived
25 from mRNA from the HeLa cells or other human cervical epithelial cells of said eukaryote, said probe is a single exon probe having a fragment identical in sequence to, or complementary in sequence to, said predicted exon, said probe is included within a microarray according to claim
30 12, and said fragment is selectively hybridizable at high stringency.

24. A method of assigning exons to a single gene, comprising:

35 identifying a plurality of exons from genomic

sequence according to the method of claim 23; and
then

measuring the expression of each of said exons in a
plurality of tissues and/or cell types using
5 hybridization to single exon microarrays having a
probe with said exon,

wherein a common pattern of expression of said exons in
said plurality of tissues and/or cell types indicates that
the exons should be assigned to a single gene.

10

25. A nucleic acid sequence as set out in any of SEQ ID
Nos: 1 - 18,392 which encodes a peptide.

26. A peptide encoded by a sequence as set out in any of
15 SEQ ID Nos: 1 - 18,392.

27. A peptide comprising a sequence as set out in any of
SEQ ID Nos: 18,393 - 26,941.

20

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Table 4
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Database Source	Top Hit Descriptor
458	9709	18949	5.87			
859	10134	19253	11.93			
1052	10278		2.08			
1309	10525	18385	19.17			
1593	10803	18982	2.78			
1613	10828	20001	12.21			
1700	10812	20099	1.72			
1721	10833	20116	1.1			
1727	10839	20122	9.25			
1858	11083	20254	1.78			
1947	11161	20353	2.13			
2131	11330	20549	1.94			
2244	11439	20683	2.03			
3148	12394	21517	3.28			
3428	12681	21781	1			
3489	12713	21849	8.63			
3535	12759		0.97			
3637	12858	21977	0.97			
3923	13139		1.02			
4179	13383	22484	1.57			
4248	13451	22542	7.61			
4285	13488	22561	0.64			
4288	13488	22562	0.64			
4330	13531		1.28			
4388	13587	22689	0.79			
4854	14043	23137	1.05			
4892	14087		0.89			
5070	14250	23333	5.18			
5404	14832		6.28			
5488	14714		6.43			
5525	14832		4.42			
5548	14770	24137	3.03			
5889	18082	24282	1.69			
5898	14908	24301	1.91			

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Table 4
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6484	15681	25150	2.19				
6830	16123	25590	5.79				
7275	16494		2.73				
7422	18078	28128	1.85				
7598	16789		3.09				
7889	17115	26847	2.51				
7997	16432	25919	2.03				
7987	16432	25920	2.03				
8034	17170		2.59				
8748	17691		1.72				
9065	17892	23898	1.79				
9278	18041		1.22				
9689	14909	24302	15.7	9.9E+00	AJ239028.1	NT	Homo sapiens LSS gene, partial, exons 15, 16, 17 and 18
9688	15693	25134	2.2	9.8E+00	U32718.1	NT	Haemophilus influenzae Rd section 31 of 163 of the complete genome
2674	12112	21240	3.14	9.4E+00	AB043785.1	NT	Mus musculus AT3 gene for antithrombin, complete cds
9766	15891	25417	3.22	9.3E+00	P11210	SWISSPROT	IMMEDIATE-EARLY PROTEIN 1 (IE1) (IMMEDIATE-EARLY PHOSPHOPROTEIN PP89)
6328	14558	23829	2.48	9.1E+00	AF095609.1	NT	Leuciscus cephalus orientalis cytochrome b (cyt b) gene, partial cds; mitochondrial gene for mitochondrial product
5328	14558	23630	2.48	9.1E+00	AF095609.1	NT	Leuciscus cephalus orientalis cytochrome b (cyt b) gene, partial cds; mitochondrial gene for mitochondrial product
5878	14898	24288	5.52	8.9E+00	BE971808.1	EST_HUMAN	60185 (C38R1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:3834582 3'
5824	15041	24444	2.15	8.7E+00	AB019788.1	NT	Cynops pyrrhogaster CpTbx3 premature mRNA, partial cds
5824	15041	24445	2.15	8.7E+00	AB019788.1	NT	Cynops pyrrhogaster CpTbx3 premature mRNA, partial cds
446	9700	18838	1.88	8.4E+00	6031804	NT	Homo sapiens insulin receptor substrate 1 (IRS1) mRNA
6898	15002	25068	2.76	8.1E+00	AJ131719.1	NT	Zea mays mRNA for legumain-like protease (see2a)
7728	16928		2.49	8.0E+00	P41820	SWISSPROT	BREFELDIN A RESISTANCE PROTEIN
6229	18410		1.77	7.6E+00	AL445065.1	NT	Thermoplasma acidophilum complete genome; segment 3/5
5572	14798	24170	4.33	7.4E+00	BF700517.1	EST_HUMAN	602128878F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4285508 5'
6703	15898	25359	2.97	7.4E+00	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
6703	15898	25360	2.97	7.4E+00	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
2834	12172	21305	3.8	7.2E+00	L12051.1	NT	Lycopodium esculentum Mill. GTPase (SAR2) mRNA, complete cds
2834	12172	21306	3.8	7.2E+00	L12051.1	NT	Lycopodium esculentum Mill. GTPase (SAR2) mRNA, complete cds
6960	18138		11.08	7.1E+00	AL161595.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 91
7824	17137	26868	4.08	7.1E+00	P05850	SWISSPROT	HYPOTHETICAL 17.3 KDA PROTEIN IN MRDA-PHPB INTERGENIC REGION

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Table 4
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7068	16245	25720	3.26	7.0E+00	P48010	SWISSPROT	ARGININE KINASE (AK)
7802	16996	26509	1.94	7.0E+00	Q22469	SWISSPROT	WD-40 REPEAT PROTEIN MS13
6553	15749	26210	5.33	6.0E+00	P35679	SWISSPROT	60S RIBOSOMAL PROTEIN L4 (L2)
7137	16314	25785	4.45	6.8E+00	Q03570	SWISSPROT	HYPOTHETICAL 157.0 KDA PROTEIN C38C10.5 IN CHROMOSOME II
7097	16274	25752	2.93	6.6E+00	Q9ZE07	SWISSPROT	URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP KINASE)
7097	16274	25753	2.93	6.6E+00	Q9ZE07	SWISSPROT	URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP KINASE)
7888	16887		2.54	6.6E+00	Q10309	SWISSPROT	PROBABLE CATION-TRANSPORTING ATPASE C8C3.05C
6824	16018	25483	6.58	6.5E+00	P03374	SWISSPROT	ENV POLYPROTEIN [CONTAINS: COAT PROTEIN GP52; COAT PROTEIN GP36]
5885	15102	24513	6.98	5.9E+00	AF155142.1	NT	Mus musculus mbcd lineage kinase 3 (Mlk3) and two pore domain K+ channel subunit (Kcnk6) genes, complete cds
3487	12721		0.84	5.8E+00	7681557	NT	Homo sapiens DESC1 protein (DESC1), mRNA
8011	16448	25636	2.42	5.6E+00	Q55278	SWISSPROT	LYCOPENE BETA CYCLASE
7380	16576		1.76	5.5E+00	AF175426.1	NT	Mus musculus DNA methyltransferase (Dnmt1) gene, exons 30, 31, and 32
8010	16445	26835	3.03	5.5E+00	P11690	SWISSPROT	PNEUMOLYSIN (THIOL-ACTIVATED CYTOLYSIN)
8222	17352		1.85	5.5E+00	AL161571.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 67
4785	13984	23089	1.28	6.3E+00	L43128.1	NT	Bovine immunodeficiency-like virus surface envelope gene, 5' end of cds
6492	15989		3.71	5.3E+00	P54098	SWISSPROT	DNA POLYMERASE GAMMA (MITOCHONDRIAL DNA POLYMERASE CATALYTIC SUBUNIT)
8147	17279	26824	1.66	5.3E+00	Q27905	SWISSPROT	PROBABLE ANTIBACTERIAL PEPTIDE POLYPROTEIN PRECURSOR
7749	16945		2.12	5.2E+00	Q10138	SWISSPROT	HYPOTHETICAL 61.1 KD PROTEIN C2E2.03C IN CHROMOSOME I
7189	16368	25846	4.81	5.0E+00	AF162445.2	NT	Canis familiaris skeletal muscle chloride channel CIC-1 (CLCN1) mRNA, complete cds
7838	17030	26546	12.07	5.0E+00	Z83860.1	NT	Mycobacterium tuberculosis H37Rv complete genome; segment 103/182
4038	13248		12.98	4.8E+00	AF185255.1	NT	Elunia australis histone H3 (H3) gene, partial cds
6638	15831		4.93	4.8E+00	AW750087.1	EST_HUMAN	PMO-BT0547-310100-002-504 BT0547 Homo sapiens cDNA
294	9568	18700	2.43	4.7E+00	BF240552.1	EST_HUMAN	601875654F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4099716 5'
295	9568	18700	2	4.7E+00	BF240552.1	EST_HUMAN	601875654F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4099716 5'
3241	12476	21606	1.02	4.7E+00	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
8131	17285	26809	1.9	4.5E+00	AE001044.1	NT	Archaeoglobus fulgidus section 63 of 172 of the complete genome
8235	17364	26902	1.67	4.5E+00	BF668841.1	EST_HUMAN	602123238F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4280216 5'
3005	12241	21371	0.96	4.4E+00	BF530893.1	EST_HUMAN	602072585F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4215284 5'
3005	12241	21372	0.96	4.4E+00	BF530893.1	EST_HUMAN	602072585F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4215284 5'
6268	15448	24887	2.48	4.3E+00	Y13402.1	NT	Plasmodium falciparum R28R+var1 gene, exon 1
7438	16847	26140	8.75	4.3E+00	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5448	14874		3.45	4.2E+00	P18444	SWISSPROT	MICROSOMAL DIPEPTIDASE PRECURSOR (MDP) (DEHYDROPEPTIDASE-I) (RENAL DIPEPTIDASE) (RDP)
5988	15270	24697	1.82	4.2E+00	P13983	SWISSPROT	EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)
5988	15270	24698	1.82	4.2E+00	P13983	SWISSPROT	EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)
6757	15952	25410	8.13	4.2E+00	A1809013.1	EST_HUMAN	wf97g03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2360692 3'
6363	15343	24868	7.72	4.1E+00	O23810	SWISSPROT	YY1 PROTEIN PRECURSOR
6408	15590	25050	3.79	4.1E+00	P28984	SWISSPROT	GENE 68 PROTEIN
6409	15590	25051	3.79	4.1E+00	P28984	SWISSPROT	GENE 68 PROTEIN
6430	15027	25092	4.55	4.1E+00	U57503.1	NT	Pan troglodytes novel repetitive scd LTR element in the RNU2 locus
7482	16870		2.98	4.1E+00	P08718	SWISSPROT	HYPOTHETICAL PROTEIN HVLP1
7643	16748		15.02	4.1E+00	BE885880.1	EST_HUMAN	601507510F1 NIH_MGC_71.Homo sapiens cDNA clone IMAGE:3908051 5'
3520	12744		0.99	4.0E+00	P38228	SWISSPROT	GLC7-INTERACTING PROTEIN 1
8009	16444	25634	1.69	4.0E+00	P14546	SWISSPROT	CYTOCHROME C OXIDASE POLYPEPTIDE III
8082	17217	26751	4.02	4.0E+00	P07584	SWISSPROT	GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE GLYCOPROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5)]
8082	17217	26762	4.02	4.0E+00	P07584	SWISSPROT	GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE GLYCOPROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5)]
3477	12701	21837	4.32	3.9E+00	X64518.1	NT	N. tabacum chitinase gene 50 for class I chitinase C
4312	13513		0.93	3.9E+00	AF055468.1	NT	Mus musculus seminal vesicle secretory protein 99 (MSVSP99) gene, promoter region
5515	14740	24105	2.78	3.9E+00	BE814357.1	EST_HUMAN	MRO-BN0070-300500-028-H05 BN0070 Homo sapiens cDNA
5515	14740	24106	2.78	3.9E+00	BE814357.1	EST_HUMAN	MRO-BN0070-300500-028-H05 BN0070 Homo sapiens cDNA
6029	15237	24660	4.25	3.9E+00	P38289	SWISSPROT	HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN AIDB-RPSF INTERGENIC REGION
6238	16419	24659	3.77	3.9E+00	M23907.1	NT	Human MHC class II lymphocyte antigen (DPw4-beta-1) gene, exon 2
6568	15702	25225	2.27	3.9E+00	X65895.1	NT	X. laevis mRNA for M4 muscarinic receptor
7828	16405	25889	3.21	3.9E+00	Y18000.1	NT	Homo sapiens NF2 gene
2593	11779		1.77	3.8E+00	AE001562.1	NT	Helicobacter pylori, strain J99 section 123 of 132 of the complete genome
3998	13209	22314	12.62	3.7E+00	AL161539.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 39
7868	17148	26863	2.5	3.7E+00	BF689279.1	EST_HUMAN	602120551F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4277748 5'
7868	17148	26864	2.5	3.7E+00	BF689279.1	EST_HUMAN	602120551F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4277748 5'
8390	17471		1.73	3.7E+00	AB013746.3	NT	Gallus gallus mRNA for hypoxia-inducible factor-1 alpha, complete cds

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
600	9847	18085	3.48	3.6E+00	AV761055.1	EST_HUMAN	AV761055 MDS Homo sapiens cDNA clone MDSBUE10 5'
4812	14001		0.86	3.6E+00	AL161472.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2
6667	15862	25321	4.86	3.6E+00	AE004447.1	NT	Pseudomonas aeruginosa PA01, section 8 of 529 of the complete genome
6667	15882	25322	4.86	3.6E+00	AE004447.1	NT	Pseudomonas aeruginosa PA01, section 8 of 529 of the complete genome
7430	16840						Escherichia coli glycerophosphate dehydrogenase (gldD) gene, partial cds; and the translation start site has been verified (gldE), the translation start site has been verified (gldG), and repressor protein (gldR) genes, complete cds
3214	12448	21580	4.12	3.6E+00	M98785.1	NT	Cryptosporidium felis heat shock protein 70 (HSP70) gene, partial cds
1501	10714	18886	1.13	3.5E+00	AF221538.1	NT	Brassica napus RPBSd mRNA, complete cds
6237	15418	24858	2.55	3.4E+00	AF254577.1	NT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT
7155	16332	25815	2.38	3.4E+00	P04052	SWISSPROT	Saccharomyces cerevisiae MSS1 gene, complete cds
8063	17188	28798	3.86	3.4E+00	AF013167.1	NT	Homo sapiens D1George syndrome critical region, centromeric end
507	9769	18886	2.13	3.4E+00	L77570.1	NT	D.refio zp-50 POU gene
4004	9759	18886	1.73	3.2E+00	X08422.1	NT	D.refio zp-50 POU gene
4738	13830	23034	0.95	3.2E+00	X08422.1	NT	Homo sapiens carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein) (CEACAM1), mRNA
5491	14717	24074	1.09	3.2E+00	P12783	SWISSPROT	PHOSPHOGLYCERATE KINASE, CYTOSOLIC
5491	14717	24075	2.88	3.2E+00	P12783	SWISSPROT	PHOSPHOGLYCERATE KINASE, CYTOSOLIC
5780	15007	24410	2.88	3.2E+00	P18831	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4
5780	15007	24411	1.78	3.2E+00	P18831	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4
6405	15588	25044	1.78	3.2E+00	Y13655.1	NT	Chlamydomonas reinhardtii chloroplast DNA for rps9, ycf4, ycf3, rps18 genes
6405	15588	25045	2.63	3.2E+00	Y13655.1	NT	Chlamydomonas reinhardtii chloroplast DNA for rps9, ycf4, ycf3, rps18 genes
6773	15888		2.53	3.2E+00	P13081	SWISSPROT	PERIPLASMIC [NIFE] HYDROGENASE SMALL SUBUNIT (NIFE HYDROGENLYASE SMALL CHAIN)
7122	18268	26781	9.1	3.2E+00	AB018081.2	NT	Oryza latipes OIG88 gene for guanylyl cyclase C, complete cds
7650	18950	26348	3.21	3.2E+00	AJ23270.1	NT	Rickettsia prowazekii strain Madrid E, complete genome, segment 1/4
8350	17444		1.75	3.2E+00	L33836.1	NT	Sus scrofa choline acetyltransferase gene, promoter region
5802	14828	24202	1.83	3.2E+00	Q10135	SWISSPROT	HYPOTHETICAL 142.5 KD PROTEIN C23E2.02 IN CHROMOSOME 1
6856	15851	25309	2.1	3.1E+00	P49884	SWISSPROT	TYPE I IODOTHYRONINE DEIODINASE (TYPE-I 5DEIODINASE) (DIOI) (TYPE 1 DI) (SDI)
6856	15851	25310	4.85	3.1E+00	P49884	SWISSPROT	TYPE I IODOTHYRONINE DEIODINASE (TYPE-I 5DEIODINASE) (DIOI) (TYPE 1 DI) (SDI)
6842	16047		4.85	3.1E+00		SWISSPROT	GLUTAMATE (NMDA) RECEPTOR SUBUNIT EPSILON 3 PRECURSOR (N-METHYL D-ASPARTATE RECEPTOR SUBTYPE 2C) (NR2C) (NMDAR2C)
7178	16355	25833	3.67	3.1E+00	Q14957	SWISSPROT	DEOXYHYPPUSINE SYNTHASE (DHS)

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Table 4
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7899	18434					SWISSPROT	GENOME POLYPROTEIN (CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE PROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5))
8016	17155		2.92	3.1E+00	P33515	NT	retinoid acid nuclear receptor isoform beta 2 [mice, embryonal carcinoma cell line, PCC7-MZ1, mRNA, 2871 nt]
8144	15328		3.7	3.1E+00	S56860.1	NT	
7241	16481	25850	12.2	3.0E+00	P18408	SWISSPROT	CYR61 PROTEIN PRECURSOR (SCH61)
			1.7	3.0E+00	Q16181	SWISSPROT	GDC10 PROTEIN HOMOLOG
7578	16784	26277				SWISSPROT	RETINAL GUANYLYL CYCLASE 2 PRECURSOR (GUANYLATE CYCLASE 2F, RETINAL) (RETGC-2)
			6.87	3.0E+00	P51842	SWISSPROT	(ROD OUTER SEGMENT MEMBRANE GUANYLATE CYCLASE 2) (ROS-GC2) (GUANYLATE CYCLASE F) (GC-F)
7579	16784	26278				SWISSPROT	RETINAL GUANYLYL CYCLASE 2 PRECURSOR (GUANYLATE CYCLASE 2F, RETINAL) (RETGC-2)
1978	11193	20391	6.87	3.0E+00	P51842	SWISSPROT	(ROD OUTER SEGMENT MEMBRANE GUANYLATE CYCLASE 2) (ROS-GC2) (GUANYLATE CYCLASE F) (GC-F)
8048	15214	24634	2.21	2.8E+00	AE002225.2	NT	Chlamydia pneumoniae AR39, section 53 of 84 of the complete genome
6170	15352	24788	1.71	2.8E+00	Z38878.1	NT	F. pringeli gdcPA gene for P-protein of the glycine cleavage system
6170	15352	24780	4.54	2.8E+00	O14514	SWISSPROT	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 1 PRECURSOR
6279	15459	24900	4.54	2.8E+00	O14514	SWISSPROT	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 1 PRECURSOR
1458	10688	18842	5.32	2.8E+00	P46589	SWISSPROT	ADHERENCE FACTOR (ADHESION AND AGGREGATION MEDIATING SURFACE ANTIGEN)
1610	10823		4.19	2.8E+00	AF186398.1	NT	Buxus harlandii maturase K (matK) gene, partial cds; chloroplast gene for chloroplast product
6210	15391	24835	2.03	2.8E+00	AL161552.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 52
238	9516	18843	4.9	2.8E+00	8393724	NT	Mus musculus endomucin (LOC53423), mRNA
238	9516	18844	13.15	2.7E+00	6878308	NT	Mus musculus per-hexamer repeat gene 3 (Phx3), mRNA
5487	14893	24048	13.15	2.7E+00	6878308	NT	Mus musculus per-hexamer repeat gene 3 (Phx3), mRNA
4677	13871	22870	1.84	2.7E+00	L14005.1	NT	Homo sapiens apoA polymorphism Kringle IV gene, exons 1 and 2
5465	14891	24043	5.08	2.8E+00	AF068749.1	NT	Mus musculus sphingosine kinase (SPHK1b) mRNA, complete cds
5465	14891	24044	2.01	2.8E+00	8755601	NT	Mus musculus SRY-box containing gene 13 (Sxr13), mRNA
5682	14808		2.01	2.8E+00	8755601	NT	Mus musculus SRY-box containing gene 13 (Sxr13), mRNA
			2.38	2.8E+00	Y17082.1	NT	Mycobacterium fortuitum furA II gene
8378	15558					NT	
6980	16158	25830	5.52	2.6E+00	AF235502.1	NT	Mus musculus SH2-containing inositol 5-phosphatase (Ship) gene, exons 16 through 27, and complete cds
7597	18900	26282	2.9	2.6E+00	AL161540.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 40
9012	18284		1.74	2.6E+00	AF143675.1	NT	Hantavirus Z10 segment M G1/G2 glycoprotein (Z10) gene, complete cds
1460	10873	19845	2.67	2.6E+00	11419220	NT	Homo sapiens ATP-binding cassette, sub-family B (MDR/TAP), member 4 (ABCB4), mRNA
			2.95	2.5E+00	AJ271844.1	NT	Aspergillus nidulans recQ gene for DNA helicase, exons 1-4

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1460	10673	19846	2.65	2.5E+00	AJ271844.1	NT	Aspergillus nidulans recQ gene for DNA helicase, exons 1-4
5576	14802	24174	2.14	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
5578	14802	24175	2.14	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
8347	17442		2.33	2.5E+00	AF286685.1	NT	Mus musculus EIF4H gene, partial cds; LIMK1 gene, complete cds; and ELN gene, partial cds
2976	12212	21350	1.68	2.4E+00	M24282.1	NT	Chicken alpha-3 collagen type VI mRNA, 3' end
4928	14116	23212	7.8	2.4E+00	4503352	NT	Homo sapiens double C2-like domains, alpha (DOC2A) mRNA
5660	14883	24271	4.18	2.4E+00	P02843	SWISSPROT	VITELLOGENIN I PRECURSOR (YOLK PROTEIN 1)
6532	16728		2.7	2.4E+00	AE001486.1	NT	Helicobacter pylori, strain J99 section 47 of 132 of the complete genome
6728	15923	25382	12.85	2.4E+00	P24081	SWISSPROT	ENDOCHITINASE B PRECURSOR (CHN-B)
7149	16326		6.73	2.4E+00	P09099	SWISSPROT	XYLULOSE KINASE (XYLULOSE KINASE)
7176	16362	26829	2.32	2.4E+00	BE326702.1	EST_HUMAN	hr03f08.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3133187 3'
7175	16352	25830	2.32	2.4E+00	BE326702.1	EST_HUMAN	hr03f08.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3133187 3'
7645	16845	26343	1.81	2.4E+00	Y14078.1	NT	Bacillus subtilis chromosomal DNA, region 75 degrees: glpPKD operon and downstream
7688	17114	26846	2.65	2.4E+00	AF158652.2	NT	Frederia x ananassa cytosolic ascorbate peroxidase (ApxSC) gene, ApxSC-c allele, complete cds
1260	10475	19837	10.92	2.3E+00	Z48724.1	NT	G. domesticus artificial single chain antibody gene (L3)
4101	13308		1.51	2.3E+00	AJ401081.1	NT	Bos taurus partial cytb gene for cytochrome b
5264	14437	23511	2.26	2.3E+00	U12024.1	NT	Aplysia mexicanus green opsin gene (g101) gene, complete cds
6277	15437	24888	2.33	2.3E+00	6978554	NT	Rattus norvegicus ATPase, Ca++ transporting, ubiquitous (Atp2a3), mRNA
6330	16386		3.14	2.3E+00	P07199	SWISSPROT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)
7380	16596	26083	1.72	2.3E+00	Q07076	SWISSPROT	ANNEXIN VII (SYNEXIN)
8247	17376	26910	2.87	2.3E+00	BF541987.1	EST_HUMAN	602069121F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4068173 5'
8247	17376	26911	2.87	2.3E+00	BF541987.1	EST_HUMAN	602069121F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4068173 5'
8579	17594	24002	4.79	2.3E+00	BE805237.1	EST_HUMAN	601433673F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918843 5'
3983	13207	22313	0.85	2.2E+00	AF020528.1	NT	Magnaporthe grisea Class IV chitin synthase (chs4) gene, complete cds
4302	13503	22588	3.87	2.2E+00	D67071.1	NT	Rat gene for regucalcin, exon1 (non-coding exon)
4302	13503	22600	3.87	2.2E+00	D67071.1	NT	Rat gene for regucalcin, exon1 (non-coding exon)
5360	14560	23687	10.24	2.2E+00	O88307	SWISSPROT	SORTLIN-RELATED RECEPTOR PRECURSOR (SORTING PROTEIN-RELATED RECEPTOR CONTAINING LDLR CLASS A REPEATS) (SORLA-1) (LOW-DENSITY LIPOPROTEIN RECEPTOR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LDLR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LR11) (>

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
							SORTILIN-RELATED RECEPTOR PRECURSOR (SORTING PROTEIN-RELATED RECEPTOR CONTAINING LDLR CLASS A REPEATS) (MSORLA-1) (SORLA-1) (LOW-DENSITY LIPOPROTEIN RECEPTOR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LDLR RELATIVE WITH 11 LIGAND- BINDING REPEATS) (LR11) (>
5380	14590	23668	10.24	2.2E+00	O88307	SWISSPROT	
5695	14915	24308	9.16	2.2E+00	BE250383.1	EST_HUMAN	600943401T1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2959777 3'
5816	15032	24433	4.17	2.2E+00	Q00335	SWISSPROT	MINOR VIRION STRUCTURAL PROTEIN MU-2
5832	15148	24558	2.98	2.2E+00	P51469	SWISSPROT	INSULIN-LIKE GROWTH FACTOR II PRECURSOR (IGF-II) (SOMATOMEDIN A)
6067	14514		3.74	2.2E+00	AA584574.1	EST_HUMAN	n85802.s1 NCI_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1058379 3'
6338	15518	24968	16.61	2.2E+00	AA449012.1	EST_HUMAN	z005g10.f1 Soares_t01a_fetus_Nb2HF8_9v Homo sapiens cDNA clone IMAGE:785634 5'
6884	16054		19.68	2.2E+00	BE741878.1	EST_HUMAN	601594733F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948581 5'
6946	18076		2.79	2.2E+00	Q04708	SWISSPROT	TRANSPONSON TY1 PROTEIN A
7080	16287	25743	2.51	2.2E+00	AI290373.1	EST_HUMAN	qmr68b03.x1 Soares_placenta_8to8weeks_2NBHP81d9W Homo sapiens cDNA clone IMAGE:1893985 3' similar to gb:Y00433 GLUTATHIONE PEROXIDASE (HUMAN);
7090	18287	25744	2.51	2.2E+00	AI290373.1	EST_HUMAN	qmr68b03.x1 Soares_placenta_8to8weeks_2NBHP81d9W Homo sapiens cDNA clone IMAGE:1893985 3'
7109	16286	25767	2.44	2.2E+00	BF248782.1	EST_HUMAN	similar to gb:Y00433 GLUTATHIONE PEROXIDASE (HUMAN);
7200	16377	25858	3.22	2.2E+00	AF183416.1	NT	601855501F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075391 5'
7977	18412	25898	4.63	2.2E+00	P07911	SWISSPROT	Homo sapiens ovarian granulosa cell 13.0 kDa protein hGR74 homolog mRNA, complete cds
8138	17271	26816	4.81	2.2E+00	P10407	SWISSPROT	UROMODULIN PRECURSOR (TAMM-HORSFALL URINARY GLYCOPROTEIN) (THP)
576	11971	18945	8.07	2.1E+00	AF132612.2	NT	EARLY E1A 28 KD PROTEIN
2878	12216	21351	1.88	2.1E+00	AF209532.1	NT	Mus musculus pre-1 cell receptor alpha gene, enhancer region and upstream region
3565	12788		1.24	2.1E+00	AW448368.1	EST_HUMAN	Homo sapiens fatty acid omega-hydroxylase CYP4A11 (CYP4A11) gene, complete cds
6000	15282	24715	3.28	2.1E+00	O70169	SWISSPROT	UIH-B13-ald-e-08-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2734550 3'
6103	15197	24615	5.28	2.1E+00	N28575.1	EST_HUMAN	ALPHA-2-HS-GLYCOPROTEIN PRECURSOR (FETUIN-A)
1204	10423	19578	1.81	2.0E+00	AF180527.1	NT	yy08a10.s1 Soares_melanocyte_2NBHM Homo sapiens cDNA clone IMAGE:270818 3' similar to gb:M56654
1204	10423	19578	1.81	2.0E+00	AF180527.1	NT	TRANSCRIPTION INITIATION FACTOR TFIIID (HUMAN);
1343	10557	19723	0.84	2.0E+00	AF204927.1	NT	Homo sapiens p22Dokdel (DOKDEL) mRNA, complete cds
1554	10788		2.32	2.0E+00	P25582	SWISSPROT	Homo sapiens p22Dokdel (DOKDEL) mRNA, complete cds
2117	11316	20533	8.65	2.0E+00	Z78279.1	NT	Oryctolagus cuniculus Na ⁺ /K ⁺ -ATPase beta 1 subunit mRNA, complete cds
2117	11316	20534	8.65	2.0E+00	Z78279.1	NT	PUTATIVE RRNA METHYLTRANSFERASE SPB1
4078	13288	22386	1.88	2.0E+00	AW664498.1	EST_HUMAN	R.norvegicus mRNA for collagen alpha1 type I R.norvegicus mRNA for collagen alpha1 type I H13c05.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2972168 3' similar to gb:X01677 GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER (HUMAN);

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Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4078	13288	22387	1.88	2.0E+00	AW684498.1	EST_HUMAN	NI13c05.x1 NC1 CGAP_GU1 Homo sapiens cDNA clone IMAGE:2972188 3' similar to gb:U01877
6472	15669	25138	6.44	2.0E+00	AB0008676.1	NT	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER (HUMAN);
6472	15669	25139	6.44	2.0E+00	AB0008676.1	NT	Escherichia coli 0157 DNA, map position at 48 min., complete cds
6472	15669	25140	6.44	2.0E+00	AB0008676.1	NT	Escherichia coli 0157 DNA, map position at 48 min., complete cds
6752	15947	25405	5.02	2.0E+00	F31500.1	EST_HUMAN	Escherichia coli 0157 DNA, map position at 48 min., complete cds
8824	19222	23694	6.36	2.0E+00	5834843	NT	HSPD22703 HM3 Homo sapiens cDNA clone s4000117B08
5489	14716	24071	4.78	1.9E+00	6764389	NT	Gallus gallus mitochondrion, complete genome
5489	14715	24072	4.78	1.9E+00	6764389	NT	Mus musculus Inositol 1,4,5-trisphosphate receptor 1 (Itp1), mRNA
5978	15183		2.35	1.8E+00	Q63627	SWISSPROT	Mus musculus Inositol 1,4,5-trisphosphate receptor 1 (Itp1), mRNA
6817	15813	25271	2.81	1.8E+00	P02467	SWISSPROT	CTD-BINDING SR-LIKE PROTEIN RA4
6817	15813	25272	2.81	1.8E+00	P02467	SWISSPROT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
6672	15867		2.81	1.8E+00	BF360206.1	EST_HUMAN	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
3058	12294	21419	2.04	1.8E+00	P21004	SWISSPROT	CM3-MT0114-010800-323-H12 MT0114 Homo sapiens cDNA
3084	12320	21441	2.26	1.8E+00	U04356.1	NT	PROTEIN B8 PRECURSOR
3084	12320	21442	2.26	1.8E+00	U04356.1	NT	Synechococcus sp. PCC7942 copper transporting P-ATPase (ctaA) and ATP synthase epsilon subunit (atpE) genes, complete cds
5589	14823		1.78	1.8E+00	P18502	SWISSPROT	Synechococcus sp. PCC7942 copper transporting P-ATPase (ctaA) and ATP synthase epsilon subunit (atpE) genes, complete cds
5708	14928	24323	1.93	1.8E+00	BF311898.1	EST_HUMAN	HEDGEHOG RECEPTOR (PATCHED PROTEIN)
8733	15928	25387	3.27	1.8E+00	O43281	SWISSPROT	601897854F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4127384 5'
7163	16340		2.67	1.8E+00	AF111849.1	NT	EMBRYONAL FYN-ASSOCIATED SUBSTRATE (HEFS)
8709	18195		5.08	1.8E+00	AF314254.1	NT	Homo sapiens PRO0530 mRNA, complete cds
8782	17718		3.48	1.8E+00	9508404	NT	Chlamydomonas reinhardtii alternative oxidase 1 (AOX1) gene, nuclear gene encoding mitochondrial protein
9100	18095	23803	1.32	1.8E+00	BF212412.1	EST_HUMAN	Rattus norvegicus Actin-related protein complex 1b (ArpC1b), mRNA
9285	18043		1.45	1.8E+00	BF316805.1	EST_HUMAN	601813714F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4048251 5'
1116	10340	19480	2.08	1.7E+00	Q60114	SWISSPROT	601803309F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4135588 5'
2238	11431	20658	2.48	1.7E+00	AL183280.2	NT	LEVANSUCRASE (BETA-D-FRUCTOFURANOSYL TRANSFERASE) (SUCROSE 6-FRUCTOSYL TRANSFERASE)
2340	11633	20758	2.43	1.7E+00	AI141087.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C080
5665	14887	24277	3.48	1.7E+00	Q81TR8	SWISSPROT	oz43105.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1678137 3'
6817	18074	25476	3.98	1.7E+00	O60479	SWISSPROT	COUP TRANSCRIPTION FACTOR 1 (COUP-TF1) (COUP-TF1)
6817	18074	25477	3.98	1.7E+00	O60479	SWISSPROT	HOMEBOX PROTEIN DLX-3
							HOMEBOX PROTEIN DLX-3

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8124	17268	28800	2.25	1.7E+00	W22424.1	EST_HUMAN	87B7 Human retina cDNA Tsp5081-cleaved sublibrary Homo sapiens cDNA not directional
8860	17637	23975	1.61	1.7E+00	AI878443.1	EST_HUMAN	U82407.x1 NCJ_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2257549 3' similar to contains MSR1.11 MSR1 repetitive element;
9178	17689	23857	2.33	1.7E+00	AI198573.1	EST_HUMAN	qf50b01.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1753417 3' similar to contains L1.11 L1 repetitive element;
2002	11205	20416	14.44	1.6E+00	AF198339.1	NT	Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds
2010	11213	20422	3.58	1.6E+00	AF077374.1	NT	Homo sapiens small proline-rich protein (SPRR3) gene, exons 1, 2, and 3 and complete cds
2016	11218	20427	1.35	1.6E+00	Y11344.1	NT	Mus musculus ST6GalNAcIII gene, exon 2
2248	11443		1.07	1.6E+00	X98373.1	NT	B.napus gene encoding endo-polygalacturonase
2815	12153	21288	1.34	1.6E+00	W58426.1	EST_HUMAN	zd25f01.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:341689 5' similar to gb:D29805 N-ACETYLLACTOSAMINE SYNTHASE (HUMAN);
4009	13221		6.38	1.6E+00	BF570077.1	EST_HUMAN	602186085T1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4310591 3'
4345	13547	22838	1.87	1.6E+00	AF15827.1	NT	Homo sapiens proliferation-associated SNF2-like protein (SMARCA6) mRNA, complete cds
4345	13547	22839	1.87	1.6E+00	AF15827.1	NT	Homo sapiens proliferation-associated SNF2-like protein (SMARCA6) mRNA, complete cds
5027	14212	23285	0.63	1.6E+00	AF075394.1	NT	Uroaethis chinensis cytochrome c oxidase subunit I (COI) gene, mitochondrial gene encoding mitochondrial protein, partial cds
5027	14212	23298	0.63	1.6E+00	AF075394.1	NT	Uroaethis chinensis cytochrome c oxidase subunit I (COI) gene, mitochondrial gene encoding mitochondrial protein, partial cds
5113	14293	23380	1.98	1.6E+00	Y11344.1	NT	Mus musculus ST6GalNAcIII gene, exon 2
5113	14293	23381	1.98	1.6E+00	Y11344.1	NT	Mus musculus ST6GalNAcIII gene, exon 2
5583	14807	24180	2.43	1.6E+00	LD4808.1	NT	Brachydanio rerio MHC class II DA-beta-2701 gene, 3' end
6182	15364	24804	2.64	1.6E+00	BE697267.1	EST_HUMAN	RC0-CT0415-200700-032-ct10 CT0415 Homo sapiens cDNA
6590	15786	25245	3.83	1.6E+00	AJ297131.1	NT	Mus musculus S1L, MAP_17, CYP_a, SCL & CYP_b genes
7420	14846	24227	6.93	1.6E+00	AF005631.1	NT	Homo sapiens transglutaminase type I (Tgase1) gene, promoter region
8197	17329	26871	3.2	1.6E+00	AF104313.1	NT	Homo sapiens unknown mRNA
9221	18000		1.43	1.6E+00	AF784043.1	EST_HUMAN	AV784043 MDS Homo sapiens cDNA clone MDSDAH08 5'
34	9330	18435	5.48	1.6E+00	U53449.1	NT	Rattus norvegicus Jun dimerization protein 2 (Jdp-2) mRNA, complete cds
237	9518	18845	2.45	1.6E+00	AE002201.2	NT	Chlamydomonas reinhardtii section 32 of 94 of the complete genome
627	9872		1.95	1.5E+00	6752981	NT	Mus musculus a disintegrin and metalloprotease domain (ADAM) 15 (metagardin) (Adam15), mRNA
1882	11089	20280	3.71	1.5E+00	AF275265.1	NT	Mus musculus receptor protein tyrosine phosphatase-rho (Ptptr) gene, exons 10 and 11 and partial cds
2373	11563	20787	2.08	1.5E+00	AJ131402.1	NT	Poliovirus A RNA complete genome, isolate U
2481	11671	20889	1.63	1.5E+00	6678350	NT	Mus musculus T-cell lymphoma invasion and metastasis 1 (Tiam1), mRNA

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Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3103	11568	20787	1.67	1.5E+00	AJ131402.1	NT	Potato virus A RNA complete genome, isolate U
3353	12581	21721	0.82	1.5E+00	AE001945.1	NT	Dainococcus radiodurans R1 section 82 of 228 of the complete chromosome 1
5828	15048	24450	2.76	1.5E+00	R17878.1	EST_HUMAN	Y910a02.r1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:31693 6'
6148	15332	24788	18.58	1.5E+00	P47179	SWISSPROT	HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR
6148	15332	24788	18.58	1.5E+00	P47179	SWISSPROT	HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR
7028	16203	25680	11.13	1.5E+00	BF376754.1	EST_HUMAN	RCO-TN0078-150800-034-g05 TN0078 Homo sapiens cDNA
7132	16309	25780	3.83	1.5E+00	AA017689.1	EST_HUMAN	z638g06.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:381308 5'
7132	16309	25791	3.83	1.5E+00	AA017689.1	EST_HUMAN	z638g06.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:381308 5'
7937	17077	26605	4.16	1.5E+00	AL134187.1	EST_HUMAN	DKFZp547P243 s1 547 (synonym: hfbt1) Homo sapiens cDNA clone DKFZp547P243 3'
8074	17209		8.7	1.5E+00	X07380.1	NT	Maize mitochondrial rRNA-Ser gene and rRNA-Phe pseudogene
8494	17537		1.33	1.5E+00	G753287	NT	Mus musculus caspase 8 associated protein 2 (Casp8ap2), mRNA
8653	18290	23687	1.24	1.5E+00	D63480.1	NT	Human mRNA for KIAA0146 gene, partial cds
8885	17780		3.71	1.5E+00	AL445085.1	NT	Thermoplasma acidophilum complete genome; segment 3/5
8888	17852		1.25	1.5E+00	6978492	NT	Rattus norvegicus 5 - Lipoygenase (Aloc5), mRNA
31	9327	18431	1.22	1.4E+00	7661685	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
31	9327	18432	1.22	1.4E+00	7661685	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
1711	10923	20108	1.26	1.4E+00	H19859.1	EST_HUMAN	y657e03.r1 Soares adult brain N2b5H55Y Homo sapiens cDNA clone IMAGE:172540 5'
2242	11437		1.38	1.4E+00	AF053357.1	NT	Helicobacter pylori glutamine synthetase (gluA) gene, complete cds
2302	11496		9.69	1.4E+00	U67822.1	NT	Ovis aries prion protein gene, complete cds
2629	11812	21030	1.38	1.4E+00	X74463.1	NT	Human papillomavirus type 7 genomic DNA
2728	11808	21122	2.38	1.4E+00	AF064564.2	NT	Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds
2729	11908	21123	2.38	1.4E+00	AF064564.2	NT	Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds
4243	13446	22538	1.72	1.4E+00	AW800455.1	EST_HUMAN	CMO-NN1005-140300-288-h06 NN1005 Homo sapiens cDNA
4243	13446	22537	1.72	1.4E+00	AW800455.1	EST_HUMAN	CMO-NN1005-140300-288-h06 NN1005 Homo sapiens cDNA
4557	12273	21401	1.2	1.4E+00	AE002324.2	NT	Chlamydia muridarum, section 65 of 85 of the complete genome
4557	12273	21402	1.2	1.4E+00	AE002324.2	NT	Chlamydia muridarum, section 65 of 85 of the complete genome
4584	13778		1.41	1.4E+00	BF081547.1	EST_HUMAN	602156887F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4297596 5'
5455	14681		5.68	1.4E+00	AB032083.1	NT	Homo sapiens mRNA for KIAA1157 protein, partial cds
5780	14988	24400	2.74	1.4E+00	Q13472	SWISSPROT	DNA TOPOISOMERASE III ALPHA
5784	18387		4.59	1.4E+00	AB020712.1	NT	Homo sapiens mRNA for KIAA0805 protein, complete cds
5832	15049	24454	2.62	1.4E+00	Q92777	SWISSPROT	SYNAPSIN II
5832	15049	24455	2.62	1.4E+00	Q92777	SWISSPROT	SYNAPSIN II

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6203	15384	24828	2.21	1.4E+00	AJ193289.1	NT	Homo sapiens caveolin-1/2 locus, Contig1, D7S522, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2)
6715	15910		8.09	1.4E+00	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
6827	16021	25487	5.92	1.4E+00	BE084687.1	EST_HUMAN	RC1-BT0313-301289-012-f05 BT0313 Homo sapiens cDNA
7637	16837	26333	2.22	1.4E+00	AA195528.1	EST_HUMAN	z36609.r1 Soares NIH-MP_u_S1 Homo sapiens cDNA clone IMAGE:865512 5' similar to contains element MER22 repetitive element;
7778	16973	26486	6.19	1.4E+00	AB006882.1	NT	Homo sapiens APECED mRNA for AIRE-1, complete cds
7943	17083	26811	3.76	1.4E+00	BE082107.2	EST_HUMAN	601655184R1 NIH_MGC 85 Homo sapiens cDNA clone IMAGE:3945805 3'
7943	17083	26612	3.76	1.4E+00	BE082107.2	EST_HUMAN	601655184R1 NIH_MGC 85 Homo sapiens cDNA clone IMAGE:3945805 3'
7965	17144	26877	2.89	1.4E+00	U30760.1	NT	Pneumocystis carinii f. sp. ratti guanine nucleotide binding protein alpha subunit (pcg1) gene, complete cds
7965	17144	26878	2.89	1.4E+00	U30760.1	NT	Pneumocystis carinii f. sp. ratti guanine nucleotide binding protein alpha subunit (pcg1) gene, complete cds
8491	18214		1.9	1.4E+00	AL101800.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 12
8999	18382		1.27	1.4E+00	11545838	NT	Homo sapiens cutaneous T-cell lymphoma tumor antigen sa70-2 (SE70-2), mRNA
9287	18033		1.22	1.4E+00	AF224668.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
577	9828		1.79	1.3E+00	Z73840.1	NT	M. mucedo gene encoding 4-Dihydroxyethyl-trispartate dehydrogenase
912	10147	16308	2.87	1.3E+00	AJ271192.1	NT	Cantharellus sp. partial 26S rRNA gene, isolate Tibet
1137	10360		17.3	1.3E+00	Y19213.1	NT	Homo sapiens putative psithHBA pseudogene for hair keratin, exons 2 to 7
1304	10520	19378	11.63	1.3E+00	4507998	NT	Homo sapiens zinc finger protein 157 (HZF22) (ZNF157) mRNA
1304	10520	19380	11.63	1.3E+00	4507998	NT	Homo sapiens zinc finger protein 157 (HZF22) (ZNF157) mRNA
1384	10579		0.94	1.3E+00	U61730.2	NT	Cox laetyma-fobi dihydrodipicolinate synthase (dapA) gene, complete cds
1589	10802		1.91	1.3E+00	AE002338.2	NT	Chlamydia muridarum, section 68 of 85 of the complete genome
2515	11704		1.76	1.3E+00	BE08735.2	EST_HUMAN	601681233R1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3915845 3'
2890	12127	21260	0.62	1.3E+00	6755621	NT	Mus musculus alpha-spectrin 1, erythrocyte (Spna1), mRNA
3575	12788	21924	0.65	1.3E+00	AF018494.1	NT	Fugu rubripes gamma-aminobutyric acid receptor beta subunit gene, partial cds; 55kd erythrocyte membrane protein (P55), synaptic vesicle-associated integral membrane protein (VAMP-1), procollagen C-proteinase enhancer protein (PCOLCE) genes, complete c-
5686	14888	24278	9.72	1.3E+00	AW362834.1	EST_HUMAN	PMO-CT0288-291189-004-f08 CT0288 Homo sapiens cDNA
5686	14888	24279	9.72	1.3E+00	AW362834.1	EST_HUMAN	PMO-CT0288-291189-004-f08 CT0288 Homo sapiens cDNA
6569	15756	26218	2.2	1.3E+00	AJ009912.1	NT	Sus scrofa plp gene
6819	16112		3.29	1.3E+00	AF042084.1	NT	Homo sapiens heparan glucosaminyl N-deacetylase/N-sulfotransferase-2 gene, complete cds
6924	16117	25582	2.21	1.3E+00	X72019.1	NT	S. alba phr-1 mRNA for photolyase

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6924	16117	25583	2.21	1.3E+00	X72019.1	NT	S. alba pfr-1 mRNA for photolase
6982	16160	25631	2.37	1.3E+00	O00754	SWISSPROT	LYSOSOMAL ALPHA-MANNOSIDASE PRECURSOR (MANNOSIDASE, ALPHA B) (LYSOSOMAL ACID ALPHA-MANNOSIDASE) (LAMAN)
7028	16205	25682	5.79	1.3E+00	BE963379.2	EST_HUMAN	601657145R1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3868195 3'
7284	16503		4.82	1.3E+00	Q14117	SWISSPROT	DIHYDROPYRIMIDINASE (DHPASE)(HYDANTOINASE)(DHP)
7480	16888	26170	2.44	1.3E+00	P25289	SWISSPROT	MRNA 3'-END PROCESSING PROTEIN RNA15
7501	16708	26195	2.28	1.3E+00	Z18892.2	NT	Mus musculus desmin gene
8072	17207	26740	3.07	1.3E+00	D42042.1	NT	Human mRNA for KIAA0085 gene, partial cds
8144	17276	26820	2.63	1.3E+00	Z98882.1	NT	Bacillus subtilis genomic DNA 23.8kb fragment
8639	17627		2.58	1.3E+00	AF187873.1	NT	Cavia porcellus inwardly-rectifying potassium channel Kir2.2 (KCNJ12) gene, complete cds
8821	17738	23930	4.23	1.3E+00	BF348043.1	EST_HUMAN	602023185F1 NCI_CGAP_Brn87 Homo sapiens cDNA clone IMAGE:4159452 5'
8833	18108		2.07	1.3E+00	P33484	SWISSPROT	E1 GLYCOPROTEIN PRECURSOR (MATRIX GLYCOPROTEIN) (MEMBRANE GLYCOPROTEIN)
8832	17814		1.4	1.3E+00	AF187035.1	NT	Stumtia lilium cytochrome b gene, complete cds; mitochondrial gene for mitochondrial product
656	8902	18028	8.38	1.2E+00	AA076246.1	EST_HUMAN	z12x08.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:431635 3'
833	10071	19228	1.12	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
833	10071	19227	1.12	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
833	10071	19228	1.12	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
888	10123		1.52	1.2E+00	8924234	NT	Homo sapiens hypothetical protein PRO3077 (PRO3077), mRNA
1169	10390	19542	3.71	1.2E+00	AF080245.2	NT	Elea clifera sesquiterpene synthase mRNA, complete cds
1213	10431	19587	1.74	1.2E+00	AJ252242.1	NT	pea seed-borne mosaic virus complete genome
1213	10431	19588	1.74	1.2E+00	AJ252242.1	NT	pea seed-borne mosaic virus complete genome
1878	11182	20390	1	1.2E+00	AF140631.1	NT	Homo sapiens G-protein coupled receptor 14 (GPR14) gene, complete cds
3074	12310	21431	1.07	1.2E+00	AB020881.1	NT	Homo sapiens mRNA for KIAA0874 protein, partial cds
3120	12384	21494	6.74	1.2E+00	AL161563.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
3120	12384	21495	6.74	1.2E+00	AL161563.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
3254	12487		2.72	1.2E+00	P54910	SWISSPROT	CONJUGAL TRANSFER PROTEIN TRBE PRECURSOR
3331	12560	21698	0.68	1.2E+00	AF188740.1	NT	Homo sapiens LHX3 gene, intron 2
3693	12813	22031	7.58	1.2E+00	U75902.1	NT	Mus musculus subtilisin-like serine protease LPC (PC7) gene, exons 1 to 9, partial cds
3864	13178	22282	2.14	1.2E+00	BF373570.1	EST_HUMAN	MR0-F70175-050900-203-g06_1 FT0175 Homo sapiens cDNA
4268	12560	21698	1.04	1.2E+00	AF188740.1	NT	Homo sapiens LHX3 gene, intron 2
4487	13685		2.05	1.2E+00	M87060.1	NT	Rattus rattus cardiac AEs3 gene, exons 1-23
4559	13763	22851	1.8	1.2E+00	AF156495.1	NT	Homo sapiens post-synaptic density 95 (DLG4) gene, complete cds
4587	13781		6.87	1.2E+00	Y09200.1	NT	T. pinnaatum chloroplast rbcL gene, partial
5468	14695	24048	2.08	1.2E+00	AW813278.1	EST_HUMAN	MR3-ST0191-140200-013-c05 ST0191 Homo sapiens cDNA

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Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5734	14953	24351	2.6	1.2E+00	X74886.1	NT	D.hydrel av1 repeat cluster DNA, fragment D
5758	14977	24378	4.03	1.2E+00	BE003113.1	EST_HUMAN	QV4-BN0080-270400-180-a03 BN0080 Homo sapiens cDNA
5804	15021	24422	37.27	1.2E+00	AA759254.1	EST_HUMAN	sh84g12.81 Scores_NHT Homo sapiens cDNA clone 1322374 3'
5877	15094	24508	2.08	1.2E+00	AW813276.1	EST_HUMAN	MR3-ST0161-140200-013-c05 ST0161 Homo sapiens cDNA
6055	15223	24642	2.84	1.2E+00	AJ002141.1	NT	Mus musculus DSPP gene
6356	15536	24890	2.81	1.2E+00	X74207.1	NT	L.lactis pyrD and pyrF genes
6844	15839	25290	5.07	1.2E+00	AB033030.1	NT	Homo sapiens mRNA for KIAA1204 protein, partial cds
6772	15987	25425	2.49	1.2E+00	AW377210.1	EST_HUMAN	MR2-CT0222-201089-001-e07 CT0222 Homo sapiens cDNA
6876	16087	25536	2.56	1.2E+00	Z32850.1	NT	R.communis gene for pyrophosphate-dependent phosphofructokinase beta subunit
6865	16143	25612	2.48	1.2E+00	D11745.1	EST_HUMAN	H.humaniM01A01 Liver HepG2 cell line. Homo sapiens cDNA clone hm01a01
7048	16226	25700	4.49	1.2E+00	X58832.1	NT	H.sapiens ENO3 gene for muscle specific endase
7886	17102	26633	2.36	1.2E+00	AW817817.1	EST_HUMAN	PM0-ST0264-181189-001-d01 ST0264 Homo sapiens cDNA
7923	17198		5.4	1.2E+00	BE160781.1	EST_HUMAN	PM1-HT0422-180200-007-g10 HT0422 Homo sapiens cDNA
7862	16427	25914	3.52	1.2E+00	U50147.1	NT	Rattus norvegicus synapse-associated protein 102 mRNA, complete cds
8605	18185	23757	20.83	1.2E+00	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
8825	17818		2.04	1.2E+00	AP001515.1	NT	Bacillus halodurans genomic DNA, section B14
470	9723	18864	1.47	1.1E+00	D66980.1	NT	Human mRNA for KIAA0227 gene, partial cds
1733	10846	20128	2.18	1.1E+00	AW985383.1	EST_HUMAN	QV0-BN0042-170300-163-g12 BN0042 Homo sapiens cDNA
3303	12534	21668	8.21	1.1E+00	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
3303	12634	21667	8.21	1.1E+00	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
3461	12686	21822	0.85	1.1E+00	8922841	NT	Homo sapiens hypothetical protein FLJ10749 (FLJ10749), mRNA
3555	12778	21907	1.18	1.1E+00	AI808380.1	EST_HUMAN	wf54h11.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2359481 3' similar to SW:P531_HUMAN Q12888 PES-BINDING PROTEIN 53BP1;
3689	12919	22038	1.52	1.1E+00	AE003886.1	NT	Xylella fastidiosa, section 32 of 228 of the complete genome
3698	12919	22037	1.52	1.1E+00	AE003886.1	NT	Xylella fastidiosa, section 32 of 228 of the complete genome
3807	13025		0.75	1.1E+00	X85374.1	NT	H.parahaemolyticus hphIM(A), hphIM(C), hphIR and menB genes
3919	13135	22252	1.03	1.1E+00	8922841	NT	Homo sapiens hypothetical protein FLJ10749 (FLJ10749), mRNA
3997	13210	22315	0.89	1.1E+00	8795205	NT	Mus musculus proteasome (prosome, macropain) subunit, beta type 7 (PsmB7), mRNA
4188	13402		7.67	1.1E+00	5835331	NT	R.uniformis complete mitochondrial genome
4688	13880		1.08	1.1E+00	U34992.1	NT	Carcharias plumbeus Ig lambda light chain gene, complete cds
5016	14203	23280	3.61	1.1E+00	U18486.1	NT	African swine fever virus, complete genome
5102	14282	23367	1.13	1.1E+00	X78425.1	NT	E.faecalis pbp5 gene
5251	14424	23501	0.82	1.1E+00	P25398	SWISSPROT	TELLURITE RESISTANCE PROTEIN TEHA
5335	14566	23640	1.89	1.1E+00	6978530	NT	Rattus norvegicus Aquaporin 4 (Aqp4), mRNA

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Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5497	14723	24081	22.14	1.1E+00	BE860184.1	EST_HUMAN	601652776R1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3825635 3'
6286	15467	24908	2.16	1.1E+00	Z72338.1	NT	Herpes simplex virus type 1 (strain KOS) UL41 gene
6286	15467	24909	2.16	1.1E+00	Z72338.1	NT	Herpes simplex virus type 1 (strain KOS) UL41 gene
6294	15475	24917	7.18	1.1E+00	AL161588.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84
6503	15700	25168	4.98	1.1E+00	BF893988.1	EST_HUMAN	602082582F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4246828 5'
7052	16228	25705	7.08	1.1E+00	AL161515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
7073	16250	25723	22.71	1.1E+00	8754021	NT	Mus musculus guanine nucleotide binding protein (G protein), gamma 3 subunit (Gng3), mRNA
7244	16484	25854	2.83	1.1E+00	11067364	NT	Homo sapiens KIAA0626 gene product (KIAA0626), mRNA
7298	16515		4.08	1.1E+00	AF068842.1	NT	Klebsiella fluitans cytochrome c oxidase subunit 2 (cox2) gene, mitochondrial gene encoding mitochondrial protein, partial cds
7684	14493		5.98	1.1E+00	8922673	NT	Homo sapiens hypothetical protein FLJ11280 (FLJ11280), mRNA
7689	16868	26370	3.89	1.1E+00	AF012862.1	NT	Petrosselinum crispum cytosolic glucose-6-phosphate dehydrogenase 1 (cG6PDH1) mRNA, complete cds
7689	16868	26371	3.89	1.1E+00	AF012862.1	NT	Petrosselinum crispum cytosolic glucose-6-phosphate dehydrogenase 1 (cG6PDH1) mRNA, complete cds
7895	17111	26842	5.2	1.1E+00	AI809099.1	EST_HUMAN	wf76e11x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2361548 3'
8103	17237	26774	1.83	1.1E+00	D89501.1	NT	Human PBI gene, complete cds
8103	17237	26776	1.83	1.1E+00	D89501.1	NT	Human PBI gene, complete cds
8578	17591		2.98	1.1E+00	P07866	SWISSPROT	LOW TEMPERATURE ESSENTIAL PROTEIN
8682	17652	23979	2.49	1.1E+00	AF216896.1	NT	Taenia solium immunogenic protein Ts76 mRNA, partial cds
8811	18182		1.81	1.1E+00	AF234169.1	NT	Dichostellum discoideum isopentenyl pyrophosphate isomerase (DipI) mRNA, complete cds
89	9392		2.08	1.0E+00	U23808.1	NT	Xenopus laevis rhodopsin gene, complete cds
113	9401	18530	1.22	1.0E+00	D88425.1	NT	Cavia cobaya mRNA for serine/threonine kinase, complete cds
424	9877		2.34	1.0E+00	AB021694.1	NT	Marchantia polymorpha genes for 28S rRNA, 5S rRNA, 18S rRNA, 5.8S rRNA and 28S rRNA
583	9832	18950	1.38	1.0E+00	AJ251680.1	NT	Gliricidia ligaria mRNA for homeodomain transcription factor (so gene)
683	9926	19057	6.39	1.0E+00	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
685	9928		0.84	1.0E+00	AF125984.1	NT	Aedes aegypti much-like protein MUC1 mRNA, complete cds
1392	11893		1.65	1.0E+00	X80416.1	NT	V. carteri Algal-CAM mRNA
1728	10940	20123	1.15	1.0E+00	AB006531.1	NT	Plautia stali intestine virus RNA for nonstructural polyprotein, capsid protein precursor, complete cds
2843	11828	21041	0.95	1.0E+00	AF131205.1	NT	Mus musculus Serf1 protein (Serf1), survival of motor neuron protein (Snm), neuronal apoptosis inhibitory protein-rs8 (Naip-rs8), and neuronal apoptosis inhibitory protein-rs3 (Naip-rs3) genes, complete cds

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Table 4
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2828	12068	21189	4.8	1.0E+00	P24008	SWISSPROT	3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 1 (STEROID 5-ALPHA-REDUCTASE 1) (SR TYPE 1)
2828	12068	21190	4.8	1.0E+00	P24008	SWISSPROT	3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 1 (STEROID 5-ALPHA-REDUCTASE 1) (SR TYPE 1)
2822	12180		1.25	1.0E+00	O14228	SWISSPROT	HYPOTHETICAL 67.9 KD PROTEIN C6F12.08C IN CHROMOSOME 1
3163	12368	21533	1.17	1.0E+00	AA628453.1	EST_HUMAN	af28908.s1 Soares, total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1032830 3' similar to
3577	9392		1.17	1.0E+00	U23808.1	NT	WP:C42D8.3 CE04204; contains element MER22 MER22 repetitive element;
3661	12882	22003	1.81	1.0E+00	AJ223816.1	NT	Xenopus laevis rhodopsin gene, complete cds
4048	13256	22357	0.84	1.0E+00	AF223391.1	NT	Agaricus bisporus mRNA for tyrosinase
5185	14361		0.97	1.0E+00	AF200817.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
5278	14450		0.6	1.0E+00	AL163218.2	NT	Pilot whale morbillivirus phosphoprotein (P) gene, partial cds
5315	14847	23616	2.5	1.0E+00	Z97022.1	NT	Homo sapiens chromosome 21 segment HS21C018
5582	14816	24180	4.53	1.0E+00	AF248054.1	NT	Hordeum vulgare gene encoding cysteine proteinase
5582	14816	24191	4.53	1.0E+00	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
5715	14933	24329	4.88	1.0E+00	P04501	SWISSPROT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
5716	14934	24330	1.82	1.0E+00	AW452782.1	EST_HUMAN	FIBER PROTEIN
5870	15088	24501	1.87	1.0E+00	U75902.1	NT	UI-H-B13-ab-d-08-0-J1.s1 NC1 CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3088969 3'
6284	15465		8.44	1.0E+00	P20273	SWISSPROT	Mus musculus subtilisin-like serine protease LPC (PC7) gene, exons 1 to 9, partial cds
6387	15567	25024	8.14	1.0E+00	AA775191.1	EST_HUMAN	B-CELL RECEPTOR CD22 PRECURSOR (LEU-14) (B-LYMPHOCYTE CELL ADHESION MOLECULE) (BL-CAM)
6505	14469		2.37	1.0E+00	D10852.1	NT	ae78908.s1 Stratagene lung (H837210) Homo sapiens cDNA clone IMAGE:888791 3'
6580	15778	25235	3.41	1.0E+00	Q02207	SWISSPROT	Rattus norvegicus mRNA for N-acetylglucosaminyltransferase III, complete cds
6580	15778	25235	3.41	1.0E+00	Q02207	SWISSPROT	PEROXISOMAL HYDRATASE-DEHYDROGENASE-EPIMERASE (HDE) (MULTIFUNCTIONAL BETA-OXIDATION PROTEIN) (MFP) [INCLUDES: 2-ENOYL-COA HYDRATASE ; D-3-HYDROXYACYL COA DEHYDROGENASE]
6590	15778	25236	3.41	1.0E+00	Q02207	SWISSPROT	PEROXISOMAL HYDRATASE-DEHYDROGENASE-EPIMERASE (HDE) (MULTIFUNCTIONAL BETA-OXIDATION PROTEIN) (MFP) [INCLUDES: 2-ENOYL-COA HYDRATASE ; D-3-HYDROXYACYL COA DEHYDROGENASE]
6634	18073		2.74	1.0E+00	BE147331.1	EST_HUMAN	RC1-H70228-181089-011-e08 HT0228 Homo sapiens cDNA
6968	18147	25618	2.2	1.0E+00	AV689554.1	EST_HUMAN	AV689554 GKC Homo sapiens cDNA clone GKCYA11 5'
7269	18386	25867	32.49	1.0E+00	AA004982.1	EST_HUMAN	zh94a02.1 Soares, fetal_liver脾脾_S1 Homo sapiens cDNA clone IMAGE:428606 5'

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7208	16388	26888	32.48	1.0E+00	AA004982.1	EST_HUMAN	zfp462.1 Source: fetal_liver_spleen_1NLS_S1 Homo sapiens cDNA clone IMAGE:428908 5'
7545	16750	26244	1.94	1.0E+00	S90825.1	NT	PBR1=praline-rich protein [Hiron 3] [human, Genomic, 898 nt]
8098	17201		1.86	1.0E+00	L47613.1	NT	Picea glauca EMB13 mRNA
8457	17514		3.4	1.0E+00	P15308	SWISSPROT	THROMBOMODULIN PRECURSOR (FETOMODULIN) (TM)
8801	17728		2.13	1.0E+00	AW978184.1	EST_HUMAN	EST388283 IMAGE resequences, MAGN Homo sapiens cDNA
2801	11785	21005	1	9.9E-01	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
3583	12805		1.14	9.9E-01	AF174585.1	NT	Apple mosaic virus RNA 2 putative polymerase gene, complete cds
6506	14730	24092	8.2	9.9E-01	P40857	SWISSPROT	SERINE/THREONINE PROTEIN KINASE MINIBRAIN
6938	16082		3.4	9.9E-01	Q28642	SWISSPROT	B2 BRADYKININ RECEPTOR (BK-2 RECEPTOR)
528	9780	18903	2.91	9.8E-01	P22567	SWISSPROT	AMINO-ACID ACETYLTRANSFERASE (N-ACETYLGLUTAMATE SYNTHASE) (AGS) (NAGS)
2268	11464		1.83	9.8E-01	AJ003108.1	NT	Callithrix jacchus UBE1 gene derived retroposon on the Y chromosome
3787	13005	22120	0.63	9.8E-01	BE967439.2	EST_HUMAN	601653583R2 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3838461 3'
3787	13005	22121	0.63	9.8E-01	BE967439.2	EST_HUMAN	601653583R2 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3838461 3'
6164	15347	24784	4.97	9.8E-01	AJ302158.1	NT	Enterobacteriaceae sp. JM883 partial groES gene for GroES-like protein and partial groEL gene for GroEL-like protein, isolate JM883
6164	15347	24785	4.97	9.8E-01	AJ302158.1	NT	Enterobacteriaceae sp. JM883 partial groES gene for GroES-like protein and partial groEL gene for GroEL-like protein, isolate JM883
7588	16771	26282	4.32	9.8E-01	BE258705.1	EST_HUMAN	601110258F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350750 5'
7588	16771	26283	4.32	9.8E-01	BE258705.1	EST_HUMAN	601110258F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350750 5'
8688	17657		1.28	9.8E-01	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
6147	15331	24767	3.07	9.7E-01	U26716.1	NT	Drosophila melanogaster sodium channel protein (para) gene, exons 9,10,11,12 and optional segments b, c, d and e, partial cds
7728	16927		4.82	9.7E-01	BF511209.1	EST_HUMAN	U1H-B14-ec-e-07-Q-UJ.s1 NCL_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085140 3'
8272	18035		1.38	9.7E-01	AL114281.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
9289	18047	23827	5.82	9.7E-01	AL181549.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 49
4430	13630	22724	1	9.6E-01	AF187825.1	NT	Bromus inermis putative cytosolic phosphoglucomutase (pgm1) mRNA, complete cds
4430	13630	22725	1	9.6E-01	AF187825.1	NT	Bromus inermis putative cytosolic phosphoglucomutase (pgm1) mRNA, complete cds
4452	13651	22748	1.53	9.6E-01	AW798874.1	EST_HUMAN	PM2-UM0053-240300-005-F12 UM0053 Homo sapiens cDNA
5552	14778	24143	3.47	9.6E-01	Z70558.1	NT	Parvovirus B19 DNA, patient C, genome position 2448-2894
5552	14778	24144	3.47	9.6E-01	Z70558.1	NT	Parvovirus B19 DNA, patient C, genome position 2448-2894
6586	16782		2.23	9.6E-01	X95276.1	NT	P.falciparum complete gene map of plastid-like DNA (IR-A)
7654	18854	26353	1.89	9.6E-01	AF041427.1	NT	Homo sapiens ribosomal protein s4 Y isoform gene, complete cds

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8051	17187	28728	4.97	9.6E-01	AV752605.1	EST_HUMAN	AV752605 NPD Homo sapiens cDNA clone NPD8AG08 5'
8051	17187	28727	4.97	9.6E-01	AV752605.1	EST_HUMAN	AV752605 NPD Homo sapiens cDNA clone NPD8AG08 5'
8358	17449		1.59	9.6E-01	11421722	NT	Homo sapiens centrosomal protein 2 (CEP2), mRNA
9010	18260	23680	2.28	9.6E-01	U91423.1	NT	Sphyrna tiburo NADH dehydrogenase subunit 2 (NADH2) gene, mitochondrial gene encoding mitochondrial protein, partial cds
2438	11629	20850	1.21	9.5E-01	7705591	NT	Homo sapiens CGI-125 protein (LOC51003), mRNA
3765	12083	22097	2.08	9.5E-01	BE902340.1	EST_HUMAN	601875639F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3858473 5'
3765	12083	22098	2.08	9.5E-01	BE902340.1	EST_HUMAN	601875639F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3858473 5'
7780	16889	26504	1.78	9.6E-01	BF218771.1	EST_HUMAN	601885183F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4103630 5'
7887	16422	26809	1.85	9.5E-01	AW203799.1	EST_HUMAN	U1H-B12-shp-f03-0-J1.s1 NCI CGAP Sub4 Homo sapiens cDNA clone IMAGE:2727677 3'
3165	12400		3.84	9.4E-01	AF165900.1	NT	Bartonella clarridgeiae RNA polymerase beta subunit (rpoB) gene, partial cds
3184	12419		2.15	9.4E-01	AF080596.1	NT	Pimpinella brachycarpa zinc finger protein (ZFP1) mRNA, complete cds
8630	17822		1.85	9.4E-01	BE781251.1	EST_HUMAN	601468703F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3889928 5'
8008	18176		1.61	9.4E-01	11419857	NT	Homo sapiens epidermal growth factor receptor (avian erythroblast leukemia viral (v-erb-b) oncogene homolog) (EGFR), mRNA
1705	10917		1.15	9.3E-01	AF242382.1	NT	Homo sapiens phytyl-CoA hydroxylase (PHYH) gene, exon 5
2598	11783	21003	1.81	9.3E-01	BE071172.1	EST_HUMAN	RCS-BT0503-271169-011-B01 BT0503 Homo sapiens cDNA
4013	13225	22325	0.76	9.3E-01	M20218.1	NT	Bovine papillomavirus type 2, complete genome
4013	13225	22326	0.76	9.3E-01	M20218.1	NT	Bovine papillomavirus type 2, complete genome
5524	14749	24118	4.02	9.3E-01	L36189.1	NT	Spodoptera frugiperda methylenetetrahydrofolate dehydrogenase mRNA, complete cds
8128	17839	23879	1.56	9.3E-01	11440288	NT	Homo sapiens inositol 1,4,5-trisphosphate receptor, type 2 (ITPR2), mRNA
9135	17044		2.19	9.3E-01	AF271207.1	NT	Aedes triseriatus putative large subunit ribosomal protein rpl34 mRNA, complete cds
3205	12439	21574	3.6	9.2E-01	BE822702.1	EST_HUMAN	601441338T1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918184 3'
4894	14082		0.79	9.2E-01	BF128973.1	EST_HUMAN	6018187814F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:4041383 5'
5849	14872	24259	4.49	9.2E-01	BF037586.1	EST_HUMAN	601461153F1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:3884881 5'
7156	16333	25818	5.03	9.2E-01	11430863	NT	Homo sapiens lysosomal apyrase-like protein 1 (LALP1), mRNA
7240	16490	25949	1.68	9.2E-01	BE563811.1	EST_HUMAN	601334943F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3688714 5'
8213	17344	26883	2.08	9.2E-01	BF132402.1	EST_HUMAN	601820312F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4052018 5'
1602	10816	18982	1.14	9.1E-01	T86875.1	EST_HUMAN	ye52701.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121369 3' similar to contains Alu repetitive element
2084	11294		1.18	9.1E-01	8923056	NT	Homo sapiens hypothetical protein FLJ20048 (FLJ20048), mRNA
3170	12405	21538	1.28	9.1E-01	T28418.1	EST_HUMAN	AB200G8R Infant brain, LNL array of Dr. M. Soares 1NIB Homo sapiens cDNA clone LLAB200G8 5'

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3170	12405	21539	1.28	9.1E-01	T28418.1	EST_HUMAN	AB200G8R Infant brain, LLNL array of Dr. M. Soares 1N1B Homo sapiens cDNA clone LLAB200G8 5'
5878	15095	24509	2.88	9.1E-01	Q61704	SWISSPROT	INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H3 PRECURSOR (ITI HEAVY CHAIN H3)
6326	15508	24952	17.88	9.1E-01	AA808623.1	EST_HUMAN	cb71g08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1338982 3'
6383	15573	25028	2.35	9.1E-01	U72895.1	NT	Rattus norvegicus Rab3 GDP/GTP exchange protein mRNA, complete cds
8726	18254		15.31	9.1E-01	AF050113.1	NT	Homo sapiens uncoupling protein-3 (UCP3) gene, complete cds
3172	12407	21542	0.8	9.0E-01	7881825	NT	Homo sapiens DKFZP564M2423 protein (DKFZP564M2423), mRNA
4373	13575	22871	2	9.0E-01	AF089810.1	NT	Homo sapiens neuroxin III-alpha gene, partial cds
5288	14441	23514	0.61	9.0E-01	A1086302.1	EST_HUMAN	cc10b05.s1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1635889 3' similar to contains Alu repetitive element;
5534	14758	24125	2.39	8.9E-01	AF026188.1	NT	Fugu rubripes neural cell adhesion molecule L1 homolog (L1-CAM) gene, complete cds; putative protein 1 (PUT1) gene, partial cds; mitosis-specific chromosome segregation protein SMC1 homolog (SMC1) gene, complete cds; and calcium channel alpha-1 subunit
8251	17379	28913	2.68	8.9E-01	AE003944.1	NT	Xylella fastidiosa, section 80 of 229 of the complete genome
8567	17579		4.11	8.9E-01	AE002188.2	NT	Chlamydia pneumoniae AR39, section 21 of 84 of the complete genome
4539	13734	22832	1.91	8.8E-01	O26350	SWISSPROT	PUTATIVE F420-DEPENDENT NADP REDUCTASE
5205	14380	23468	3.88	8.8E-01	AW856840.1	EST_HUMAN	RC2-CT0288-150200-015-b01 CT0288 Homo sapiens cDNA
7847	18847	28345	3.08	8.8E-01	Z28337.1	NT	M.aeruginosa (HUB 5-2-4) DNA from plasmid PM1
8372	18344		2.12	8.8E-01	D80911.1	NT	Synechocystis sp. PCC6803 complete genome, 13/27, 1576593-1718643
471	9724	18855	1.29	8.7E-01	AF106953.2	NT	Homo sapiens SOS1 (SOS1) gene, partial cds
2827	12068	21187	5.87	8.7E-01	AA595863.1	EST_HUMAN	nr05f11.s1 NCI_CGAP_Pr4.1 Homo sapiens cDNA clone IMAGE:1076877
6031	14218		2.76	8.7E-01	AF121970.1	NT	Pseudomonas aeruginosa topoisomerase (top), putative transcriptional regulatory protein OhbR (ohbR), ortho-halobenzoside 1,2-dioxygenase beta-ISP protein OhbA (ohbA), OhbC (ohbC), ortho-halobenzoside 1,2-dioxygenase alpha-ISP protein OhbB (ohbB), and put
7408	18620	28112	6.23	8.7E-01	BF363970.1	EST_HUMAN	QV0-NN1021-100800-337-c03 NN1021 Homo sapiens cDNA
8226	17356	28894	3.87	8.7E-01	BF107694.1	EST_HUMAN	601823884R1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4043564 3'
8226	17356	28895	3.87	8.7E-01	BF107694.1	EST_HUMAN	601823884R1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4043564 3'
8775	18144		2.27	8.7E-01	AV681898.1	EST_HUMAN	AV681898 GLC Homo sapiens cDNA clone GLCGYG07 3'
481	9733		1.49	8.6E-01	X17012.1	NT	Rat IGFI gene for insulin-like growth factor II
888	10104	19287	7.48	8.6E-01	W68089.1	EST_HUMAN	zd44e03.r1 Soares fetal_heart_NbH19W Homo sapiens cDNA clone IMAGE:343516 5'
2235	11430	20855	0.95	8.6E-01	4503210	NT	Homo sapiens cytochrome P450, subfamily XXVIIA (steroid 27-hydroxylase, cerebrotendinous xanthomatosis), polypeptide 1 (CYP27A1b) mRNA
3598	12820	21841	1.09	8.6E-01	AL161585.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65
3784	13002	22117	1.49	8.6E-01	U49724.1	NT	Drosophila melanogaster merlin (Dmerlin) mRNA, complete cds

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5614	14837	24214	7.93	8.6E-01	X60547.1	NT	Chicken lipoprotein lipase gene
5614	14837	24215	7.93	8.6E-01	X60547.1	NT	Chicken lipoprotein lipase gene
5669	15184	24600	1.77	8.6E-01	AF143732.1	NT	Grus canadensis recombinant activating protein 1 (RAG-1) gene, partial cds
5669	15184	24601	1.77	8.6E-01	AF143732.1	NT	Grus canadensis recombinant activating protein 1 (RAG-1) gene, partial cds
8662	18082		1.58	8.6E-01	AL112182.1	NT	Bovine chimeric strain T4 cDNA library under conditions of nitrogen deprivation
4491	13689	22781	0.85	8.5E-01	AI701028.1	EST_HUMAN	we08h02.x1 NC1_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2340827 3'
6301	15482	24826	2.42	8.5E-01	BE542612.1	EST_HUMAN	601087107F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453505 5'
7180	16357	25835	2.22	8.5E-01	AB006799.1	NT	Cyanidium caldarium gene for SigC, complete cds
7180	16357	25836	2.22	8.5E-01	AB006799.1	NT	Cyanidium caldarium gene for SigC, complete cds
8711	18256		2.74	8.5E-01	11418543	NT	Homo sapiens human immunodeficiency virus type 1 enhancer-binding protein 1 (HIVEP1), mRNA
8717	17672		4	8.5E-01	9507008	NT	Rattus norvegicus protein tyrosine phosphatase, non-receptor type 6 (Ptpn6), mRNA
5440	18055	23820	2.81	8.4E-01	L78726.1	NT	Human fibroblast growth factor receptor 3 (FGFR3) gene, intron 7
5440	18055	23821	2.81	8.4E-01	L78726.1	NT	Human fibroblast growth factor receptor 3 (FGFR3) gene, intron 7
7057	16234		4.37	8.4E-01	AJ248287.1	NT	Pyrococcus abyssi complete genome; segment 5/8
749	9890	19133	2.79	8.3E-01	M93437.1	NT	Thermus thermophilus cytochrome c-552 (cycA) and CycB (cycB) genes, complete cds
3060	12296	21420	3.24	8.3E-01	AL161508.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 18
3768	13016	22128	0.71	8.3E-01	AB010879.1	NT	Nicotiana tabacum mRNA for chloroplast ribosomal protein L10, complete cds
3988	13202	22310	3.75	8.3E-01	Y18177.1	NT	Streptomyces antibioticus polyketide biosynthetic gene cluster
5308	14540	23545	2.38	8.3E-01	AL161540.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 40
7140	16317	25766	4.78	8.3E-01	AF108133.1	NT	Mus musculus neuro-d4 gene, exons 3 through 12 and partial cds
7266	16485	25877	2.68	8.3E-01	AE000903.1	NT	Methanobacterium thermoautotrophicum from bases 1270510 to 1283409 (section 109 of 148) of the complete genome
7282	18501		2.2	8.3E-01	7212472	NT	Phytophthora infestans mitochondrion, complete genome
7851	17041	26558	2.88	8.3E-01	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
2018	11220	20428	2.47	8.2E-01	AB000489.1	NT	Rattus norvegicus mRNA for RPHO-1, complete cds
2059	11260		1.69	8.2E-01	AF145589.1	NT	Mus musculus trophalin (Trn) gene, complete cds
2639	11822		1.02	8.2E-01	AW376880.1	EST_HUMAN	IL3-CT0218-161189-031-C08 CT0218 Homo sapiens cDNA
3878	13095	22212	0.61	8.2E-01	AB014574.1	NT	Homo sapiens mRNA for KIAA0674 protein, partial cds
4111	13318	22417	0.99	8.2E-01	Z72584.1	NT	S. cerevisiae chromosome VII reading frame ORF YGL082w
4111	13318	22418	0.99	8.2E-01	Z72584.1	NT	S. cerevisiae chromosome VII reading frame ORF YGL082w
6040	15248	24670	3.49	8.2E-01	AW376433.1	EST_HUMAN	CM4-HT0243-081189-037-401 HT0243 Homo sapiens cDNA
6196	18072	24618	4.4	8.2E-01	Z12126.1	NT	S. cerevisiae MET, LEU4, and POL1 genes encoding MET4 protein, alpha-isopropylmalate (alpha-IPM) synthetase (partial), and DNA polymerase alpha (partial)

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Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7094	18271	25748	2.43	8.2E-01	AF052859.1	NT	Homo sapiens thioredoxin-related protein mRNA, complete cds
7184	16361	25840	3.29	8.2E-01	Q8J170	SWISSPROT	MCKUSICK-KAUFMAN/BARDET-BIEDL SYNDROMES PUTATIVE CHAPERONIN
7184	16361	26841	3.29	8.2E-01	Q8J170	SWISSPROT	MCKUSICK-KAUFMAN/BARDET-BIEDL SYNDROMES PUTATIVE CHAPERONIN
8155	17287	26831	3.09	8.2E-01	L10127.1	NT	Molluscum contagiosum virus type 1 ORF1 and ORF2 DNA
8221	17351	26889	7.78	8.2E-01	P10383	SWISSPROT	OVARIAN TUMOR LOCUS PROTEIN
8227	17357	26896	8.88	8.2E-01	H87398.1	EST_HUMAN	yw14002.1 Soares_placenta_8kbOwaka_2NbtHP8ts9W Homo sapiens cDNA clone IMAGE:252195 5'
8734	17680	23952	1.91	8.2E-01	AJ001261.1	NT	similar to gb:M38072.60S RIBOSOMAL PROTEIN L7A (HUMAN);
2714	11893		1.1	8.1E-01	AF181839.1	NT	Mus musculus mRNA for NIPSNAP2 protein
3435	12660	21781	3.11	8.1E-01	AF055086.1	NT	Mus musculus TANK binding kinase TBK1 (Tbk1) mRNA, complete cds
3435	12660	21792	3.11	8.1E-01	AF055086.1	NT	Homo sapiens MHC class 1 region
4841	14128		0.82	8.1E-01	AF202634.1	NT	Homo sapiens MHC class 1 region
5943	15159	24571	2.59	8.1E-01	Q13491	SWISSPROT	Drosophila melanogaster Na/K-ATPase beta subunit isoform 4 (JYbeta2) mRNA, complete cds
5943	15159	24572	2.59	8.1E-01	Q13491	SWISSPROT	NEURONAL MEMBRANE GLYCOPROTEIN M8-B
8017	17166	26891	3.68	8.1E-01	BE938558.1	SWISSPROT	NEURONAL MEMBRANE GLYCOPROTEIN M8-B
8017	17166	26892	3.58	8.1E-01	BE938558.1	EST_HUMAN	RC00-TN0080-220800-025-d10 TN0080 Homo sapiens cDNA
8430	17496	24013	1.63	8.1E-01	AE001711.1	EST_HUMAN	RC00-TN0080-220800-025-d10 TN0080 Homo sapiens cDNA
180	9480		2.95	8.0E-01	AJ271510.1	NT	Thermoboga maritima section 23 of 138 of the complete genome
283	9587	18688	9.28	8.0E-01	AJ132772.1	NT	Staphylococcus aureus partial pla gene for phosphatase allele 15
2003	11206		1.53	8.0E-01	BF530982.1	EST_HUMAN	Bos taurus furf and rtf genes
3284	12515	21846	1.71	8.0E-01	AB006193.1	NT	602072473F1 NCI_CGAP_Brm87 Homo sapiens cDNA clone IMAGE:4215091 5'
4530	13726	22823	5.94	8.0E-01	X63739.2	NT	Mus musculus gene for oxiductal glycoprotein, complete cds
5001	14188	23278	1.29	8.0E-01	7657352	NT	G.gallus mRNA for nicotinic acetylcholine receptor (nAChR) beta 3 subunit
6828	15825	25287	2.21	8.0E-01	Y11095.1	NT	Mus musculus myosin IXb (Myc9b), mRNA
460	8713	18948	1.01	7.9E-01	D11476.1	NT	Rice stripe virus RNA 3
722	8984		1.09	7.9E-01	AE002130.1	NT	Lymnaea dispar nuclear polyhedrosis virus gene for DNA polymerase, complete cds
1584	10797		25.24	7.9E-01	AB040885.1	NT	Ureaplasma urealyticum section 31 of 59 of the complete genome
1631	10845		1	7.9E-01	U2739.1	NT	Homo sapiens mRNA for KIAA1452 protein, partial cds
2228	11424	20650	6.52	7.9E-01	AB004816.1	NT	Haemophilus influenzae Rd section 54 of 163 of the complete genome
2229	11425	20651	2.33	7.9E-01	AF130459.1	NT	Oryctolagus cuniculus mRNA for mitsuguthin29, complete cds
3490	12714	21850	2.71	7.9E-01	AF228664.1	NT	Danio rerio Trp4-associated protein Tap1A (tap1A) mRNA, complete cds
4287	13489		0.71	7.9E-01	BE263612.1	EST_HUMAN	Gallus gallus SOX8 transcription factor (SOX8) mRNA, complete cds
4613	13907	22899	1.03	7.9E-01	8753745	NT	601192033F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535785 5'
4613	13907	22900	1.03	7.8E-01	8753745	NT	Mus musculus embigin (Emb), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6497	15694	25158	4.39	7.9E-01	X00998.1	NT	P. sativum GR gene
6834	16128	25594	4.56	7.9E-01	U01912.1	NT	Giardia lamblia variant-specific surface protein G3M-B (vapG3M-B) mRNA, partial cds
7089	16268	25742	2.99	7.9E-01	P19719	SWISSPROT	SMALL HYDROPHOBIC PROTEIN
7577	16782		2.29	7.9E-01	7862471	NT	Homo sapiens KIAA1072 protein (KIAA1072), mRNA
7764	18960	26470	3	7.9E-01	P18022	SWISSPROT	NEURAL-CADHERIN PRECURSOR (N-CADHERIN)
888	10121		2.22	7.8E-01	Z43785.1	EST_HUMAN	HSC1KH041 normalized infant brain cDNA Homo sapiens cDNA clone c-1kh04
2240	11435	20859	4.11	7.8E-01	AW959567.1	EST_HUMAN	EST371637 MAGE resequences, MAGF Homo sapiens cDNA
4712	13903	23003	0.74	7.8E-01	U87305.1	NT	Rattus norvegicus transmembrane receptor Unc5H1 mRNA, complete cds
5062	14242		1.12	7.8E-01	AW753353.1	EST_HUMAN	RC3-CT0254-130100-023-c02 CT0284 Homo sapiens cDNA
5227	14401		1.33	7.8E-01	Z43785.1	EST_HUMAN	HSC1KH041 normalized infant brain cDNA Homo sapiens cDNA clone c-1kh04
5697	14917	24311	2.41	7.8E-01	AF115856.1	NT	Sphenodon punctatus alpha endase mRNA, partial cds
8705	18234		1.54	7.8E-01	L28280.1	NT	Arabidopsis thaliana 1-aminio-1-cyclopropanecarboxylate synthase (ACS5) gene, complete cds
141	9423	18556	5.87	7.7E-01	AF184345.1	NT	Lycopodium hirsutum ADP-glucose pyrophosphorylase large subunit (AGP-L1) mRNA, complete cds
733	9974		2.1	7.7E-01	AF050157.1	NT	Mus musculus major histocompatibility locus class II region: major histocompatibility protein class II alpha chain (IAA1pha) and major histocompatibility protein class II beta chain (IEbeta) genes, complete cds; butyrophilin-like (NG9), butyrophilin-1p>
2872	11854	21070	1.39	7.7E-01	O33915	SWISSPROT	CITRATE SYNTHASE
3978	12800	21928	4.2	7.7E-01	AF118085.1	NT	Homo sapiens PRO1975 mRNA, complete cds
4390	13591	22893	3.15	7.7E-01	AF189488.1	NT	Coturnix coturnix japonica sub-species japonica beta-actin mRNA, partial cds
4390	13591	22894	3.15	7.7E-01	AF189488.1	NT	Coturnix coturnix japonica sub-species japonica beta-actin mRNA, partial cds
5203	14438		1.46	7.7E-01	L78833.1	NT	Human BRCA1, Rho7 and vatl genes, complete cds, and prf35 gene, partial cds
8479	9423	18556	1.35	7.7E-01	AF184345.1	NT	Lycopodium hirsutum ADP-glucose pyrophosphorylase large subunit (AGP-L1) mRNA, complete cds
8586	17598		5.33	7.7E-01	11497821	NT	Archaeoglobus fulgidus, complete genome
5707	14928	24320	4.05	7.6E-01	AF059510.1	NT	Arabidopsis thaliana 3-methylcrotonyl-CoA carboxylase non-biotinylated subunit (MCCB) mRNA, complete cds
5707	14928	24321	4.05	7.6E-01	AF059510.1	NT	Arabidopsis thaliana 3-methylcrotonyl-CoA carboxylase non-biotinylated subunit (MCCB) mRNA, complete cds
6501	15698	25163	2.5	7.6E-01	6857752	NT	Mus musculus adiolin (Adiol-pending), mRNA
6501	15698	25164	2.5	7.6E-01	6857752	NT	Mus musculus adiolin (Adiol-pending), mRNA
6849	16038	25502	7.49	7.6E-01	P30372	SWISSPROT	MUSCARINIC ACETYLCHOLINE RECEPTOR M2
6849	16038	25503	7.49	7.6E-01	P30372	SWISSPROT	MUSCARINIC ACETYLCHOLINE RECEPTOR M2
7897	17113	26844	2.88	7.6E-01	X88347.1	NT	H. aspersa mRNA for neurofilament NF70

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7897	17113	28845	2.88	7.8E-01	X86347.1	NT	H. aspersa mRNA for neurofilament NF70
8201	17333		6.71	7.8E-01	AL181592.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 88
8334	17432		3.62	7.8E-01	AB020702.1	NT	Homo sapiens mRNA for KIAA0885 protein, partial cds
519	9770		1.25	7.5E-01	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
591	9839	18958	1.51	7.5E-01	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (PHIT) gene, exon 5
7708	16984	26477	1.71	7.5E-01	AB047819.1	NT	Homo sapiens GCMa/GCM1 gene for chordin-specific transcription factor GCMa, complete cds
8858	17635		4.34	7.5E-01	AF163151.2	NT	Homo sapiens dentin sialophosphoprotein precursor (DSPP) gene, complete cds
8204	17889	23863	1.8	7.5E-01	AE000823.1	NT	Methanobacterium thermoautotrophicum from bases 317350 to 328792 (section 29 of 148) of the complete genome
1138	10361	19510	1.26	7.4E-01	AI598146.1	EST_HUMAN	tn14609.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2167577 3' similar to contains Alu repetitive element/contains element MIR repetitive element ;
2311	11505	20726	0.63	7.4E-01	AB011106.1	NT	Homo sapiens mRNA for KIAA0534 protein, partial cds
3707	12827	22045	0.59	7.4E-01	AF112538.1	NT	Malva pusilla actin (Act1) mRNA, complete cds
4299	13500	22596	8.84	7.4E-01	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
6804	15988	25458	9.91	7.4E-01	BE747503.1	EST_HUMAN	601573026F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3834174 5'
8168	17300	26843	1.64	7.4E-01	AB021490.2	NT	Oryza latipes gene for membrane guanylyl cyclase OIGC1, complete cds
8168	17300	26844	1.64	7.4E-01	AB021490.2	NT	Oryza latipes gene for membrane guanylyl cyclase OIGC1, complete cds
8302	17410		2.98	7.4E-01	6753217	NT	Mus musculus complement component 1 inhibitor (C1inh), mRNA
8415	17488		1.42	7.4E-01	AI472841.1	EST_HUMAN	ta13h01.x1 NCI_CGAP_Lym5 Homo sapiens cDNA clone IMAGE:2043985 3'
3952	13167		0.68	7.3E-01	AP000082.1	NT	Aeropyrum pernix genomic DNA, section 5/7
4818	13812	22802	0.67	7.3E-01	AE001188.1	NT	Borrelia burgdorferi (section 52 of 70) of the complete genome
4711	13902	23002	5.65	7.3E-01	AF225421.1	NT	Homo sapiens HT017 mRNA, complete cds
5130	14303	23399	0.91	7.3E-01	O43103	SWISSPROT	FERRICHRONE SIDEROPHORE PEPTIDE SYNTHETASE
5936	15152	24562	6.03	7.3E-01	L35772.1	NT	Mus musculus antigen (OD72) gene
5936	15152	24563	6.03	7.3E-01	L35772.1	NT	Mus musculus antigen (OD72) gene
6310	15491	24635	8.23	7.3E-01	M28511.1	NT	V. alginolyticus sucrase (scrB) gene, complete cds
6310	15491	24636	8.23	7.3E-01	M28511.1	NT	V. alginolyticus sucrase (scrB) gene, complete cds
7868	17147	26681	3.69	7.3E-01	AA678019.1	EST_HUMAN	225508.s1 Soares_fetal_liver_spleen_1NFS_S1 Homo sapiens cDNA clone IMAGE:431789 3'
7868	17147	26682	3.69	7.3E-01	AA678019.1	EST_HUMAN	225508.s1 Soares_fetal_liver_spleen_1NFS_S1 Homo sapiens cDNA clone IMAGE:431789 3'
841	10078		2.68	7.2E-01	L29281.1	NT	Rattus norvegicus initiation factor-2 kinase (eIF-2a) mRNA, complete cds
1827	11131	20326	4.35	7.2E-01	X79140.1	NT	N. tabacum NeIF-4A13 mRNA
2424	11615	20837	2.18	7.2E-01	AB009805.1	NT	Gallus gallus gene for melanocortin 2-receptor, complete cds
3031	12267	21394	1.35	7.2E-01	AF198100.1	NT	Fowlpox virus, complete genome

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3430	12855	21785	3.04	7.2E-01	AF065806.1	NT	Giardia intestinalis variant-specific surface protein (vsp417-6) gene, vsp417-6(A-I) allele, complete cds
3582	12813	21834	1.13	7.2E-01	AB002307.1	NT	Human mRNA for KIAA0309 gene, partial cds
4039	13248		0.81	7.2E-01	AF108093.1	NT	Homo sapiens IA-2 gene, intron 18
4780	13968	23071	3.68	7.2E-01	D80314.1	NT	L-mesentericoides gene for sucrose phosphorylase (EC 2.4.1.7)
6335	15516		6.78	7.2E-01	8625875	NT	Human herpesvirus 3, complete genome
7325	16541	26030	6.88	7.2E-01	U82623.1	NT	Rattus norvegicus cytochrome mRNAs, complete cds
7715	16814	26423	1.7	7.2E-01	S76838.1	NT	Dba-DBI guanine nucleotide exchange factor homolog [mice, 32D murine hemopoietic cell line, mRNA, 3823 nt]
8857	17760		4.28	7.2E-01	AP000063.1	NT	Aeropyrum pernix genomic DNA, section 8/7
689	8841	19075	12.1	7.1E-01	D21070.1	NT	Rana catesbeiana mRNA for bullfrog skeletal muscle calcium release channel (ryanodine receptor) alpha isoform(RyR1), complete cds
3027	12263	21391	15.67	7.1E-01	AJ270777.1	NT	Homo sapiens partial TCF-4 gene for T-cell transcription factor-4, exons 15-16
4160	13394	22493	3.47	7.1E-01	7305360	NT	Mus musculus otogelin (Otog), mRNA
4180	13394	22494	3.47	7.1E-01	7305360	NT	Mus musculus otogelin (Otog), mRNA
6063	16283	24977	7.74	7.1E-01	U36232.1	NT	Drosophila melanogaster 6-pyruvyltetrahydropterin synthase (pr) gene, complete cds
8840	18160		1.97	7.1E-01	AA421492.1	EST_HUMAN	z008h11.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:731109 3'
1236	10453	19811	2.88	7.0E-01	AB014514.1	NT	Homo sapiens mRNA for KIAA0614 protein, partial cds
1236	10453	19812	2.88	7.0E-01	AB014514.1	NT	Homo sapiens mRNA for KIAA0614 protein, partial cds
2412	11604	20825	1.49	7.0E-01	N82412.1	EST_HUMAN	yz73e07.s1 Soares_multiple_sclerosis_2NBHMS Homo sapiens cDNA clone IMAGE:288708 3' similar to contains Alu repetitive element
2412	11604	20826	1.49	7.0E-01	N82412.1	EST_HUMAN	yz73e07.s1 Soares_multiple_sclerosis_2NBHMS Homo sapiens cDNA clone IMAGE:288708 3' similar to contains Alu repetitive element
5098	14268		2.07	7.0E-01	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
5207	14382	23468	0.61	7.0E-01	AE003921.1	NT	Xyella fastidiosa, section 67 of 229 of the complete genome
5253	14426	23502	8.3	7.0E-01	T88328.1	EST_HUMAN	yc41h03.s1 Stratiogene liver (#837224) Homo sapiens cDNA clone IMAGE:83285 3' similar to gb:K03020 PHENYLALANINE-4-HYDROXYLASE (HUMAN);
6588	15785		9.8	7.0E-01	AE000253.1	NT	Escherichia coli K-12 MG1655 section 143 of 400 of the complete genome
7680	16878	26385	2.01	7.0E-01	AV763842.1	EST_HUMAN	AV763842 MDS Homo sapiens cDNA clone MDSCH04 5'
7680	16878	26386	2.01	7.0E-01	AV763842.1	EST_HUMAN	AV763842 MDS Homo sapiens cDNA clone MDSCH04 5'
977	10208	18384	11.39	6.9E-01	U69874.1	NT	Candida albicans squalene epoxidase (CAERG1) gene, complete cds and translational regulator gene, partial cds
977	10209	18385	11.39	6.9E-01	U69874.1	NT	Candida albicans squalene epoxidase (CAERG1) gene, complete cds and translational regulator gene, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1317	10533	19895	2.41	6.9E-01	AA563530.1	EST_HUMAN	nr28409.s1 NCI_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1085178 3'
3185	12420	21653	1.68	6.8E-01	AE002271.2	NT	Chlamydia muridarum, section 3 of 85 of the complete genome
6248	14419	23496	0.02	6.9E-01	BE782751.1	EST_HUMAN	601495594F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3888943 5'
8455	15852	25120	3.94	6.9E-01	AL161573.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 89
8455	15852	25121	3.94	6.9E-01	AL161573.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 89
7810	17003	28518	2.35	6.9E-01	D89013.1	NT	Homo sapiens DAN gene, complete cds
7810	17003	28517	2.35	6.9E-01	D89013.1	NT	Homo sapiens DAN gene, complete cds
8278	18154		3.81	6.9E-01	Q69958	SWISSPROT	FORKHEAD BOX PROTEIN C2 (FORKHEAD-RELATED PROTEIN FKHL14) (MESENCHYME FORK HEAD PROTEIN 1) (MFH-1 PROTEIN) (TRANSCRIPTION FACTOR FKH-14)
884	10187	18352	0.82	6.8E-01	AF017784.1	NT	Giardia intestinalis carboxamide kinase gene, complete cds
2634	11817		1.32	6.8E-01	D80917.1	NT	Synechocystis sp. PCC6803 complete genome, 27/27, 3418852-3573470
2781	10807	19983	1.28	6.8E-01	AA854475.1	EST_HUMAN	q75a05.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1402256 3' similar to gb:56411.1_mai1 ALCOHOL DEHYDROGENASE CLASS II PI CHAIN (HUMAN);
4588	13763	22859	1.35	6.8E-01	J00762.1	NT	Rat(hooded) protectin gene : exon iii and flanks
6976	18164	26626	3.23	6.8E-01	AB037768.1	NT	Homo sapiens mRNA for KIAA1345 protein, partial cds
7653	16853	26351	2.57	6.8E-01	AJ270687.1	NT	Stagonospora avenae bgj1 gene for beta-glucosidase, exons 1-4
7653	16853	26352	2.57	6.8E-01	AJ270687.1	NT	Stagonospora avenae bgj1 gene for beta-glucosidase, exons 1-4
7675	16874	26378	2.41	6.8E-01	AF038839.1	NT	Mus musculus zinc finger protein (Peg3) mRNA, complete cds
7675	16874	26380	2.41	6.8E-01	AF038839.1	NT	Mus musculus zinc finger protein (Peg3) mRNA, complete cds
7848	17037	26553	1.85	6.8E-01	AF184151.1	NT	Anopheles gambiae strain M2 translation initiation factor 4C (1A) (eIF-4C) mRNA, complete cds
303	9578	18709	27.9	6.7E-01	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
344	9812	18739	21.23	6.7E-01	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
1876	11083		1.07	6.7E-01	M12132.1	NT	Quail fast skeletal muscle tropomyosin I gene, complete cds
2115	11314	20530	1.38	6.7E-01	AA451884.1	EST_HUMAN	zx12g12.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:786310 3' similar to contains element TAR1 repetitive element;
2132	12011	20550	3.16	6.7E-01	AF186073.1	NT	Drosophila melanogaster Mst85C gene, complete cds; NMDMC isoform (Nmdmc) gene, complete cds, alternatively spliced; and transcription factor (Relish) gene, complete cds, alternatively spliced
2953	12191	21325	4.18	6.7E-01	6878560	NT	Mus musculus Wiskott-Aldrich syndrome protein (Wasp), mRNA
4447	13648	22742	0.8	6.7E-01	X74421.1	NT	S.tuberosum mRNA for glucose-6-phosphate dehydrogenase
4885	14172	23262	1.04	6.7E-01	AW079110.1	EST_HUMAN	xs85g12.x1 NCI_CGAP_Co17 Homo sapiens cDNA clone IMAGE:2574588 3'
6215	15398		4.48	6.7E-01	AE004608.1	NT	Pseudomonas aeruginosa PAO1, section 167 of 629 of the complete genome

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7527	18732	26222	2.59	6.7E-01	BF354649.1	EST_HUMAN	CM3-HT0769-010800-197-03 HT0769 Homo sapiens cDNA
7894	18429	25918	3.48	6.7E-01	O14357	SWISSPROT	N-ACETYLGLUCOSAMINYL-PHOSPHATIDYLINOSITOL BIOSYNTHETIC PROTEIN GPI1
2465	11056	20877	0.91	6.6E-01	AF075240.1	NT	Homo sapiens SLIT1 protein (SLIL2) mRNA, partial cds
2681	11842	21056	1.09	6.6E-01	AF199339.1	NT	Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds
3484	12689	21825	1.22	6.6E-01	4508980	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A) mRNA
3638	12859	21978	3.98	6.6E-01	Y07869.1	NT	Calicains random DNA marker, 282bp
4087	13286		1.19	6.6E-01	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rar1 gene, and sodium phosphate transporter (NP73) gene, complete cds
5803	15020	24421	4.35	6.6E-01	6880577	NT	Mus musculus kinesin light chain 2 (Klc2), mRNA
6369	15349	25005	3.49	6.6E-01	AV680508.1	EST_HUMAN	AV680508 GLC Homo sapiens cDNA clone GLCGID04.3'
629	9874	18995	2.11	6.5E-01	M75140.1	NT	H. vulgaris Na,K-ATPase alpha subunit mRNA, complete cds
629	9874	18998	2.11	6.5E-01	M75140.1	NT	H. vulgaris Na,K-ATPase alpha subunit mRNA, complete cds
3411	12637	21768	5.25	6.5E-01	AB041225.1	NT	Mus musculus gene for Tob2, complete cds
4287	13470	22563	4.63	6.5E-01	AJ272285.1	NT	Homo sapiens SP2 gene for secreted phosphoprotein 24 precursor, exons 1-8
4301	13502	22598	0.97	6.5E-01	AL181539.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 39
5095	14275	23358	1.84	6.5E-01	U28921.1	NT	Phaeodactylus vulgaris ATPase gamma subunit mRNA, nuclear gene encoding mitochondrial protein, partial cds
6413	18054	23773	2.09	6.5E-01	P18480	SWISSPROT	TRANSCRIPTION REGULATORY PROTEIN SNF5 (SWISNF COMPLEX COMPONENT SNF5)
7177	18354	25832	3.78	6.5E-01	AF19976.1	NT	(TRANSCRIPTION FACTOR TFE4)
7228	18449	25938	3.68	6.5E-01	H87583.1	EST_HUMAN	Mus musculus small GTP-binding protein RAB25 (Rab25) gene, complete cds
7278	18497	25989	4.84	6.5E-01	AA601287.1	EST_HUMAN	yy1706.r1 Soares placenta 8to9weeks_2NblP8ts9W Homo sapiens cDNA clone IMAGE:252515 5'
7371	16587		4.71	6.5E-01	AU138078.1	EST_HUMAN	no15c07.s1 NCI_CGAP_Pho1 Homo sapiens cDNA clone IMAGE:1100748 3'
8127	17261	26804	2.85	6.5E-01	AF014115.1	NT	AU138078 PLACE1 Homo sapiens cDNA clone PLACE1007810 5'
8700	17668		3.08	6.5E-01	BE465050.1	EST_HUMAN	Plasmodium berghei cytochrome c oxidase subunit III, cytochrome c oxidase subunit I, and cytochrome b genes, mitochondrial genes encoding mitochondrial proteins, complete cds
8948	18098		1.75	6.5E-01	Z74145.1	NT	hy74810.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3179130 3'
256	9532	18663	8.75	6.4E-01	U48848.1	NT	S. cerevisiae chromosome IV reading frame ORF YDL097c
3433	12658	21789	2.87	6.4E-01	U48854.2	NT	Drosophila melanogaster 8kd dynein light chain mRNA, complete cds
4490	13688	22779	0.73	6.4E-01	Y12488.1	NT	Mus musculus dystroglycan 1 (DAG1) gene, exons 1 and 2 and complete cds
4490	13688	22780	0.73	6.4E-01	Y12488.1	NT	M.musculus whn gene

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7105	16282	25762	0.92	6.4E-01	U82828.1	NT	Homo sapiens ataxia telangiectasia (ATM) gene, complete cds
8816	17734		7.45	6.4E-01	AV759212.1	EST_HUMAN	AV759212 MDS Homo sapiens cDNA clone MDSGCG09 5'
440	9694	18833	4.65	6.3E-01	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
541	9792	18915	2.33	6.3E-01	U32889.1	NT	Haemophilus influenzae Rd section 4 of 183 of the complete genome
2126	11327	20545	2.37	6.3E-01	U81136.1	NT	Shigella flexneri multi-antigenic resistance locus
2542	11730	20848	2.44	6.3E-01	U75331.1	NT	Gallus gallus bone morphogenetic protein 1 (BMP1) mRNA, partial cds
2542	11730	20949	2.44	6.3E-01	U75331.1	NT	Gallus gallus bone morphogenetic protein 1 (BMP1) mRNA, partial cds
2979	12216		0.69	6.3E-01	Y17275.1	NT	Lycopodium obscurum p88a gene, complete CDS
6896	16077	25545	4.49	6.3E-01	8627521	NT	Varicella virus, complete genome
6896	16077	25548	4.49	6.3E-01	8627521	NT	Varicella virus, complete genome
7627	16829	26326	1.86	6.3E-01	AA877715.1	EST_HUMAN	h09h08.s1 NCI_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1161371 3' similar to TR:002816 002916 HLARK :
7679	17067	26392	14.1	6.3E-01	AB04160.1	EST_HUMAN	CM-BT043-060289-046 BT043 Homo sapiens cDNA
7663	17142	26675	2.07	6.3E-01	P47003	SWISSPROT	HYPOTHETICAL 13.7 KD PROTEIN IN INO1-JDS2 INTERGENIC REGION
8116	17250	26790	1.95	6.3E-01	P36073	SWISSPROT	HYPOTHETICAL 15.3 KD PROTEIN IN YMA12-APN1 INTERGENIC REGION
6392	18320	23596	8.86	6.3E-01	8910283	NT	Mus musculus keratin complex 2, gene 6g (Krt2-6g), mRNA
8490	17534		1.48	6.3E-01	AF105227.1	NT	Homo sapiens 3'-phosphoadenosine 5'-phosphosulfate synthetase (PAPS) mRNA, complete cds
8716	18230		2.12	6.3E-01	X33528.1	NT	Cilicicda pect gene
5600	14824	24200	1.94	6.2E-01	Q10135	SWISSPROT	HYPOTHETICAL 142.5 KD PROTEIN C23E2.02 IN CHROMOSOME 1
6286	15469		2.85	6.2E-01	AF022253.1	NT	Mus musculus calcium-sensing receptor related protein 4 (Casr-ra4) mRNA, partial cds
6561	15757	25220	8.38	6.2E-01	H72255.1	EST_HUMAN	ys01e08.s1 Soares fetal liver spleen 1NFS Homo sapiens cDNA clone IMAGE:213542 3'
6915	16103		3.47	6.2E-01	M24461.1	NT	Human pulmonary surfactant-associated protein SP-B (SFTP3) mRNA, complete cds
7100	16277	25757	10.3	6.2E-01	AL161511.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 23
7215	16392	25874	5.08	6.2E-01	P27410	SWISSPROT	NON-STRUCTURAL POLYPROTEIN [CONTAINS: RNA-DIRECTED RNA POLYMERASE ; THIOL
7215	16392	25875	5.08	6.2E-01	P27410	SWISSPROT	PROTEASE P3C ; HELICASE (2C LIKE PROTEIN); COAT PROTEIN]
2358	11651		6.54	6.1E-01	8678078	NT	NON-STRUCTURAL POLYPROTEIN [CONTAINS: RNA-DIRECTED RNA POLYMERASE ; THIOL
6026	16233	24654	3.81	6.1E-01	M64733.1	NT	PROTEASE P3C ; HELICASE (2C LIKE PROTEIN); COAT PROTEIN]
6026	16233	24655	3.81	6.1E-01	M64733.1	NT	Mus musculus secreted acidic cysteine rich glycoprotein (Spero), mRNA
6537	15733	25187	4.68	6.1E-01	AF033535.1	NT	Rat TRPM-2 gene, complete cds
6885	16076	25543	26.49	6.1E-01	AF236117.1	NT	Rat TRPM-2 gene, complete cds
6885	16076	25544	26.49	6.1E-01	AF236117.1	NT	Arabidopsis thaliana putative zinc transporter (ZIP1) mRNA, complete cds
							Homo sapiens G-protein coupled receptor EDG-7 mRNA, complete cds
							Homo sapiens G-protein coupled receptor EDG-7 mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8225	17355	26882	2.27	6.1E-01	S83182.1	NT	hyaluronan-binding protein=hepatocyte growth factor activator homolog [human, plasma, mRNA, 2408 nt]
8225	17355	26883	2.27	6.1E-01	S83182.1	NT	hyaluronan-binding protein=hepatocyte growth factor activator homolog [human, plasma, mRNA, 2408 nt]
8488	18116	23810	1.39	6.1E-01	AB041350.1	NT	Mus musculus Col4a5 mRNA for type IV collagen alpha 5 chain, complete cds
9150	17953		1.38	6.1E-01	X95287.1	NT	M.mazaei orfA, orfB, and orfC of archaeal ABC-transporter system
501	8753	18881	0.83	6.0E-01	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
568	8818		2.86	6.0E-01	5802989	NT	Homo sapiens adaptor-related protein complex 3, mu 2 subunit (CLA20), mRNA
1370	10584	19751	1.71	6.0E-01	AF065253.1	NT	Human respiratory syncytial virus strain CH183-53b attachment protein (G) gene, complete cds
3804	13022	22133	0.92	6.0E-01	AJ233398.1	NT	Viral hemorrhagic septicemia virus N, P, M, G, Nv, L genes, French strain 07-71
4011	13223	22324	1.39	6.0E-01	X16842.1	NT	Xenopus mRNA for desmin
4170	13374		1.31	6.0E-01	AF058895.1	NT	Homo sapiens Notch3 (NOTCH3) gene, exons 26, 27, and 28
5314	14546	23815	1.92	6.0E-01	P20288	SWISSPROT	D(2) DOPAMINE RECEPTOR
5412	14841	23772	2.63	6.0E-01	AW139713.1	EST_HUMAN	UI-H-811-eeb-e-10-Q-UJ.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2718819 3'
5897	15114	24525	2.64	6.0E-01	U98813.1	NT	Musca domestica insecticide-susceptible strain voltage-sensitive sodium channel mRNA, complete cds
6232	15413	24854	6.27	6.0E-01	AJ277881.1	NT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
6500	15897	25161	5.08	6.0E-01	P02835	SWISSPROT	SEGMENTATION PROTEIN FUSHI TARAZU
6500	15897	25162	5.08	6.0E-01	P02835	SWISSPROT	SEGMENTATION PROTEIN FUSHI TARAZU
7019	16186	25672	2.66	6.0E-01	AB008193.1	NT	Homo sapiens genes for leukotriene B4 receptor BLT2, leukotriene B4 receptor BLT1, complete cds
7159	16336		2.39	6.0E-01	Q01497	SWISSPROT	PEROXISOMAL MEMBRANE PROTEIN PERO (PEROXIN-3)
7824	16826	26323	1.98	6.0E-01	AJ131892.1	NT	Gallus gallus mRNA for Hyperion protein, 419 kD isoform
7824	16826	26324	1.98	6.0E-01	AJ131892.1	NT	Gallus gallus mRNA for Hyperion protein, 419 kD isoform
8085	17220	26756	2.68	6.0E-01	AJ420623.1	EST_HUMAN	h08f07.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2085621 3'
8788	17715	23960	1.73	6.0E-01	11421683	NT	Homo sapiens nuclear factor (erythroid-derived 2)-like 3 (NFE2L3), mRNA
8886	17760		1.55	6.0E-01	AA708087.1	EST_HUMAN	Homo sapiens RNA binding motif protein 3 (RBM3), mRNA
9052	18161		2.62	6.0E-01	5803136	NT	Homo sapiens cGMP-inhibited phosphodiesterase (Pde3a), mRNA
9093	18165	23755	1.87	6.0E-01	0055303	NT	Mus musculus cGMP-inhibited phosphodiesterase (Pde3a), mRNA
9121	18090		2.38	6.0E-01	BE157617.1	EST_HUMAN	RC1-HT0376-030500-015-c03 HT0375 Homo sapiens cDNA
1008	10239	18391	2.5	5.9E-01	U32701.1	NT	Haemophilus influenzae Rd section 16 of 163 of the complete genome
3237	12471	21802	5.43	5.9E-01	AL163287.2	NT	Homo sapiens chromosome 21 segment HS21C087
3237	12471	21603	5.43	5.9E-01	AL163287.2	NT	Homo sapiens chromosome 21 segment HS21C087
4205	13408		3.92	5.9E-01	AF162756.1	NT	Rattus norvegicus ceraxin 2 mRNA, partial cds

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5854	15072	24483	5.05	5.9E-01	AF065440.2	NT	Homo sapiens low density lipoprotein receptor-related protein II (LRP2) gene, exon 1 and partial cds
6195	15377	24817	1.84	5.9E-01	AB072348.1	NT	Homo sapiens gene for histamine H2 receptor, promoter region and complete cds
7130	16307	25787	2.2	5.9E-01	P55284	SWISSPROT	VASCULAR ENDOTHELIAL-CADHERIN PRECURSOR (VE-CADHERIN) (CADHERIN-5)
7264	16463	25976	3.21	5.9E-01	Q8X0J3	SWISSPROT	THYMIDYLATE KINASE (DTMP KINASE)
7269	16488	25978	1.76	5.9E-01	AF197844.1	NT	Xenopus laevis receptor protein tyrosine phosphatase delta (XPTP-D) mRNA, complete cds
7632	16737	26227	2.97	5.9E-01	AW837175.1	EST_HUMAN	PM1-DT0041-190100-002-h03 DT0041 Homo sapiens cDNA
7748	16844	26456	2.23	5.9E-01	AF068426.1	NT	Mus spretus strain SPRET/EI CD48 antigen (Cd48) gene, partial cds
8428	17495	24012	1.87	5.9E-01	L42320.1	NT	Oryctolagus cuniculus alpha 1 anti-trypsin (alpha 1 AT) gene, promoter region
8884	17653		1.53	5.9E-01	AB0117705.1	NT	Aspergillus oryzae pyrG gene for orotidine-5'-phosphate decarboxylase, complete cds
8910	17789		6.21	5.9E-01	P34928	SWISSPROT	MICROTUBULE-ASSOCIATED PROTEIN 1A [CONTAINS: MAP1 LIGHT CHAIN LC2]
1873	11080	20270	0.93	5.8E-01	P40472	SWISSPROT	SIM1 PROTEIN
3682	13177	22280	0.95	5.8E-01	BF685738.1	EST_HUMAN	601852474F1 NIH_MGC 58 Homo sapiens cDNA clone IMAGE:4076131 5'
4516	13711	22804	2.77	6.8E-01	AB009077.1	NT	Vigna radiata mRNA for proton pyrophosphatase, complete cds
4808	13897		1.44	5.8E-01	AF110848.1	NT	Megascella scalaris sex-lethal homolog (Mgsxl) gene, partial cds, alternatively spliced products
6003	15285		2.43	5.8E-01	S85091.1	NT	cyclic AMP-regulated phosphoprotein [rats, mRNA, 1030 nt]
6525	15721	25185	2.9	5.8E-01	P14328	SWISSPROT	SPORE COAT PROTEIN SP88
6525	15721	25186	2.9	5.8E-01	P14328	SWISSPROT	SPORE COAT PROTEIN SP88
6741	15938	25397	12.15	5.8E-01	AJ270774.1	NT	Homo sapiens partial TCF-4 gene for T-cell transcription factor-4, exons 6-11
7681	18788	26257	9.84	5.8E-01	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
7698	18809		3.72	5.8E-01	BF700082.1	EST_HUMAN	602127577F1 NIH_MGC 58 Homo sapiens cDNA clone IMAGE:4284403 5'
7701	18900		2.14	5.8E-01	BF700082.1	EST_HUMAN	602127577F1 NIH_MGC 58 Homo sapiens cDNA clone IMAGE:4284403 5'
3008	12244		0.88	5.7E-01	8765263	NT	Mus musculus plasmacytoma variant translocation 1 (Pvt1), mRNA
3189	12424	21557	1.5	5.7E-01	Q8W1J2	SWISSPROT	PUTATIVE TRANSCRIPTION FACTOR OVO-LIKE 1 (MOV01) (MOV01A)
3478	12702		3.08	5.7E-01	AB033503.1	NT	Populus euramericana pease-2 mRNA for 1-aminocyclopropane-1-carboxylate synthase, complete cds
3881	13087	22214	1.81	6.7E-01	AF011581.1	NT	Homo sapiens T cell receptor beta chain (BV8S72-BJ1S1) mRNA, partial cds
5818	15033	24434	4.41	5.7E-01	BF035413.1	EST_HUMAN	601454962F1 NIH_MGC 68 Homo sapiens cDNA clone IMAGE:3858580 5'
6400	15581	25038	2.26	5.7E-01	P00373	SWISSPROT	PYRROLINE-5-CARBOXYLATE REDUCTASE (P5CR) (P5C REDUCTASE)
8386	17487		1.31	5.7E-01	BE715051.1	EST_HUMAN	MR3-HT0738-180700-003-a02 HT0738 Homo sapiens cDNA
3340	12568	21707	1.22	5.6E-01	AB018283.2	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
3340	12568	21708	1.22	5.6E-01	AB018283.2	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
6718	15913	25372	4.84	5.6E-01	AV684703.1	EST_HUMAN	AV684703 GKC Homo sapiens cDNA clone GKCF5F05 5'
6718	15913	25373	4.84	5.6E-01	AV684703.1	EST_HUMAN	AV684703 GKC Homo sapiens cDNA clone GKCF5F05 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8284	17400		2.94	5.6E-01	BE888280.1	EST_HUMAN	601514007F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3916457 5'
8401	17478	28595	1.58	5.6E-01	AA493535.1	EST_HUMAN	hg75g10.s1 NCI_CGAP_P16 Homo sapiens cDNA clone IMAGE:940874 similar to contains element PTR7 repetitive element;
8788	14404	23583	1.7	5.6E-01	AL181501.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 13
8812	17732		2.41	5.6E-01	P50505	SWISSPROT	HIGH AFFINITY POTASSIUM TRANSPORTER
8238	18010		4.08	5.6E-01	BF573829.1	EST_HUMAN	602132028F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271334 5'
1219	10437	19583	1.49	5.5E-01	8393012	NT	Rattus norvegicus Propionyl Coenzyme A carboxylase, beta polypeptide (Pccb), mRNA
2882	11843	21057	2.75	5.5E-01	P03341	SWISSPROT	GAG POLYPROTEIN [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]
2882	11843	21058	2.75	5.5E-01	P03341	SWISSPROT	GAG POLYPROTEIN [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]
2889	12107	21238	1	5.5E-01	5902085	NT	Homo sapiens superkiller virulicidic activity 2 (S. cerevisiae homolog)-like (SKIV2L), mRNA
3030	12266		1.75	5.5E-01	H48219.1	EST_HUMAN	yo18a10.s1 Soares adult brain N2b5f1B55Y Homo sapiens cDNA clone IMAGE:178288 3'
3200	12435	21570	3.18	5.5E-01	AF227240.1	NT	Rabbit oral papillomavirus, complete genome
3871	12882	22013	1.23	5.5E-01	P48755	SWISSPROT	FOS-RELATED ANTIGEN-1
5171	14350		1.05	5.5E-01	AF083688.1	NT	Melanoplus sanguinipes entomopoxvirus, complete genome
142	9424	18557	10.17	5.4E-01	7657288	NT	Homo sapiens KIAA0928 protein Mx2 interacting nuclear target (MINT) homolog (KIAA0928), mRNA
142	9424	18558	10.17	5.4E-01	7657288	NT	Homo sapiens KIAA0928 protein Mx2 interacting nuclear target (MINT) homolog (KIAA0928), mRNA
592	9840	18959	1.84	5.4E-01	AF232008.1	NT	Pseudomonas syringae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and GsaA (gsaA) genes, complete cds; and unknown genes
592	9840	18960	1.84	5.4E-01	AF232008.1	NT	Pseudomonas syringae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and GsaA (gsaA) genes, complete cds; and unknown genes
1278	10493	19652	3.59	5.4E-01	AW896037.1	EST_HUMAN	QV4-NN0040-070400-180-c04 NN0040 Homo sapiens cDNA
2076	11278	20641	2.48	5.4E-01	AE002247.2	NT	Chlamydomonas reinhardtii AR39, section 74 of 84 of the complete genome
2219	11418	20641	2.25	5.4E-01	AJ276682.1	NT	Drosophila melanogaster mRNA for 15.15 beta carotene dioxygenase (beta-diox gene)
5280	14433		1.89	5.4E-01	X85973.1	NT	A. thaliana mRNA for phospholipase-specific phospholipase C
5514	14739	24104	1.87	5.4E-01	AW842327.1	EST_HUMAN	PM2-CN0030-030200-003-c10 CN0030 Homo sapiens cDNA
7070	16247		2.44	5.4E-01	BF572538.1	EST_HUMAN	602078545F1 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:4243690 5'
7844	16844	28342	3.44	5.4E-01	P36858	SWISSPROT	NITRATE REDUCTASE [NADPH] (NR)
8141	17273	28817	6.26	5.4E-01	Q00675	SWISSPROT	LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSIN HEAVY CHAIN)
8141	17273	28818	6.28	5.4E-01	Q00675	SWISSPROT	LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSIN HEAVY CHAIN)

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8348	17443		2.44	5.4E-01	A1858398.1	EST_HUMAN	w37g04.x1 NCI_CGAP_UH1 Homo sapiens cDNA clone IMAGE:2427128 3' similar to gb:M13452 LAMIN A (HUMAN);
522	9773	18888	1.4	5.3E-01	AF019413.1	NT	Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SKI2W), RD, complement factor B (Bf), and complement component C2 (C2) genes, >
2737	11916	21128	7.07	5.3E-01	4508328	NT	Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPRZ1) mRNA
2737	11916	21130	7.07	5.3E-01	4508328	NT	Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPRZ1) mRNA
3208	12443	21675	3.37	5.3E-01	AF087658.1	NT	Homo sapiens secreted C-type lectin precursor (LSLCL) gene, complete cds
4194	13398		1.36	5.3E-01	U39887.1	NT	Mycoplasma genitalium section 8 of 51 of the complete genome
5423	14850	23785	1.82	5.3E-01	A1820921.1	EST_HUMAN	zu42h12.y5 Soares ovary tumor NtHOT Homo sapiens cDNA clone IMAGE:740711 5'
5423	14850	23788	1.82	5.3E-01	A1820921.1	EST_HUMAN	zu42h12.y5 Soares ovary tumor NtHOT Homo sapiens cDNA clone IMAGE:740711 5'
5510	14735	24087	2.05	5.3E-01	BE945620.1	EST_HUMAN	7e73c12.x1 NCI_CGAP_P728 Homo sapiens cDNA clone IMAGE:3288118 3' similar to gb:J02783 PROTEIN DISULFIDE ISOMERASE PRECURSOR (HUMAN);
5510	14735	24088	2.05	5.3E-01	BE945620.1	EST_HUMAN	7e73c12.x1 NCI_CGAP_P728 Homo sapiens cDNA clone IMAGE:3288118 3' similar to gb:J02783 PROTEIN DISULFIDE ISOMERASE PRECURSOR (HUMAN);
6745	15940		2.53	5.3E-01	L01950.2	NT	Roridula gorgonias ribulose 1,5-bisphosphate carboxylase (rbcl) gene, partial cds; chloroplast gene for chloroplast product
8095	17229	26767	6.25	5.3E-01	BE568291.1	EST_HUMAN	601339867F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3682168 5'
8277	18162		3.58	5.3E-01	AA916053.1	EST_HUMAN	cg30a05.s1 NCI_CGAP_Br7 Homo sapiens cDNA clone IMAGE:1441376 3' similar to gb:J02811 APOLIPOPROTEIN D PRECURSOR (HUMAN);
826	10084	18218	10.97	5.2E-01	L20770.1	NT	Drosophila melanogaster helix-loop-helix mRNA, complete cds
1172	10383	19545	11.35	5.2E-01	Q9WV30	SWISSPROT	NUCLEAR FACTOR OF ACTIVATED T CELLS 5 (T CELL TRANSCRIPTION FACTOR NFAT5) (NF-AT5) (REL DOMAIN-CONTAINING TRANSCRIPTION FACTOR NFAT5)
1188	10419	19572	2.73	5.2E-01	AF224492.1	NT	Homo sapiens phospholipid scramblase 1 gene, complete cds
1851	11058		3.64	5.2E-01	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
2114	11313	20529	2.33	5.2E-01	AB018283.2	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
2461	11652	20873	10.39	5.2E-01	AF199339.1	NT	Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds
2461	11652	20874	10.39	5.2E-01	AF199339.1	NT	Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds
3083	12319	21440	1.91	5.2E-01	U65942.1	NT	Chlamydomonas reinhardtii strain S293 POMP81A and POMP80A precursor, genes, complete cds
3203	12438		0.77	5.2E-01	D73443.1	NT	Azotobacter vinelandii lcd gene for isocitrate dehydrogenase, complete cds
3383	12610		1.54	5.2E-01	AL119780.1	NT	Bacillus cereus strain T4 cDNA library under conditions of nitrogen deprivation
3421	12648	21776	2.28	5.2E-01	AA984165.1	EST_HUMAN	am77g05.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1616504 3'
3610	12831		0.6	5.2E-01	AF020269.1	NT	Medicago sativa chloroplast malate dehydrogenase precursor (p1mdh) mRNA, nuclear gene encoding chloroplast protein, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4482	13680		1.07	5.2E-01	AF083786.1	NT	Aden infectious bronchitis virus isolate variant 2 S1 spike glycoprotein gene, partial cds
4808	13602	22892	0.7	5.2E-01	6752947	NT	Mus musculus acetylcholine receptor beta (Acrb), mRNA
9208	17891		4.88	5.2E-01	P18516	SWISSPROT	RETINOIC ACID RECEPTOR GAMMA (RAR-GAMMA) (RETINOIC ACID RECEPTOR DELTA) (RAR-DELTA)
623	9888	18980	1.82	5.1E-01	M58509.1	NT	Human adrenodoxin reductase gene, exons 3 to 12
654	9900	19025	4.85	5.1E-01	AJ233944.1	NT	Pyangium vitellinum (strain PI vt1) 16S rRNA gene
654	9900	19028	4.85	5.1E-01	AJ233944.1	NT	Pyangium vitellinum (strain PI vt1) 16S rRNA gene
1892	11185		1.2	5.1E-01	BF683085.1	EST_HUMAN	602139319F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4288117 5'
4054	13284	22367	4.8	5.1E-01	A1859495.1	EST_HUMAN	W39012.1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2427263 3'
4188	13372	22471	3.35	5.1E-01	P68380	SWISSPROT	TRANSCRIPTION-REPAIR COUPLING FACTOR (TRCF)
6049	15217	24637	1.74	6.1E-01	R80873.1	EST_HUMAN	Y04609.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:148872 3'
6986	16164	25638	6.52	5.1E-01	J05412.1	NT	Human regenerating protein (reg) gene, complete cds
6887	16165	25637	4.7	5.1E-01	W22302.1	EST_HUMAN	6581 Human retina cDNA Tap5091-cleaved sublibrary Homo sapiens cDNA not directional
8501	18084		3.24	5.1E-01	BF030207.1	EST_HUMAN	601556863F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3826767 5'
8769	17700		2.09	5.1E-01	BF439882.1	EST_HUMAN	nec51f10.x1 NCI_CGAP_Bim23 Homo sapiens cDNA clone IMAGE:3406218 3' similar to contains element TAR1 repetitive element:
2104	11304	20517	1.06	5.0E-01	4885552	NT	Homo sapiens postmitotic segregation Increased 2-like 9 (PMS2L9), mRNA
2104	11304	20518	1.06	5.0E-01	4885552	NT	Homo sapiens postmitotic segregation Increased 2-like 9 (PMS2L9), mRNA
2112	11311	20525	1.53	5.0E-01	AF008210.1	NT	Buchnera aphidicola genomic fragment containing (chaperone Hsp60) groEL, DNA biosynthesis initiating protein (dnaA), ATP operon (apCDGAHFEB), and putative chromosome replication protein (gidA) genes, complete cds; and termination factor Rho (rho) gene>
2112	11311	20528	1.63	5.0E-01	AF008210.1	NT	Buchnera aphidicola genomic fragment containing (chaperone Hsp60) groEL, DNA biosynthesis initiating protein (dnaA), ATP operon (apCDGAHFEB), and putative chromosome replication protein (gidA) genes, complete cds; and termination factor Rho (rho) gene>
3729	12948	22068	0.64	5.0E-01	U55574.1	NT	Mus musculus anti-DNA immunoglobulin light chain IgM mRNA, antibody 383p.138, partial cds
3854	13070	22184	3.27	5.0E-01	AB033010.1	NT	Homo sapiens mRNA for KIAA1184 protein, partial cds
6898	15804	25069	4.28	5.0E-01	BF317212.1	EST_HUMAN	601903871F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4136832 5'
8434	17500		1.92	5.0E-01	AF029215.1	NT	Mus musculus MIR3 OX-2 antigen homolog gene, exons 2-5, and complete cds
9174	17867		2.88	5.0E-01	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
9185	17976		3.84	5.0E-01	O13961	SWISSPROT	NUCLEAR ENVELOPE PROTEIN CUT11
789	10038	19189	2.7	4.9E-01	BF571462.1	EST_HUMAN	602076849F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4243860 5'
1635	10849	20027	2.86	4.9E-01	AJ243955.1	NT	Xenopus laevis mRNA for c-Jun protein, 1978 BP
1870	11077	20287	1.33	4.9E-01	U40889.1	NT	Cavia porcellus pulmonary surfactant protein A (SP-a) mRNA, complete cds
5677	14897	24289	3.1	4.9E-01	AF020831.1	NT	Homo sapiens diacylglycerol kinase 3 (DAGK3) gene, exon 10

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5677	14997	24280	3.1	4.9E-01	AF020931.1	NT	Homo sapiens diacylglycerol kinase 3 (DAGK3) gene, exon 10
6275	15455	24898	1.68	4.9E-01	AB040051.1	NT	Oryza sativa subsp. japonica mEF-G mRNA for mitochondrial elongation factor G, complete cds
6853	18389		2.73	4.9E-01	10948883	NT	Mus musculus unc13 homolog (C. elegans) 1 (Unc13h1), mRNA
8328	17428		1.61	4.8E-01	AF178912.1	NT	Homo sapiens neurotrophin-1/B-cell stimulating factor-3 gene, complete cds
9167	18354		4.8	4.8E-01	AA613562.1	EST_HUMAN	h22611.s1 NCL CGAP Co10 Homo sapiens cDNA clone IMAGE:1144852 3'
9249	18019		1.47	4.9E-01	11431438	NT	Homo sapiens eukaryotic translation initiation factor 4 gamma, 1 (EIF4G1), mRNA
3512	12736		0.88	4.8E-01	AA612842.1	EST_HUMAN	d32a09.s1 Soaree_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1525144 3'
4324	13525		0.69	4.8E-01	4504850	NT	Homo sapiens potassium channel, subfamily K, member 5 (TASK-2) (KCNK5) mRNA, and translated products
4678	13825		0.68	4.8E-01	4504850	NT	Homo sapiens potassium channel, subfamily K, member 5 (TASK-2) (KCNK5) mRNA, and translated products
5443	14688	23828	8.14	4.8E-01	J02987.1	NT	Saccharomyces cerevisiae sporulation protein (SPO11) gene required for meiotic recombination, complete cds
5961	15178		3.78	4.8E-01	AA659878.1	EST_HUMAN	nu85f09.s1 NCL CGAP_Alv1 Homo sapiens cDNA clone IMAGE:1217513
6218	15397		2.3	4.8E-01	5031650	NT	Homo sapiens reproduction 8 (D8S2288E) mRNA
6399	15590	25038	3.91	4.8E-01	AL181492.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 4
6399	15580	25037	3.91	4.8E-01	AL181492.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 4
7310	16334		2.05	4.8E-01	X83502.1	NT	S.cerevisiae ORF6 from chromosome X
8408	17483		1.28	4.8E-01	AL183227.2	NT	Homo sapiens chromosome 21 segment HS21C027
8645	18122		3.04	4.8E-01	AF227565.1	NT	Trypanosoma cruzi transposon VIP II SIRE repeat region
3039	12276		0.78	4.7E-01	AF182387.1	NT	Felis catus feline leukemia virus subgroup C receptor (FLVCR1) mRNA, complete cds
5882	15099	24510	8.23	4.7E-01	BF217173.1	EST_HUMAN	601883880F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4096387 5'
7424	18834		8.28	4.7E-01	AF102873.1	NT	Influenza A virus isolate h51897 hemagglutinin (HA) gene, partial cds
7651	16851	26349	2.42	4.7E-01	U41069.1	NT	Human collagen alpha2(XI) (COL11A2) gene, exons 8 through 18, and partial cds
7915	17130	26680	2.99	4.7E-01	AW889448.1	EST_HUMAN	RC8-NT0029-240400-011-E08 NT0029 Homo sapiens cDNA
8687	17843		1.41	4.7E-01	AW341561.1	EST_HUMAN	h11c08.x1 Soaree_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2909188 3'
3724	12944	22061	1.64	4.6E-01	BF883300.1	EST_HUMAN	602081103F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4245481 5'
3724	12944	22082	1.84	4.6E-01	BF883300.1	EST_HUMAN	602081103F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4245481 5'
5428	14855	23782	3.65	4.6E-01	Q90843	SWISSPROT	INTERFERON REGULATORY FACTOR 3 (IRF-3)
5428	14855	23783	3.65	4.6E-01	Q90843	SWISSPROT	INTERFERON REGULATORY FACTOR 3 (IRF-3)
5464	14880	24042	1.88	4.6E-01	BE734781.1	EST_HUMAN	601588755F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3843637 5'
5473	14899	24052	1.88	4.6E-01	AI247679.1	EST_HUMAN	qh59h02.x1 Soaree_fetal_liver_splice_1NLS_S1 Homo sapiens cDNA clone IMAGE:1848011 3' similar to TR:O15338 O15338 BUTYROPHILIN.;

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5473	14689	24053	1.88	4.6E-01	A1247678.1	EST_HUMAN	qh50h02.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849011 3' similar to TR:O15338 O15338 BUTYRPHILIN.;
5885	15267	24692	1.84	4.6E-01	U62332.1	NT	Emertocella nidulans NEMPA (nemPA) gene, mitochondrial gene encoding putative mitochondrial protein, complete cds
5985	15267	24693	1.84	4.6E-01	U62332.1	NT	Emertocella nidulans NEMPA (nemPA) gene, mitochondrial gene encoding putative mitochondrial protein, complete cds
6398	15588	25025	2.25	4.6E-01	AA493577.1	EST_HUMAN	rh04h05.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943353 similar to contains Alu repetitive element; contains element L1 repetitive element;
6598	15764	25226	21.67	4.6E-01	BF697399.1	EST_HUMAN	602130953F1 NIH_MGC 56 Homo sapiens cDNA clone IMAGE:4287828 5'
7063	16240	25713	3.37	4.6E-01	A1915634.1	EST_HUMAN	w073612.x1 Soares_NSF_F8_GW_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:4287828 5'
7063	16240	25714	3.37	4.6E-01	A1915634.1	EST_HUMAN	w073612.x1 Soares_NSF_F8_GW_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2370768 3'
7563	16768		3.16	4.6E-01	P88163	SWISSPROT	PUTATIVE VITELLOGENIN RECEPTOR PRECURSOR (YL)
7571	16776	26268	3.63	4.6E-01	BE185449.1	EST_HUMAN	IL5-HT0730-100500-075-g05 HT0730 Homo sapiens cDNA
7571	16778	26269	3.63	4.6E-01	BE185449.1	EST_HUMAN	IL5-HT0730-100500-075-g05 HT0730 Homo sapiens cDNA
8007	16442	25930	5.97	4.6E-01	AF018369.1	NT	Human thiopurine methyltransferase (TPMT) gene, exon 10 and complete cds
8007	16442	25931	5.97	4.6E-01	AF018369.1	NT	Human thiopurine methyltransferase (TPMT) gene, exon 10 and complete cds
8588	17597		1.24	4.6E-01	D53316.1	EST_HUMAN	HUM105F03B Clontech human fetal brain polyA+ mRNA (#8535) Homo sapiens cDNA clone GEN-105F03 5'
1875	11082	20272	1.17	4.5E-01	AE001831.1	NT	Deinococcus radiodurans R1 section 68 of 229 of the complete chromosome 1
1875	11082	20273	1.17	4.5E-01	AE001831.1	NT	Deinococcus radiodurans R1 section 68 of 229 of the complete chromosome 1
2822	12061	21184	5.81	4.5E-01	AA677086.1	EST_HUMAN	z155d02.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:454178 3'
3289	12520	21631	4.15	4.5E-01	Q05793	SWISSPROT	BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN
3358	12584	21723	1.2	4.5E-01	AF126376.1	NT	PRECURSOR (HSPG) (PERLECAN) (PLC)
4008	13218		1.27	4.5E-01	Q28247	SWISSPROT	Mus musculus DNA polymerase epsilon catalytic subunit (Pole) gene, exons 2 through 12
4052	13262	22365	0.86	4.5E-01	A1708808.1	EST_HUMAN	COLLAGEN ALPHA 5(IV) CHAIN
4157	14479		5.3	4.5E-01	AW873495.1	EST_HUMAN	es08609.x1 Barstead aorta HPLR58 Homo sapiens cDNA clone IMAGE:2353480 3'
4962	14149	23241	1.17	4.5E-01	BE963445.2	EST_HUMAN	hcd0g02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3041810 3'
6340	15520	24987	2.51	4.5E-01	A1858849.1	EST_HUMAN	601867225R1 NIH_MGC 67 Homo sapiens cDNA clone IMAGE:3869023 3'
6802	15798	25255	4.3	4.5E-01	A1848596.1	EST_HUMAN	w132602.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2426618 3' similar to TR:Q92823 Q92823
6710	15805		2.22	4.5E-01	11444786	NT	SWISNF NCF 170 KDA SUBUNIT.;
7212	16389	25871	18.01	4.5E-01	M86008.1	EST_HUMAN	ts58g11.x1 NCI_CGAP_Ov35 Homo sapiens cDNA clone IMAGE:2282644 3'
7212	16389	25872	18.01	4.5E-01	M86008.1	EST_HUMAN	Homo sapiens hypothetical protein DKFZp547G183 (DKFZp547G183), mRNA

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7440	16648	26141	3.36	4.5E-01	AW591271.1	EST_HUMAN	xc14h01.x1 NCI_CGAP_U13 Homo sapiens cDNA clone IMAGE:2703985 3' similar to SW:INT6_MOUSE
7804	16987		1.8	4.5E-01	AV719382.1	EST_HUMAN	Q64252 VIRAL INTEGRATION SITE PROTEIN INT-8, [1];
8036	17172	26711	2.23	4.5E-01	BE068472.1	EST_HUMAN	AV719382 GLO Homo sapiens cDNA clone GLCCED12 5'
8298	18348		3.39	4.5E-01	BE871461.1	EST_HUMAN	RC3-BT0333-160300-016-403 BT0333 Homo sapiens cDNA
8693	17854		1.42	4.5E-01	BF337531.1	EST_HUMAN	601449201F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3852981 5'
9097	17894		3.3	4.5E-01	11422089	NT	602035275F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4183290 5'
2004	11207		1.99	4.4E-01	6680503	NT	Homo sapiens testis-specific kinase 2 (TESK2), mRNA
2352	11645	20767	3.37	4.4E-01	P49765	SWISSPROT	Mus musculus integral membrane-associated protein 1 (Imap1), mRNA
3287	12518	21849	1.37	4.4E-01	AF058790.1	NT	VASCULAR ENDOTHELIAL GROWTH FACTOR B PRECURSOR (VEGF-B) (VEGF RELATED FACTOR)
3287	12518	21850	1.37	4.4E-01	AF058790.1	NT	Rattus norvegicus SynGAP-b mRNA, complete cds
3291	12522	21853	2.03	4.4E-01	BF056726.1	EST_HUMAN	Rattus norvegicus SynGAP-b mRNA, complete cds
4219	13422		1.4	4.4E-01	BE378707.1	EST_HUMAN	J91602.y1 NCI_CGAP_B116 Homo sapiens cDNA clone IMAGE:3393795 5'
5242	14416		4.05	4.4E-01	Q11082	SWISSPROT	601237139F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3808393 5'
5770	14988	24389	1.93	4.4E-01	AW080795.1	EST_HUMAN	PROBABLE G PROTEIN-COUPLED RECEPTOR B0563.6
6411	16608		19.38	4.4E-01	Z11678.1	NT	xc27468.x1 NCI_CGAP_Cot18 Homo sapiens cDNA clone IMAGE:2585510 3' similar to TR:095154
7058	16235		2.74	4.4E-01	P28922	SWISSPROT	AF1403XIN B1-ALDEHYDE REDUCTASE, ;
7110	16287	25768	4.94	4.4E-01	P35590	SWISSPROT	S.tuberosum mRNA for induced staton tip protein (partial)
8570	17598	23998	3.41	4.4E-01	6877874	NT	GLYCOPROTEIN B PRECURSOR (GLYCOPROTEIN 14)
8591	18279		4.39	4.4E-01	AL163282.2	NT	TYROSINE-PROTEIN KINASE RECEPTOR TIE-1 PRECURSOR
9035	17879	23893	3.59	4.4E-01	8627742	NT	Mus musculus sodium channel, type X, alpha polypeptide (Scn10a), mRNA
9137	17045		1.88	4.4E-01	P54725	SWISSPROT	Homo sapiens chromosome 21 segment HS21C082
417	9670	18810	2.15	4.3E-01	AF155218.1	NT	Autographa californica nucleopolyhedrovirus, complete genome
417	9670	18811	2.15	4.3E-01	AF155218.1	NT	UV EXCISION REPAIR PROTEIN PROTEIN RAD23 HOMOLOG A (HHR23A)
1693	10798	19973	0.92	4.3E-01	AW886550.1	EST_HUMAN	Callithrix jacchus MW/LW opsin gene, upstream flanking region
2824	12063		1.01	4.3E-01	AW835289.1	EST_HUMAN	Callithrix jacchus MW/LW opsin gene, upstream flanking region
3025	12261	21399	0.87	4.3E-01	AW899477.1	EST_HUMAN	QV4-SN0024-200400-183-b01 SN0024 Homo sapiens cDNA
4133	13339	22438	1.3	4.3E-01	J00308.1	NT	CM2-DT0003-010200-077-c01 DT0003 Homo sapiens cDNA
4400	9670	18810	0.99	4.3E-01	AF155218.1	NT	MRO-BN0070-270300-008-g04 BN0070 Homo sapiens cDNA
4400	9670	18811	0.99	4.3E-01	AF155218.1	NT	Human somatostatin 1 gene and flanks
5618	14841	24219	2.04	4.3E-01	AF178825.1	NT	Callithrix jacchus MW/LW opsin gene, upstream flanking region
5998	15183	24598	4.69	4.3E-01	AJ001078.1	NT	Callithrix jacchus MW/LW opsin gene, upstream flanking region
							Salmix silureus olfactory receptor (SSC186) gene, partial cds
							Coturnix coturnix japonica ifnG gene

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Table 4
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6283	15444		1.94	4.3E-01	BF348001.1	EST_HUMAN	602023134F1 NCI_CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4158298 5'
6608	15905		3.13	4.3E-01	U97040.1	NT	Methanococcus voltae flagellar-related protein C-1 (flaC-fla) genes, complete cds
7505	15275	24705	2.79	4.3E-01	AF075629.1	NT	Equus caballus microsatellite LEX027
7757	16953	28460	1.8	4.3E-01	AW993658.1	EST_HUMAN	RC3-BN0034-280200-013-c12 BN0034 Homo sapiens cDNA
7757	16953	28461	1.8	4.3E-01	AW993658.1	EST_HUMAN	RC3-BN0034-280200-013-c12 BN0034 Homo sapiens cDNA
9238	18009		2.07	4.3E-01	AJ003022.1	NT	Streptomyces coelicolor whiH gene
1368	11992	19747	1.62	4.2E-01	Q39102	SWISSPROT	CELL DIVISION PROTEIN FTSH HOMOLOG PRECURSOR
1917	11122		0.89	4.2E-01	AA761853.1	EST_HUMAN	nt24409.s1 NCI_CGAP_G0B1 Homo sapiens cDNA clone IMAGE:1288696 3'
3587	12608	21830	5.31	4.2E-01	AE003947.1	NT	Xylella fastidiosa, section 93 of 228 of the complete genome
3818	12837	21958	1.03	4.2E-01	AI280338.1	EST_HUMAN	q94b01.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1879945 3'
3692	14478		0.8	4.2E-01	N81203.1	EST_HUMAN	788IE1 fetal brain cDNA Homo sapiens cDNA clone 788IE1-K similar to R07879, Z40498
3960	13175	22289	1.16	4.2E-01	Q04886	SWISSPROT	SOX-8 PROTEIN
4707	13998	22697	7.2	4.2E-01	AA534063.1	EST_HUMAN	nt80h01.s1 NCI_CGAP_P110 Homo sapiens cDNA clone IMAGE:997777 similar to gb:M33600 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR-1 BETA CHAIN (HUMAN);
4780	13978	23083	4.08	4.2E-01	R13467.1	EST_HUMAN	y77e01.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:28278 5'
6064	15254	24678	9.98	4.2E-01	AU158472.1	EST_HUMAN	AU158472 PLACE2 Homo sapiens cDNA clone PLACE2000470 3'
6084	15254	24679	9.08	4.2E-01	AU158472.1	EST_HUMAN	AU158472 PLACE2 Homo sapiens cDNA clone PLACE2000470 3'
6093	18071	24726	1.88	4.2E-01	S82504.1	NT	Brcal=breast cancer gene [rat, WF, spleen, Genomic, 418 nt, segment 2 of 2]
6122	15306	24739	5.87	4.2E-01	AL161547.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 47
6461	15658	25129	5.45	4.2E-01	AW957448.1	EST_HUMAN	EST389413 MAGE resequences, MAGE Homo sapiens cDNA
6481	15658	25130	5.45	4.2E-01	AW957448.1	EST_HUMAN	EST389413 MAGE resequences, MAGE Homo sapiens cDNA
7612	16816	26311	2.08	4.2E-01	AB023489.1	NT	Oryzias latipes OIGC7 mRNA for membrane guanylyl cyclase, complete cds
7833	17073	26600	2.55	4.2E-01	BE968485.2	EST_HUMAN	601880352R1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3908085 3'
9178	17971		1.28	4.2E-01	AV731815.1	EST_HUMAN	AV731815 HTF Homo sapiens cDNA clone HTFBH05 5'
1102	10326	19476	1.44	4.1E-01	AI905481.1	EST_HUMAN	RC-BT081-210183-142 BT081 Homo sapiens cDNA
1111	10335	19485	0.85	4.1E-01	AV705243.1	EST_HUMAN	AV705243 ADB Homo sapiens cDNA clone ADBAHF08 5'
1111	10336	19488	0.85	4.1E-01	AV705243.1	EST_HUMAN	AV705243 ADB Homo sapiens cDNA clone ADBAHF08 5'
2871	11852	21068	1.14	4.1E-01	7705283	NT	Homo sapiens anaphase-promoting complex subunit 7 (APC7), mRNA
2891	12128	21261	2.32	4.1E-01	AL161536.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 38
2891	12128	21262	2.32	4.1E-01	AL161536.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 38
3272	12505	21636	0.6	4.1E-01	AA909344.1	EST_HUMAN	q94b08.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1505943 3'
3753	12972	22087	0.74	4.1E-01	AA9081282.1	EST_HUMAN	EST373364 MAGE resequences, MAGG Homo sapiens cDNA
3753	12972	22088	0.74	4.1E-01	AA9081282.1	EST_HUMAN	EST373364 MAGE resequences, MAGG Homo sapiens cDNA
4260	13463	22555	2.88	4.1E-01	AJ249207.1	NT	Rhodococcus sp. AD45 isoG, [isoH, isoI, isoJ, isoK, isoL, isoM, isoN, isoO, isoP, isoQ, isoR, isoS, isoT, isoU, isoV, isoW, isoX, isoY, isoZ, isoAA, isoAB, isoAC, isoAD, isoAE, isoAF, isoAG, isoAH, isoAI, isoAJ, isoAK, isoAL, isoAM, isoAN, isoAO, isoAP, isoAQ, isoAR, isoAS, isoAT, isoAU, isoAV, isoAW, isoAX, isoAY, isoAZ, isoBA, isoBB, isoBC, isoBD, isoBE, isoBF, isoBG, isoBH, isoBI, isoBJ, isoBK, isoBL, isoBM, isoBN, isoBO, isoBP, isoBQ, isoBR, isoBS, isoBT, isoBU, isoBV, isoBW, isoBX, isoBY, isoBZ, isoCA, isoCB, isoCC, isoCD, isoCE, isoCF, isoCG, isoCH, isoCI, isoCJ, isoCK, isoCL, isoCM, isoCN, isoCO, isoCP, isoCQ, isoCR, isoCS, isoCT, isoCU, isoCV, isoCW, isoCX, isoCY, isoCZ, isoDA, isoDB, isoDC, isoDD, isoDE, isoDF, isoDG, isoDH, isoDI, isoDJ, isoDK, isoDL, isoDM, isoDN, isoDO, isoDP, isoDQ, isoDR, isoDS, isoDT, isoDU, isoDV, isoDW, isoDX, isoDY, isoDZ, isoEA, isoEB, isoEC, isoED, isoEE, isoEF, isoEG, isoEH, isoEI, isoEJ, isoEK, isoEL, isoEM, isoEN, isoEO, isoEP, isoEQ, isoER, isoES, isoET, isoEU, isoEV, isoEW, isoEX, isoEY, isoEZ, isoFA, isoFB, isoFC, isoFD, isoFE, isoFF, isoFG, isoFH, isoFI, isoFJ, isoFK, isoFL, isoFM, isoFN, isoFO, isoFP, isoFQ, isoFR, isoFS, isoFT, isoFU, isoFV, isoFW, isoFX, isoFY, isoFZ, isoGA, isoGB, isoGC, isoGD, isoGE, isoGF, isoGG, isoGH, isoGI, isoGJ, isoGK, isoGL, isoGM, isoGN, isoGO, isoGP, isoGQ, isoGR, isoGS, isoGT, isoGU, isoGV, isoGW, isoGX, isoGY, isoGZ, isoHA, isoHB, isoHC, isoHD, isoHE, isoHF, isoHG, isoHH, isoHI, isoHJ, isoHK, isoHL, isoHM, isoHN, isoHO, isoHP, isoHQ, isoHR, isoHS, isoHT, isoHU, isoHV, isoHW, isoHX, isoHY, isoHZ, isoIA, isoIB, isoIC, isoID, isoIE, isoIF, isoIG, isoIH, isoII, isoIJ, isoIK, isoIL, isoIM, isoIN, isoIO, isoIP, isoIQ, isoIR, isoIS, isoIT, isoIU, isoIV, isoIW, isoIX, isoIY, isoIZ, isoJA, isoJB, isoJC, isoJD, isoJE, isoJF, isoJG, isoJH, isoJI, isoJJ, isoJK, isoJL, isoJM, isoJN, isoJO, isoJP, isoJQ, isoJR, isoJS, isoJT, isoJU, isoJV, isoJW, isoJX, isoJY, isoJZ, isoKA, isoKB, isoKC, isoKD, isoKE, isoKF, isoKG, isoKH, isoKI, isoKJ, isoKK, isoKL, isoKM, isoKN, isoKO, isoKP, isoKQ, isoKR, isoKS, isoKT, isoKU, isoKV, isoKW, isoKX, isoKY, isoKZ, isoLA, isoLB, isoLC, isoLD, isoLE, isoLF, isoLG, isoLH, isoLI, isoLJ, isoLK, isoLL, isoLM, isoLN, isoLO, isoLP, isoLQ, isoLR, isoLS, isoLT, isoLU, isoLV, isoLW, isoLX, isoLY, isoLZ, isoMA, isoMB, isoMC, isoMD, isoME, isoMF, isoMG, isoMH, isoMI, isoMJ, isoMK, isoML, isoMM, isoMN, isoMO, isoMP, isoMQ, isoMR, isoMS, isoMT, isoMU, isoMV, isoMW, isoMX, isoMY, isoMZ, isoNA, isoNB, isoNC, isoND, isoNE, isoNF, isoNG, isoNH, isoNI, isoNJ, isoNK, isoNL, isoNM, isoNO, isoNP, isoNQ, isoNR, isoNS, isoNT, isoNU, isoNV, isoNW, isoNX, isoNY, isoNZ, isoOA, isoOB, isoOC, isoOD, isoOE, isoOF, isoOG, isoOH, isoOI, isoOJ, isoOK, isoOL, isoOM, isoON, isoOO, isoOP, isoOQ, isoOR, isoOS, isoOT, isoOU, isoOV, isoOW, isoOX, isoOY, isoOZ, isoPA, isoPB, isoPC, isoPD, isoPE, isoPF, isoPG, isoPH, isoPI, isoPJ, isoPK, isoPL, isoPM, isoPN, isoPO, isoPP, isoPQ, isoPR, isoPS, isoPT, isoPU, isoPV, isoPW, isoPX, isoPY, isoPZ, isoQA, isoQB, isoQC, isoQD, isoQE, isoQF, isoQG, isoQH, isoQI, isoQJ, isoQK, isoQL, isoQM, isoQN, isoQO, isoQP, isoQQ, isoQR, isoQS, isoQT, isoQU, isoQV, isoQW, isoQX, isoQY, isoQZ, isoRA, isoRB, isoRC, isoRD, isoRE, isoRF, isoRG, isoRH, isoRI, isoRJ, isoRK, isoRL, isoRM, isoRN, isoRO, isoRP, isoRQ, isoRR, isoRS, isoRT, isoRU, isoRV, isoRW, isoRX, isoRY, isoRZ, isoSA, isoSB, isoSC, isoSD, isoSE, isoSF, isoSG, isoSH, isoSI, isoSJ, isoSK, isoSL, isoSM, isoSN, isoSO, isoSP, isoSQ, isoSR, isoSS, isoST, isoSU, isoSV, isoSW, isoSX, isoSY, isoSZ, isoTA, isoTB, isoTC, isoTD, isoTE, isoTF, isoTG, isoTH, isoTI, isoTJ, isoTK, isoTL, isoTM, isoTN, isoTO, isoTP, isoTQ, isoTR, isoTS, isoTT, isoTU, isoTV, isoTW, isoTX, isoTY, isoTZ, isoUA, isoUB, isoUC, isoUD, isoUE, isoUF, isoUG, isoUH, isoUI, isoUJ, isoUK, isoUL, isoUM, isoUN, isoUO, isoUP, isoUQ, isoUR, isoUS, isoUT, isoUU, isoUV, isoUW, isoUX, isoUY, isoUZ, isoVA, isoVB, isoVC, isoVD, isoVE, isoVF, isoVG, isoVH, isoVI, isoVJ, isoVK, isoVL, isoVM, isoVN, isoVO, isoVP, isoVQ, isoVR, isoVS, isoVT, isoVU, isoVV, isoVW, isoVX, isoVY, isoVZ, isoWA, isoWB, isoWC, isoWD, isoWE, isoWF, isoWG, isoWH, isoWI, isoWJ, isoWK, isoWL, isoWM, isoWN, isoWO, isoWP, isoWQ, isoWR, isoWS, isoWT, isoWU, isoWV, isoWW, isoWX, isoWY, isoWZ, isoXA, isoXB, isoXC, isoXD, isoXE, isoXF, isoXG, isoXH, isoXI, isoXJ, isoXK, isoXL, isoXM, isoXN, isoXO, isoXP, isoXQ, isoXR, isoXS, isoXT, isoXU, isoXV, isoXW, isoXX, isoXY, isoXZ, isoYA, isoYB, isoYC, isoYD, isoYE, isoYF, isoYG, isoYH, isoYI, isoYJ, isoYK, isoYL, isoYM, isoYN, isoYO, isoYP, isoYQ, isoYR, isoYS, isoYT, isoYU, isoYV, isoYW, isoYX, isoYY, isoYZ, isoZA, isoZB, isoZC, isoZD, isoZE, isoZF, isoZG, isoZH, isoZI, isoZJ, isoZK, isoZL, isoZM, isoZN, isoZO, isoZP, isoZQ, isoZR, isoZS, isoZT, isoZU, isoZV, isoZW, isoZX, isoZY, isoZZ

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4262	13494		0.78	4.1E-01	AA909257.1	EST_HUMAN	om33402 s1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1642819 3'
4670	13884	22865	1.28	4.1E-01	AV747880.1	EST_HUMAN	AV747880 NPC Homo sapiens cDNA clone NPCBDF10 5'
5257	14430		0.85	4.1E-01	BF345483.1	EST_HUMAN	602019232F1 NCI_CGAP_Bim67 Homo sapiens cDNA clone IMAGE:4155102 5'
5650	14873	24260	4.51	4.1E-01	BF681393.1	EST_HUMAN	602156500F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4297319 5'
6265	15446	24895	2.7	4.1E-01	U67535.1	NT	Methanococcus jannaschii section 77 of 150 of the complete genome
7410	16028	26120	50.16	4.1E-01	X58700.1	NT	Zea mays ZIMPMS2 gene for 19 kDa zein protein
7630	16406	25890	2.89	4.1E-01	Q09470	SWISSPROT	VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.1 (HUK1) (HBK1)
8918	18326		1.76	4.1E-01	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
138	11960		3.52	4.0E-01	AW847123.1	EST_HUMAN	RC2-CT0201-290898-012-410 CT0201 Homo sapiens cDNA
1046	10271	19422	1.06	4.0E-01	8404656	NT	Laqueus rubellus mitochondrion, complete genome
1347	10562	18727	1.04	4.0E-01	AF203478.1	NT	Drosophila melanogaster Dalmatian (dm1) mRNA, complete cds
1478	10681		3.71	4.0E-01	6679258	NT	Mus musculus platelet derived growth factor receptor, beta polypeptide (Pdgfrb), mRNA
1974	12007	20364	1.88	4.0E-01	Z89833.1	NT	Ascoebolus limnerius msc2 gene
1974	12007	20365	1.86	4.0E-01	Z89833.1	NT	Ascoebolus limnerius msc2 gene
2157	9421	18555	2.61	4.0E-01	6878460	NT	Mus musculus ubiquitin-protein ligase e3 component n-recognin (Ubr1), mRNA
2823	12161	21265	1.49	4.0E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
2823	12161	21266	1.49	4.0E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
							Streptococcus pneumoniae Y11C (Y11C), Y11D (Y11D), penicillin-binding protein 2x (pbp2x), and undecaprenyl-phosphate-UDP-MurNAc-pentapeptide phospho-MurNAc-pentapeptide transferase (mraY) genes, complete cds
3673	12894	22016	2.17	4.0E-01	AF068903.1	NT	Ovis aries partial JD2 gene for T cell receptor delta chain (TCRDJ2), exon 1
3817	13035	22148	3.33	4.0E-01	AJ277511.1	NT	Ovis aries partial JD2 gene for T cell receptor delta chain (TCRDJ2), exon 1
3817	13035	22147	3.33	4.0E-01	AJ277511.1	NT	NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 5, CHLOROPLAST
4832	14021		9.93	4.0E-01	Q31849	SWISSPROT	Synechocystis sp. PCC 6413 transposase gene, complete cds
8212	17343		3.53	4.0E-01	L76080.1	NT	Homo sapiens chromosome 21 segment HS21C100
8587	18178		2.26	4.0E-01	AL163300.2	NT	HYPOTHETICAL 49.7 KD PROTEIN IN GIN2-STE3 INTERGENIC REGION
9138	17946		1.4	4.0E-01	P36049	SWISSPROT	Gorilla gorilla carboxyl-ester lipase (CEL) gene, complete cds
1384	10568	18765	1.52	3.9E-01	AF206818.1	NT	Homo sapiens mRNA for KIAA1183 protein, partial cds
2805	11769	21008	3.23	3.9E-01	AB033018.1	NT	H. sapiens B-myb gene
2868	11847	21061	4.38	3.9E-01	X82032.1	NT	H. sapiens B-myb gene
2868	11847	21062	4.39	3.9E-01	X82032.1	NT	Simulium mellei egl, eglB2, eglB3 genes and orf3
3062	12298	21422	4.8	3.9E-01	XJ25686.1	NT	Simulium mellei egl, eglB2, eglB3 genes and orf3
4055	12285	22368	1.53	3.9E-01	BF592811.1	EST_HUMAN	761d01.x1 NCI_CGAP_Bim67 Homo sapiens cDNA clone IMAGE:3339189 3'
5014	14201	23288	2.1	3.9E-01	BE728687.1	EST_HUMAN	601563948F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3833689 5'
5630	14854	24237	4.01	3.9E-01	BF208036.1	EST_HUMAN	601862362F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:4082055 5'

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7032	16209	25688	3.45	3.9E-01	M19879.1	NT	Human clabindin 27 gene, exons 10 and 11, and L1 and Alu repeats
7397	16810		1.94	3.9E-01	AV685974.1	EST_HUMAN	AV685974 GKC Homo sapiens cDNA clone GKC8QC11 5'
8352	18255		4.15	3.9E-01	AF304354.1	NT	Homo sapiens proteoglycan 3 (PRG3) gene, complete cds
8475	17528		2.15	3.9E-01	Q61670	SWISSPROT	HOMEBOX PROTEIN HLX1
8561	17582	23697	1.37	3.9E-01	AE001811.1	NT	Thermotoga maritima section 123 of 136 of the complete genome
9011	17865		1.31	3.9E-01	11433335	NT	Homo sapiens hypothetical protein FLJ10583 (FLJ10583), mRNA
163	9445		16.12	3.9E-01	7019488	NT	Homo sapiens protein kinase PKNbeta (pknbeta), mRNA
512	9763		6.69	3.9E-01	AB023291.1	NT	Mus musculus pom-1 mRNA for pericentriolar material-1, complete cds
1838	11044		1.28	3.9E-01	AE003870.1	NT	Xylella fastidiosa, section 18 of 228 of the complete genome
2535	11723	20940	3.41	3.9E-01	AF214117.1	NT	Arabidopsis thaliana putative c-myc-like transcription factor (MYB3R-3) mRNA, complete cds
2698	12021	21000	4.04	3.9E-01	6678002	NT	Mus musculus solute carrier family 1, member 6 (Slc1a6), mRNA
2861	12189		0.92	3.9E-01	AJ251057.1	NT	Human immunodeficiency virus type 1 complete genome (isolate 88SE-MP1213)
3013	12249	21360	2.35	3.9E-01	AF043383.1	NT	Pleuronectes americanus aminopeptidase N (ampn) gene, partial cds
3458	12883	21817	9.08	3.9E-01	AL161618.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 30
3513	12737		0.75	3.9E-01	AI807218.1	EST_HUMAN	W38b12.x1 Soares_NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:2357855 3'
3528	12737		0.66	3.9E-01	AI807218.1	EST_HUMAN	W38b12.x1 Soares_NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:2357855 3'
3558	12779	21908	6.64	3.9E-01	AF109372.1	NT	Danio rerio blue-sensitive opsin (bluops) mRNA, complete cds
3558	12778	21909	6.64	3.9E-01	AF109372.1	NT	Danio rerio blue-sensitive opsin (bluops) mRNA, complete cds
3739	12959	22074	1.09	3.9E-01	BE154080.1	EST_HUMAN	PMO-HT0339-200400-010-G01 HT0339 Homo sapiens cDNA
3894	13110	22228	0.69	3.9E-01	6754095	NT	Mus musculus general transcription factor II I (Gtf2i), mRNA
5079	14259	23344	1.14	3.9E-01	AF038833.1	NT	Homo sapiens Mpv17 protein (MPV17) gene, partial cds; and urocorin gene, complete cds
5221	14395	23480	4.31	3.9E-01	AF158835.1	NT	Triticum ventricosum V8 (V6) gene, partial cds
5945	15161	24574	5.59	3.9E-01	BE072399.1	EST_HUMAN	QV3-BT0537-271289-049-402 BT0537 Homo sapiens cDNA
5984	15268	24691	4.68	3.9E-01	A1374601.1	EST_HUMAN	ta54f11.x1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:2047817 3' similar to contains Alu repetitive element
6297	16478		4.51	3.9E-01	X81597.1	NT	M.musculus gene for kallikrein-binding protein
6841	16838	25297	3.65	3.9E-01	AB048851.1	NT	Homo sapiens mRNA for KIAA1631 protein, partial cds
6944	16888		7.37	3.9E-01	T95413.1	EST_HUMAN	ye43h08.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:120539 5' similar to contains Alu repetitive element; contains PTR5 repetitive element
8065	17200		3.41	3.9E-01	BE19219.1	EST_HUMAN	RCO-HT0841-040800-032-b12 HT0841 Homo sapiens cDNA
8190	17322	26865	3.07	3.9E-01	R42550.1	EST_HUMAN	y92h11.s1 Soares Infant brain 1NIB Homo sapiens cDNA clone IMAGE:30289 3'
8190	17322	26866	3.07	3.9E-01	R42550.1	EST_HUMAN	y92h11.s1 Soares Infant brain 1NIB Homo sapiens cDNA clone IMAGE:30289 3'
8571	17589		2.97	3.9E-01	AE001124.1	NT	Borrelia burgdorferi (section 10 of 70) of the complete genome
8703	18278		1.58	3.9E-01	U64788.1	NT	Human p53 (TP53) gene, complete cds

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8818	17736		1.91	3.8E-01	BE828258.1	EST_HUMAN	QV3-ET0063-190700-271-605 ET0063 Homo sapiens cDNA
9237	18251		1.26	3.8E-01	AF201483.1	NT	Mus musculus vomeronasal receptor V1RA4 (V1ra4) gene, complete cds
9255	18023	23852	1.24	3.8E-01	AF194972.1	NT	Mus musculus developmental control protein mRNA, partial cds
2443	11834	20854	8.52	3.7E-01	AB037831.1	NT	Homo sapiens mRNA for KIAA1410 protein, partial cds
3437	12882	21794	10.32	3.7E-01	AF056838.1	NT	Danio rerio bone morphogenetic protein 4 precursor (BMP4) gene, complete cds
3852	13068	22183	1	3.7E-01	AA319482.1	EST_HUMAN	EST21715 Adrenal gland tumor Homo sapiens cDNA 5' end
4214	13417	22513	8.6	3.7E-01	AI218707.1	EST_HUMAN	dk39c07.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:1510188 3'
4311	13512	22608	1.22	3.7E-01	AW878037.1	EST_HUMAN	MP3-OT0007-080300-104-b02 OT0007 Homo sapiens cDNA
4384	13585	22887	2.79	3.7E-01	AE002408.1	NT	Neisseria meningitidis serogroup B strain MC58 section 50 of 208 of the complete genome
5272	14474	23516	7.85	3.7E-01	BE865837.1	EST_HUMAN	601678239F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3981138 5'
6135	15319	24763	3.37	3.7E-01	11525843	NT	Homo sapiens tumor endothelial marker 7 precursor (TEM7), mRNA
6571	15787	25229	3.35	3.7E-01	11436739	NT	Homo sapiens chromosome 12 open reading frame 4 (C12ORF4), mRNA
6571	15787	25230	3.35	3.7E-01	11436739	NT	Homo sapiens chromosome 12 open reading frame 4 (C12ORF4), mRNA
7138	18315	25798	3.64	3.7E-01	AI338411.1	EST_HUMAN	qt48b07.x1 Soares_Tetral_Ling_NBHL19W Homo sapiens cDNA clone IMAGE:1950987 3'
7589	18802	26295	2.8	3.7E-01	AJ297357.1	NT	Homo sapiens partial LIMD1 gene for LIM domains containing protein 1 and KIAA0851 gene
7589	18802	26296	2.8	3.7E-01	AJ297357.1	NT	Homo sapiens partial LIMD1 gene for LIM domains containing protein 1 and KIAA0851 gene
7604	18807	26304	2.62	3.7E-01	AF149788.1	NT	Erythrocyte p60 protein isoform #3288 decay-accelerating factor (CD55) gene, partial cds
8002	18437	26924	4.81	3.7E-01	X04122.1	NT	Bovine mRNA for terminal deoxynucleotidyltransferase (TdT) (EC 2.7.7.31)
8239	17588		3.16	3.7E-01	6677678	NT	Mus musculus retinoblastoma 1 (Rb1), mRNA
8288	17918		1.53	3.7E-01	J04982.1	NT	Human heart/skeletal muscle ATP/ADP translocator (ANT1) gene, complete cds
8441	17504		3.72	3.7E-01	AJ243525.1	NT	Chlamydomonas reinhardtii partial omp1 gene for outer membrane protein 1
8542	17567		2.37	3.7E-01	D80976.1	NT	Human mRNA for KIAA0223 gene, partial cds
8831	17813		1.89	3.7E-01	AL121154.1	EST_HUMAN	DKFZp762K075.1 762 (synonym: hmel2) Homo sapiens cDNA clone DKFZp762K075 5'
9000	17880	23888	2.65	3.7E-01	Y18000.1	NT	Homo sapiens NF2 gene
9232	18210		1.23	3.7E-01	X91182.1	NT	H. sapiens PLC beta 3 gene (exon 1) and SOM172 gene (exon 1)
265	9540	18670	1.16	3.8E-01	AJ009609.1	NT	Brassica napus mRNA for MAP4K alpha2 protein
1003	10234		7.24	3.8E-01	U86241.1	NT	Human mlbp gene, partial cds
1321	10536	19700	2.68	3.8E-01	T80255.1	EST_HUMAN	yc03e05.1 Soares infant brain INIB Homo sapiens cDNA clone IMAGE:24443 5'
1321	10536	19701	2.68	3.8E-01	T80255.1	EST_HUMAN	yc03e05.1 Soares infant brain INIB Homo sapiens cDNA clone IMAGE:24443 5'
1881	11088	20278	6.2	3.8E-01	AW590184.1	EST_HUMAN	hg33f02.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2947419 3'
1881	11088	20279	6.2	3.8E-01	AW590184.1	EST_HUMAN	hg33f02.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2947419 3'
1922	11126	20322	5.48	3.8E-01	AF216207.1	NT	Mus musculus ribosomal protein S19 (Rps19) gene, complete cds
2234	11429		1.19	3.8E-01	AB002321.1	NT	Human mRNA for KIAA0323 gene, partial cds
2353	11546		1.98	3.8E-01	X76725.1	NT	P. irregularis (P3804) gene for actin

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2450	11841	20862	1.18	3.6E-01	AW812033.1	EST_HUMAN	RC5-ST0171-181098-011-g07 ST0171 Homo sapiens cDNA
2584	11780	20988	1.3	3.6E-01	P24208	SWISSPROT	PROTEIN-L-ISOASPARTATE O-METHYLTRANSFERASE (PROTEIN-BETA-ASPARTATE METHYLTRANSFERASE) (PMT) (PROTEIN L-ISOASPARTYL METHYLTRANSFERASE) (L-ISOASPARTYL PROTEIN CARBOXYL METHYLTRANSFERASE)
2851	14478		9.22	3.6E-01	AF189485.1	NT	Drosophila melanogaster sugar transporter 3 (sug3) mRNA, complete cds
3448	12871	21805	2.88	3.6E-01	X76758.1	NT	H. sapiens serotonin transporter gene, exons 9 and 10
3448	12871	21806	2.88	3.6E-01	X76758.1	NT	H. sapiens serotonin transporter gene, exons 9 and 10
4402	13802	22702	1.01	3.6E-01	BE707983.1	EST_HUMAN	RC1-HT0545-150600-014-512 HT0545 Homo sapiens cDNA
4700	13891	22891	0.94	3.6E-01	AJ009809.1	NT	Brassica napus mRNA for MAP4K alpha2 protein
4730	13921	23024	0.97	3.6E-01	AF071838.1	NT	Mus musculus protein tyrosine kinase Tec (Tec) gene, alternative exons 4 and 4a, exons 5 through 7 and Tec1 isoform, complete cds
4730	13921	23025	0.97	3.6E-01	AF071838.1	NT	Mus musculus protein tyrosine kinase Tec (Tec) gene, alternative exons 4 and 4a, exons 5 through 7 and Tec1 isoform, complete cds
4765	13954	23055	0.71	3.6E-01	Y11528.1	NT	Z. mays mRNA for casein kinase II alpha subunit
4802	13981	23099	5.78	3.6E-01	AJ228237.1	NT	Bacteria from anode bulk soil 16S rRNA gene (strain XB45)
5033	14218	23303	2.58	3.6E-01	AW339383.1	EST_HUMAN	hs02004.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2872568 3'
5131	14309	23400	0.78	3.6E-01	BE087690.1	EST_HUMAN	MIR4-BT0358-270300-005-c10 BT0358 Homo sapiens cDNA
5882	15080	24492	1.85	3.6E-01	Y10198.1	NT	Homo sapiens PHEX gene
6198	16322		4.03	3.6E-01	R94090.1	EST_HUMAN	X74c06.r1 Soares fetal liver spleen 1NF5L Homo sapiens cDNA clone IMAGE:275887 5'
6202	15383	24825	1.81	3.6E-01	AW027174.1	EST_HUMAN	wf72c10.x1 Soares thymus NHFTb Homo sapiens cDNA clone IMAGE:2513010 3' similar to TRC015117
6552	15748	25209	21.1	3.6E-01	AL181583.2	NT	O15117 FYN BINDING PROTEIN. [1];
						NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 79
6765	15980	25415	5.02	3.6E-01	4504958	NT	Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), transcript variant LAMP2A, mRNA
6765	15980	25416	5.02	3.6E-01	4504958	NT	Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), transcript variant LAMP2A, mRNA
7027	18204	25681	24.7	3.6E-01	Q53194	SWISSPROT	PROBABLE PEPTIDE ABC TRANSPORTER ATP-BINDING PROTEIN Y4TS
7618	18723	26213	2.34	3.6E-01	BE002390.1	EST_HUMAN	601678418F1 NIH MGC_21 Homo sapiens cDNA clone IMAGE:3858997 5'
7672	16871	26374	3.94	3.6E-01	AB004283.1	NT	Arabidopsis thaliana mRNA for SigB, complete cds
7880	16416	25802	3.78	3.6E-01	AE000856.1	NT	Methanobacterium thermoautotrophicum from bases 702375 to 714311 (section 82 of 148) of the complete genome
8305	18383		2.02	3.6E-01	Y19210.1	NT	Homo sapiens Hb5 gene for hair keratin, exons 1 to 9
8391	17472		5.38	3.6E-01	AE000335.1	NT	Escherichia coli K-12 MG1655 section 225 of 400 of the complete genome
8553	17576		3.98	3.6E-01	U88888.1	NT	Mus musculus Emr1 mRNA, complete cds

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8837	17817		1.52	3.6E-01	11432598	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (t(11q24) (Drosophila) homolog); translocated to, 10 (AF10), mRNA
9208	18327		2.18	3.6E-01	AW190228.1	EST_HUMAN	x160e11.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2678116 3' similar to gb:K00558 TUBULIN
9259	18027		1.86	3.6E-01	L27208.1	NT	ALPHA-1 CHAIN (HUMAN);
115	9403	18332	0.79	3.5E-01	AL161536.2	NT	Oryza sativa root-specific RCs3 mRNA, complete cds
214	9494	18628	2.07	3.5E-01	6678933	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 36
684	9927	19058	1.16	3.5E-01	AL161581.2	NT	Mus musculus mannose receptor, C type 2 (Mrc2), mRNA
732	9973	19112	1.36	3.5E-01	7706136	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 77
732	9973	19113	1.36	3.5E-01	7708136	NT	Homo sapiens GAP-like protein (LOC51308), mRNA
789	10029	19178	3.99	3.5E-01	BF129786.1	EST_HUMAN	Homo sapiens GAP-like protein (LOC51308), mRNA
1617	10830	20005	1.84	3.5E-01	U35776.1	NT	601811060R1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4053951 3'
2247	11442	20668	0.93	3.5E-01	P06798	SWISSPROT	Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds
2567	12020	20872	2.03	3.5E-01	AA223252.1	EST_HUMAN	HOMEOBOX PROTEIN HOX-A4 (HOX-1.4) (MH-3)
2957	12195	21329	0.78	3.5E-01	AA057691.1	EST_HUMAN	zr08e08.s1 Stratagene NT2 neuronal precursor 837230 Homo sapiens cDNA clone IMAGE:850872 3'
3763	13011		1.23	3.5E-01	AA642138.1	EST_HUMAN	z164f03.r1 Stratagene corneal stroma (8337222) Homo sapiens cDNA clone IMAGE:51285 5'
4249	13432	22543	2.33	3.5E-01	AF071253.1	NT	nr60d03.s1 NCI_CGAP_Lym3 Homo sapiens cDNA clone IMAGE:1172367 3'
4953	14140	23234	4.58	3.5E-01	M18349.1	NT	Danio rerio homeobox protein (hoxb-5b) gene, complete cds
5147	14328		3.22	3.5E-01	AA825140.1	EST_HUMAN	Rat leukocyte common antigen (L-CA) gene, exons 1 through 5
5356	14588	23662	1.81	3.5E-01	Q86687	SWISSPROT	ce62b07.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1416181 3'
5356	14588	23663	1.81	3.5E-01	Q86687	SWISSPROT	EARLY E2A DNA-BINDING PROTEIN
6107	15201		3.88	3.5E-01	X98505.1	NT	EARLY E2A DNA-BINDING PROTEIN
6489	15686		3.28	3.5E-01	X98505.1	NT	S. cerevisiae mRNA for CD31 protein (PEGAM-1)
7320	16537	26025	3.47	3.5E-01	X61084.1	NT	Homo sapiens tumor protein p53-binding protein, 2 (TP53BP2), mRNA
7592	16706	26289	2.15	3.5E-01	AJ243178.1	NT	C. gigas rhodopsin gene for opsin protein
7592	16706	26290	2.15	3.5E-01	AJ243178.1	NT	Gallus gallus SPARC gene for osteonectin, promoter and exon 1
8119	17253	26794	2.04	3.5E-01	N77597.1	EST_HUMAN	Gallus gallus SPARC gene for osteonectin, promoter and exon 1
8181	17313	26855	1.67	3.5E-01	L05145.1	NT	yz80h12.r1 Soares_multiple_sclerosis_2NbhMSP Homo sapiens cDNA clone IMAGE:280375 5'
8472	17525		2.16	3.5E-01	X84565.1	NT	Human glucokinase (GCK) gene, repeat polymorphism
8943	17626		1.95	3.5E-01	AE001774.1	NT	B. taurus alpA1 gene for F(0)F(1) ATP synthase alpha-subunit
9263	18227	23697	2.45	3.5E-01	H80814.1	EST_HUMAN	Thermoboga maritima section 86 of 136 of the complete genome
9263	18227	23698	2.45	3.5E-01	H80814.1	EST_HUMAN	ys64f11.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:219597 5'
							ys64f11.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:219597 5'

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
714	8958		1.87	3.4E-01	AJ242958.1	NT	Homo sapiens partial N-myc (exon 3), HPV45 L2, HPV45 L1, HPV45 E8, HPV45 E7 and HPV45 E1 genes isolated from IC4 cervical carcinoma cell line
983	10214	18370	5.03	3.4E-01	Y09788.2	NT	Pseudomonas fluorescens colR, colS genes, orf222 and partial lnaA gene
1334	10549	19713	1.91	3.4E-01	Y00554.1	NT	Azotobacter vinelandii nifA gene for NifA protein (positive regulatory element)
2368	11559	20781	2.41	3.4E-01	D90809.1	NT	Synechocystis sp. PCC6803 complete genome, 11/27, 1311235-1430418
2959	12197	21331	0.97	3.4E-01	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
2959	12197	21332	0.97	3.4E-01	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3125	12360	21489	8.49	3.4E-01	U83905.1	NT	Carls familiaris rod photoreceptor cGMP-gated channel alpha-subunit (CNGC1) mRNA, complete cds
3317	12647	21680	0.94	3.4E-01	AF034862.1	NT	Homo sapiens pulmonary surfactant protein D, promoter region and exon 1
3505	12729	21868	4.83	3.4E-01	AF106835.1	NT	Methylovorus sp. strain SS1 putative GrpE (grpE), DnaK (dnaK), and putative DnaJ (dnaJ) genes, complete cds
3772	12980		1.4	3.4E-01	BF448010.1	EST_HUMAN	7r84a01.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3572232 3' similar to TR:Q8JU15
4029	13239		1.43	3.4E-01	AA684196.1	EST_HUMAN	Q8JU15.D18C9.1
4490	13694	22788	0.68	3.4E-01	AF166341.1	NT	no11b10.s1 NCI_CGAP_Pho1 Homo sapiens cDNA clone IMAGE:1100347 3'
4845	13839	22829	2.14	3.4E-01	BE068912.1	EST_HUMAN	Homo sapiens Integrin alpha 6 (ITGA6) gene, exons 12 through 23
4971	14158		4.38	3.4E-01	A1240973.1	EST_HUMAN	MR4-BT0403-230200-202-c01 BT0403 Homo sapiens cDNA
5529	14753	24120	3.01	3.4E-01	AL161594.2	NT	ql95c05.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1887208 3' similar to contains Alu repetitive element
5577	14801		5.91	3.4E-01	AA085313.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 80
5657	14880		1.84	3.4E-01	U02971.1	NT	zn12d11.s1 Strategene HNT neuron (#837233) Homo sapiens cDNA clone IMAGE:647221 3'
5711	14830	24324	1.89	3.4E-01	AW204505.1	EST_HUMAN	Echovirus 22 1AB, 1C, 1D, 2A, 2B, 2C, 3A, 3B, 3C, 3D proteins RNA, complete mature peptides and cds
5788	14887	24387	1.88	3.4E-01	AL120544.1	EST_HUMAN	UI-H-B11-ae1-6-12-Q-U1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2718582 3'
6831	16025	25490	5.51	3.4E-01	P28013	SWISSPROT	DKFZp781A249_r1 781 (synonym: hamy2) Homo sapiens cDNA clone DKFZp781A249 5'
6831	16025	25491	5.51	3.4E-01	P28013	SWISSPROT	INTEGRIN BETA-3 PRECURSOR
6892	15598	25083	8.48	3.4E-01	U19492.1	NT	INTEGRIN BETA-3 PRECURSOR
6892	15598	25084	8.48	3.4E-01	U19492.1	NT	Saccharomyces cerevisiae Maf1p (MAF1) gene, complete cds
7037	16214	25691	3.24	3.4E-01	AJ225084.1	NT	Saccharomyces cerevisiae Maf1p (MAF1) gene, complete cds
7598	16791		4.26	3.4E-01	AE000881.1	NT	Homo sapiens FAA gene, exon 18, 17 and 18
7621	16824	26320	2.64	3.4E-01	P06925	SWISSPROT	Methanobacterium thermoautotrophicum from bases 1018444 to 1028212 (section 87 of 148) of the complete genome
							PROBABLE E4 PROTEIN

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7657	16857	26358	2.78	3.4E-01	AF045981.1	NT	Rutilus arcasii cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, partial cds
7832	17024	26339	1.89	3.4E-01	M25856.1	NT	Human von Willebrand factor gene, exons 36 and 37
7832	17024	26340	1.89	3.4E-01	M25856.1	NT	Human von Willebrand factor gene, exons 36 and 37
8032	17169	26708	1.9	3.4E-01	AB035507.1	NT	Rattus norvegicus mRNA for a-galactin/MUC18, complete cds
8038	17183	26731	4.69	3.4E-01	AL161515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
8250	17378	26912	1.85	3.4E-01	BF081948.1	EST_HUMAN	7k68d12.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:3480848 3'
8282	17368		1.9	3.4E-01	U93604.1	NT	Citrus variegation virus putative replicase gene, partial cds
8394	17473		1.37	3.4E-01	Z21621.1	NT	S. cerevisiae RIB5 gene encoding Riboflavin synthase
8500	18118		1.58	3.4E-01	AF254351.1	NT	Schizosaccharomyces pombe Cwif9p (cwif9) gene, complete cds
8623	17617		6.12	3.4E-01	L26339.1	NT	Human autoantigen mRNA, complete cds
8855	18149		2.98	3.4E-01	BE218652.1	EST_HUMAN	h42h08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176127 3' similar to contains PTR5.13
8713	18262		1.9	3.4E-01	8938361	NT	PTR5 repetitive element:
8925	17739	23931	1.88	3.4E-01	AJ297131.1	NT	Beta vulgaris mitochondrion, complete genome
						NT	Mus musculus SIL, MAP_17, CYP_a, SCL & CYP_b genes
9142	17948		2.18	3.4E-01	AF019413.1	NT	Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, hemicase (SK12W), RD, complement factor B (BF), and complement component C2 (C2) genes,>
14	8310	18412	14.06	3.3E-01	X07890.1	NT	Rhizobium leguminosarum sym plasmid pRL5J1 nodX gene
105	8310	18412	5.73	3.3E-01	X07890.1	NT	Rhizobium leguminosarum sym plasmid pRL5J1 nodX gene
464	9707	18845	0.77	3.3E-01	AL161546.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 45
639	9885	19010	1.85	3.3E-01	7662485	NT	Homo sapiens KIAA1100 protein (KIAA1100), mRNA
1208	10427	19584	3.17	3.3E-01	Q12448	SWISSPROT	PROLINE-RICH PROTEIN LAS17
1314	10530	19692	3.14	3.3E-01	BF568880.1	EST_HUMAN	602184016T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300251 3'
1595	10788	19874	1.04	3.3E-01	6753685	NT	Mus musculus disintegrin 5 (Dign5), mRNA
1710	10822		1.41	3.3E-01	AA332734.1	EST_HUMAN	EST36722 Embryo, 8 week 1 Homo sapiens cDNA 5' end
2368	11582		4.41	3.3E-01	4507834	NT	Homo sapiens uridine monophosphate synthetase (uridine phosphorylase transferase and orotidine-5'-decarboxylase) (UMPS) mRNA
2901	12139	21276	2.03	3.3E-01	AJ251805.1	NT	Bacteriophage phi-YeO3-12 complete genome
2977	12214		0.87	3.3E-01	O02743	SWISSPROT	INTERLEUKIN-12 ALPHA CHAIN PRECURSOR (IL-12A) (CYTOTOXIC LYMPHOCYTE MATURATION FACTOR 35 KD SUBUNIT) (CLMF P36)
3020	12256	21385	1.04	3.3E-01	AJ007832.2	NT	Streptomyces argillaceus mithramycin biosynthetic genes
3470	12895	21831	0.97	3.3E-01	AB012922.1	NT	Homo sapiens MTA1-L1 gene, complete cds
3763	13001	22116	0.6	3.3E-01	D14015.1	NT	Rat mRNA for cyclin E, complete cds

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3787	13016	22128	2.2	3.3E-01	O84645	SWISSPROT	EXODEOXYRIBONUCLEASE V BETA CHAIN
3808	13028	22138	1	3.3E-01	P22602	SWISSPROT	GENOME POLYPROTEIN [CONTAINS: N-TERMINAL PROTEIN (P1); HELPER COMPONENT PROTEINASE (HC-PRO); PROTEIN P3]
3842	13168	22275	1.97	3.3E-01	AL161488.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 10
3878	13182	22300	2.17	3.3E-01	AF200448.1	NT	Hypoxylon fragiforme chitin synthase gene, partial cds
4361	13563		2.43	3.3E-01	D31682.1	NT	Rattus norvegicus DNA for regucalcin, partial cds
4698	13887		1.58	3.3E-01	A1539114.1	EST_HUMAN	bp78612x1 NCI CGAP U13 Homo sapiens cDNA clone IMAGE:2205407 3' similar to gb:57522 ANTIGEN PEPTIDE TRANSPORTER 1 (HUMAN);
4856	14044	23138	1.36	3.3E-01	D84003.1	NT	Synechocystis sp. PCC6803 complete genome, 22/27, 2755703-2668766
5222	14398	23481	1.51	3.3E-01	AW884408.1	EST_HUMAN	QV3-OT0065-280300-137-911 OT0065 Homo sapiens cDNA
5348	14578	23654	2.48	3.3E-01	X69819.1	NT	R. norvegicus mRNA for 3'UTR of ubiquitin-like protein
5348	14578	23655	2.48	3.3E-01	X69819.1	NT	R. norvegicus mRNA for 3'UTR of ubiquitin-like protein
5836	14860	24244	1.78	3.3E-01	BE619650.1	EST_HUMAN	601472768T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875763 3'
5836	14860	24245	1.76	3.3E-01	BE619650.1	EST_HUMAN	601472768T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875763 3'
5678	14888	24281	6.34	3.3E-01	P05691	SWISSPROT	CIRCUMSPOROZOITE PROTEIN (CS)
6035	15243	24684	4.81	3.3E-01	A1628131.1	EST_HUMAN	ly64h01.x1 NCI CGAP Kid11 Homo sapiens cDNA clone IMAGE:2285809 3' similar to contains Alu repetitive element; contains element L1 repetitive element;
6035	15243	24685	4.61	3.3E-01	A1628131.1	EST_HUMAN	ly64h01.x1 NCI CGAP Kid11 Homo sapiens cDNA clone IMAGE:2285809 3' similar to contains Alu repetitive element; contains element L1 repetitive element;
6408	15588	25049	1.8	3.3E-01	N85146.1	EST_HUMAN	J2498F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J2498 5' similar to TEGT
6642	15837	25298	14.61	3.3E-01	BF683954.1	EST_HUMAN	602140372F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4301800 5'
6916	16104	25570	3.78	3.3E-01	N68898.1	EST_HUMAN	z687h01.s1 Soares_fetal_lung_NIH_MGC_48 Homo sapiens cDNA clone IMAGE:287849 3'
6935	16079	25549	3.25	3.3E-01	BF376745.1	EST_HUMAN	RC4-TN0077-250800-011-g04 TN0077 Homo sapiens cDNA
7308	16527	26017	2.71	3.3E-01	X63953.1	NT	D.mauritiana Adh gene
7308	16527	26018	2.71	3.3E-01	X63953.1	NT	D.mauritiana Adh gene
7565	16798		1.89	3.3E-01	BF526403.1	EST_HUMAN	602070802F1 NCI CGAP Bim64 Homo sapiens cDNA clone IMAGE:4213585 5'
7783	16978	26491	11.77	3.3E-01	BE218351.1	EST_HUMAN	h61g02.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:3176978 3'
7885	17101	26832	4.85	3.3E-01	P47953	SWISSPROT	GALECTIN-3 (GALACTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (IGE-BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35) (LAMININ-BINDING PROTEIN) (LECTIN L-29) (CBP30)
8209	17340		4.68	3.3E-01	AA806821.1	EST_HUMAN	cd71g02.s1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1336850 3'
8228	8310	18412	2.53	3.3E-01	X07680.1	NT	Rhizobium leguminosarum sym plasmid pRLSJ1 nodX gene
8381	17465	26560	1.58	3.3E-01	6588319	NT	Homo sapiens aldehyde oxidase 1 (AOX1), mRNA

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Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9131	17941		12.3	3.3E-01	AP000002.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 287001-544000 nt. position (277)
463	9718		2.22	3.2E-01	AF018281.1	NT	Rattus norvegicus EH domain binding protein Epsin mRNA, complete cds
725	9967		0.82	3.2E-01	AL181581.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 61
1170	10391	19543	18.32	3.2E-01	AF047013.1	NT	Fusarium poae virus 1 RNA2 putative RNA dependent RNA polymerase gene, complete cds
1289	10504	19685	1.74	3.2E-01	Z50202.1	NT	P. vulgaris arcs-1 gene
1394	10608	19772	6.8	3.2E-01	Q48024	SWISSPROT	LACTOSE PERMEASE (LACTOSE-PROTON SYMPORT) (LACTOSE TRANSPORT PROTEIN)
1744	10858	20139	1.28	3.2E-01	Z38041.1	NT	S. cerevisiae chromosome II reading frame ORF YBR172c
1754	10868	20151	5.41	3.2E-01	AW957184.1	EST_HUMAN	EST369284 MAGE resequences, MAGD Homo sapiens cDNA
1754	10868	20152	5.41	3.2E-01	AW957184.1	EST_HUMAN	EST369284 MAGE resequences, MAGD Homo sapiens cDNA
1810	11019	20211	1.34	3.2E-01	AL111655.1	NT	Borlyis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
2128	11325	20543	2.6	3.2E-01	BF203817.1	EST_HUMAN	601868804F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4111512 5'
2508	11694		2.24	3.2E-01	7710079	NT	Mus musculus Pdxfructid 1 homeobox (Pdxfruct), mRNA
2670	11851	21087	1.35	3.2E-01	AF060568.1	NT	Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds
3588	12807		0.67	3.2E-01	D10872.1	NT	Human h NAT allele 3-2 gene for arylamine N-acetyltransferase
4387	13588	22680	1.44	3.2E-01	M18818.1	NT	Rabbit beta-like globin gene cluster encoding the epsilon, gamma, delta (pseudogene) and beta globin polypeptides, complete cds
4501	13689	22763	1.34	3.2E-01	Q10288	SWISSPROT	HYPOTHETICAL 81.7 KD PROTEIN C13G7.04C IN CHROMOSOME I PRECURSOR
4748	13940		7.91	3.2E-01	BF683617.1	EST_HUMAN	602081972F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4248505 5'
4901	14089	23182	0.69	3.2E-01	Q57081	SWISSPROT	CYTADHERENCE HIGH MOLECULAR WEIGHT PROTEIN 3 (CYTADHERENCE ACCESSORY PROTEIN 3) (ACCESSORY ADHESIN PROTEIN 3) (P89)
5310	14541	23610	3.05	3.2E-01	BE173964.1	EST_HUMAN	CM0-HT05689-060300-269-110 HT05689 Homo sapiens cDNA
6516	15712	25177	2.43	3.2E-01	M60266.1	NT	Rat ISO-atrial natriuretic factor gene, complete cds
6585	15781	25241	13.9	3.2E-01	X02508.1	NT	H. sapiens gene fragment for acetylcholine receptor (AChR) alpha subunit exons 8, 9 and 3' flanking region
6587	15783	25244	22.45	3.2E-01	BF311635.1	EST_HUMAN	601897107F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4128833 5'
6845	15840	25300	2.84	3.2E-01	AE002015.1	NT	Deinococcus radiodurans R1 section 152 of 228 of the complete chromosome 1
6796	15981		2.69	3.2E-01	M86611.1	NT	Human monocyte antigen CD14 (CD14) mRNA, complete cds
7071	16248	25721	2.71	3.2E-01	U44914.1	NT	Borrelia burgdorferi plasmid cp32-2, erpC and erpD genes, complete cds; and unknown genes
7170	16347		2.78	3.2E-01	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
7261	16480	25972	3.47	3.2E-01	T08813.1	EST_HUMAN	EST04702 Fetal brain, Stragene (cat#836208) Homo sapiens cDNA clone HFBDZ21
8417	18278		2.4	3.2E-01	L07288.1	NT	Drosophila melanogaster laminin A (Lam-A) mRNA, complete cds
8988	17838		2.92	3.2E-01	O83217	SWISSPROT	ELONGATION FACTOR TU (EF-TU)
9111	17829		1.43	3.2E-01	L39874.1	NT	Homo sapiens deoxycytidylate deaminase gene, complete cds
9171	18318	23595	1.92	3.2E-01	BE385776.1	EST_HUMAN	601275480F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3818748 5'

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2631	11814	21033	3.26	3.1E-01	R18051.1	EST_HUMAN	ye00h08.r1 Soares fetal liver spleen 1NFS Homo sapiens cDNA clone IMAGE:126051 5' similar to gb:MB4241 QM PROTEIN (HUMAN);
2658	11855	21052	3.57	3.1E-01	7681971	NT	Homo sapiens KIAA0174 gene product (KIAA0174), mRNA
2658	11855	21053	3.57	3.1E-01	7681971	NT	Homo sapiens KIAA0174 gene product (KIAA0174), mRNA
2810	12050		1.15	3.1E-01	AW629036.1	EST_HUMAN	hi46h08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2875391 3'
3138	12373		3.8	3.1E-01	AB028069.1	NT	Mus musculus gene for Ser/Thr kinase KIAAMRE, exon 6
3865	13101	22218	1	3.1E-01	AJ251588.1	NT	Daucus carota mRNA for transcription factor E2F (E2F gene)
4983	14170	23260	0.69	3.1E-01	AE003984.1	NT	Xyella fastidiosa, section 130 of 229 of the complete genome
5430	14657	23795	9.75	3.1E-01	AF176111.1	NT	Homo sapiens hepatocyte nuclear factor-3 alpha (HNF3A) gene, exon 1
5561	14784	24154	2.13	3.1E-01	AF184122.1	NT	Homo sapiens filamin 2 (FLN2) gene, exons 10 through 22
6073	18049	23562	2.71	3.1E-01	BE737392.1	EST_HUMAN	601306121F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3840420 5'
7119	16296	25778	2.92	3.1E-01	A1244001.1	EST_HUMAN	q161e11.x1 NCI_CGAP_K143 Homo sapiens cDNA clone IMAGE:1863980 3' similar to gb:S55700 HYDROXYMETHYLGLUTARYL-COA LYASE PRECURSOR (HUMAN);
7414	16628	26119	1.86	3.1E-01	BF216117.1	EST_HUMAN	601883592F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4085814 5'
8068	17204	26737	2.43	3.1E-01	7682291	NT	Homo sapiens KIAA0764 gene product (KIAA0764), mRNA
8551	17574		1.55	3.1E-01	AF294308.1	NT	Ancalis opatinus isolate QS NADH dehydrogenase subunit 2 (ND2) gene, complete cds; mitochondrial gene for mitochondrial product
8580	17599		1.62	3.1E-01	AF304162.1	NT	Stizobedion vitreum 40S ribosomal protein S11 mRNA, partial cds
8740	17690		2.6	3.1E-01	AF195953.1	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds
9116	17834						Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T64 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel α
9155	18314		3.2	3.1E-01	AF198779.1	NT	
72	11935	18494	1.52	3.1E-01	10946823	NT	Mus musculus peptidoglycan recognition protein-like (Pglyrpl-pending), mRNA
258	9534	18663	1.46	3.0E-01	6755083	NT	Mus musculus protein kinase C, epsilon (Pkc ϵ), mRNA
1231	10449	19605	8.66	3.0E-01	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
1497	10710	19883	2.2	3.0E-01	AW300400.1	EST_HUMAN	xs63f08.x1 NCI_CGAP_K1411 Homo sapiens cDNA clone IMAGE:2774343 3'
3169	12404		5.25	3.0E-01	AJ008765.1	NT	Balaenoptera physalus gene encoding atrial natriuretic peptide
3178	12413		0.84	3.0E-01	X83615.1	NT	S.pombe plc1 gene
3372	12600	21736	1.29	3.0E-01	AB030481.1	NT	Corynebacterium sp. ALY-1 alvPG gene for polyglutamate lyase, complete cds
3848	13063	22177	0.62	3.0E-01	P23825	SWISSPROT	GATA BINDING FACTOR-3 (TRANSCRIPTION FACTOR NF-E1C)(GATA-3)
3951	13168	22280	1.68	3.0E-01	AW817765.1	EST_HUMAN	PM1-ST0282-261189-001-g01 ST0282 Homo sapiens cDNA
4514	13710	22803	1.08	3.0E-01	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
5180	12600	21736	1.88	3.0E-01	AJ008755.1	NT	Balaenoptera physalus gene encoding atrial natriuretic peptide
			0.63	3.0E-01	P23825	SWISSPROT	GATA BINDING FACTOR-3 (TRANSCRIPTION FACTOR NF-E1C)(GATA-3)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6368	14586	23873	5.84	3.0E-01	BE741828.1	EST_HUMAN	601594960F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948734 5'
5441	14687	23822	3.77	3.0E-01	BE683575.1	EST_HUMAN	RC3-BT0333-180700-111-e03 BT0333 Homo sapiens cDNA
5441	14687	23823	3.77	3.0E-01	BE683575.1	EST_HUMAN	RC3-BT0333-180700-111-e03 BT0333 Homo sapiens cDNA
5462	14688	24039	4.58	3.0E-01	U01247.1	NT	Mus musculus 128/sv Clara cell 10 kd protein (mCC10) gene, complete cds
6011	15261	24695	2.88	3.0E-01	D16313.1	NT	Mouse cytokerafin 15 gene, complete cds
6221	15402	24843	3.34	3.0E-01	10947007	NT	Mus musculus mtndnln (Mltn-pending), mRNA
6260	15471	24912	1.75	3.0E-01	AF071810.1	NT	Streptococcus pneumoniae strain DBL5 Papa (pspa) gene, partial cds
6588	15784		4.68	3.0E-01	9910161	NT	Mus musculus C-type (calcium dependent, carbohydrate recognition domain) lectin, superfamily member 9 (Clec5f9), mRNA
6620	15916	25275	2.38	3.0E-01	BE568083.1	EST_HUMAN	6013339076F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3681594 5'
7188	16363	25843	2.78	3.0E-01	AB030231.1	NT	Aspergillus oryzae bpaA gene for ER chaperone BiP, complete cds
8240	17368	26804	3.04	3.0E-01	H51029.1	EST_HUMAN	yp84b10.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:194107 5'
8240	17368	26805	3.04	3.0E-01	H51029.1	EST_HUMAN	yp84b10.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:194107 5'
8852	18261		1.68	3.0E-01	AJ287631.1	NT	Rattus norvegicus mRNA for glyceraldehyde-3-phosphate dehydrogenase type 2 (gapdh-2 gene)
8149	18311		3.57	3.0E-01	6877788	NT	Mus musculus ribose 5-phosphate isomerase A (Rpia), mRNA
1706	10918		1.72	2.8E-01	AJ249895.1	NT	Mus musculus mas proto-oncogene and Igf2r gene for insulin-like growth factor type 2 and L41ps and Au76 pseudogenes
1983	11198	20405	1.33	2.9E-01	AE000736.1	NT	Aquifex aeolicus section 68 of 109 of the complete genome
3217	12451	21583	1.78	2.9E-01	AW754239.1	EST_HUMAN	PM1-CT0328-171289-001-f12 CT0328 Homo sapiens cDNA
3217	12451	21584	1.78	2.9E-01	AW754239.1	EST_HUMAN	PM1-CT0328-171289-001-f12 CT0328 Homo sapiens cDNA
4048	13258	22360	0.66	2.8E-01	AB018428.1	NT	Cavia porcellus mRNA for glutathione S-transferase, complete cds
4061	13272		0.66	2.8E-01	AW002802.1	EST_HUMAN	wr02f10.x1 NCI_CGAP_GC81 Homo sapiens cDNA clone IMAGE:2480395 3'
4483	13681	22770	1.18	2.9E-01	AA284468.1	EST_HUMAN	zs57d12.11 NCI_CGAP_GC81 Homo sapiens cDNA clone IMAGE:701591 5' similar to contains Alu repetitive element;
4852	14041	23134	4.7	2.9E-01	AB019029.1	NT	Mus musculus gene, complete cds, similar to EXLM1
5144	14323		1.21	2.9E-01	A1870899.1	EST_HUMAN	wa06f03.x1 NCI_CGAP_Kd11 Homo sapiens cDNA clone IMAGE:2287309 3' similar to contains L1.12 L1 repetitive element;
5557	14781	24149	5.09	2.8E-01	X56088.1	NT	B.subtilis levanase operon levD, levE, levF, levG and sacC (partial) genes for fructose phosphotransferase system polypeptides P16,18,28,30 and levanase
5557	14781	24150	5.09	2.8E-01	X56088.1	NT	B.subtilis levanase operon levD, levE, levF, levG and sacC (partial) genes for fructose phosphotransferase system polypeptides P16,18,28,30 and levanase
5503	14787	24158	6.3	2.9E-01	6679662	NT	Mus musculus Eph receptor A8 (EphA8), mRNA
5799	15018	24419	2.5	2.9E-01	U03420.1	NT	Bos taurus myosin I mRNA, complete cds
6123	15307	24740	3.4	2.9E-01	Q04388	SWISSPROT	PUTATIVE MULTICOPPER OXIDASE YDR506C

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7470	16878	26160	2.13	2.9E-01	AF128843.1	NT	Tyrosinase cruz stage-specific surface glycoprotein gp82 (gp82) mRNA, partial cds
7721	16820	26427	2.67	2.9E-01	V01394.1	NT	Torpedo californica mRNA encoding acetylcholine receptor gamma subunit
7721	16920	26428	2.67	2.9E-01	V01394.1	NT	Torpedo californica mRNA encoding acetylcholine receptor gamma subunit
8111	17245	26785	2.54	2.9E-01	AA835373.1	EST_HUMAN	ny96h02.s1 NCI_CGAP_P112 Homo sapiens cDNA clone IMAGE:1273779 similar to contains LTR8.12 LTR8 repetitive element;
8114	17248	26788	4.72	2.8E-01	AL139078.2	NT	Campylobacter jejuni NC1C11168 complete genome; segment 5/6
8802	17727	23929	1.34	2.9E-01	AW005671.1	EST_HUMAN	wz8805.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2565821 3' similar to contains element
8893	17787	23920	3.11	2.9E-01	AF092453.1	NT	MER29 repetitive element;
9202	17987	23860	1.67	2.9E-01	Y08637.1	NT	Homo sapiens TNF- α -inducible RNA binding protein (TIRP) gene, complete cds
9202	17987	23861	1.57	2.9E-01	Y08637.1	NT	Chlamydomonas reinhardtii mRNA for nitrite reductase structural locus
576	9825		1.73	2.8E-01	U67138.1	NT	Chlamydomonas reinhardtii mRNA for nitrite reductase structural locus
580	9828		0.78	2.8E-01	L28145.1	NT	Rattus norvegicus A-kinase anchoring protein AKAP150 mRNA, complete cds
1081	10316	19469	3.05	2.8E-01	AF169050.1	NT	Prune dwarf virus movement protein, complete cds; coat protein, complete cds
1284	10489	19659	1.07	2.8E-01	BE313442.1	EST_HUMAN	Gulra guinea oocyte maturation factor Mos (e-mos) gene, partial cds
1284	10499	19660	1.07	2.8E-01	BE313442.1	EST_HUMAN	601148733F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3163886 5'
1288	10513	19671	0.68	2.8E-01	D86550.1	NT	601148733F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3163886 5'
1702	10914	20102	1.41	2.8E-01	AW860020.1	EST_HUMAN	Human mRNA for serine/threonine protein kinase, complete cds
1980	11184	20392	1.49	2.8E-01	AL047620.1	EST_HUMAN	QV1-CT0364-120200-065-b05 CT0384 Homo sapiens cDNA
2101	11301	20515	1.13	2.8E-01	AW511106.1	EST_HUMAN	DKFZp58612321_r1 586 (synonym: hufet1) Homo sapiens cDNA clone DKFZp58612321
2435	11626	20848	2.08	2.8E-01	AE000494.1	NT	h444b03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2812333 3'
2435	11626	20849	2.08	2.8E-01	AE000494.1	NT	Escherichia coli K-12 MG1655 section 394 of 400 of the complete genome
2512	11701		1.48	2.8E-01	AL181565.2	NT	Escherichia coli K-12 MG1655 section 394 of 400 of the complete genome
2825	12163		1.58	2.8E-01	AF170480.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65
2828	12164	21288	1.96	2.8E-01	Z14037.1	NT	Toxoplasma gondii 90kDa heat-shock protein (HSP90) mRNA, partial cds
2828	12164	21289	1.96	2.8E-01	Z14037.1	NT	B. taurus microsatellite (ETH121)
3357	12585	21724	1.07	2.8E-01	AF000004.1	NT	B. taurus microsatellite (ETH121)
3973	13187	22285	2.91	2.8E-01	AE001180.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 777001-984000 nt. position (47)
4104	13311		0.75	2.8E-01	AE004450.1	NT	Borrelia burgdorferi (section 66 of 70) of the complete genome
4180	13384		2.26	2.8E-01	AI080808.1	EST_HUMAN	Pseudomonas aeruginosa PA01, section 11 of 528 of the complete genome
4454	13652	22747	2.77	2.8E-01	P13615	SWISSPROT	ov44g10.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640228 3' similar to contains Alu repetitive element; contains element MER22 repetitive element;
4792	13981	23085	1.17	2.8E-01	D15050.1	NT	RNA POLYMERASE BETA SUBUNIT (LARGE STRUCTURAL PROTEIN)(L PROTEIN)
4792	13981	23086	1.17	2.8E-01	D15050.1	NT	Human mRNA for transcription factor AREB8, complete cds
						NT	Human mRNA for transcription factor AREB8, complete cds

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4839	14028	23120	0.95	2.8E-01	AF075238.1	NT	Hepatitis G virus isolate 60 (SZNAE12) polyprotein precursor, gene, partial cds
4846	14035	23128	2.98	2.8E-01	AF030154.1	NT	Bovine adenovirus 3 complete genome
4877	14085	23160	1.52	2.8E-01	BF528188.1	EST_HUMAN	602042601F1 NC1_CGAP_Bim67 Homo sapiens cDNA clone IMAGE:4180128 5'
4908	14094	23187	2.89	2.8E-01	AI272668.1	EST_HUMAN	q159c11.x1 Soares_NihMPu_S1 Homo sapiens cDNA clone IMAGE:4180128 5'
5209	14384	23469	1.85	2.8E-01	AW808625.1	EST_HUMAN	repetitive element/contains element LTR5 repetitive element
5240	14414	23494	0.79	2.8E-01	U65949.1	NT	MR1-ST0111-111189-010-g07 ST0111 Homo sapiens cDNA
5291	14482	23530	0.83	2.8E-01	6878618	NT	Mus musculus hepatocyte growth factor-like protein receptor (Ran) gene, complete cds
5338	18051	23843	22.74	2.8E-01	AA348997.1	EST_HUMAN	Mus musculus Yamaguchi sarcoma viral (v-yes) oncogene homolog (Yes), mRNA
5494	14720	24077	2.89	2.8E-01	AB016625.1	NT	EST57072 Infant brain Homo sapiens cDNA 5' end
5976	15100	24807	7.37	2.8E-01	BF511216.1	EST_HUMAN	Homo sapiens OCTN2 gene, complete cds
6531	15727	25192	3.85	2.8E-01	U51688.1	EST_HUMAN	U1H-B14-act-f-04-0-UI.s1 NC1_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085182 3'
6851	15848	25192	8.12	2.8E-01	BF347847.1	EST_HUMAN	Homo sapiens lanosterol 14-alpha demethylase cytochrome P450 (CYP51) gene, exon 5
7095	16272	25749	4.31	2.8E-01	7708163	NT	602022887F1 NC1_CGAP_Bim67 Homo sapiens cDNA clone IMAGE:4185526 5'
7328	16545	26034	2.35	2.8E-01	BF241002.1	EST_HUMAN	Homo sapiens hypothetical protein (LOC51319), mRNA
7328	16545	26035	2.35	2.8E-01	BF241082.1	EST_HUMAN	601880784F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4108350 5'
7354	16570	26061	3.21	2.8E-01	BF695970.1	EST_HUMAN	601880784F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4108350 5'
7457	16665	26154	2.95	2.8E-01	AF051862.1	NT	601852148F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4078028 5'
7827	17019		4.12	2.8E-01	BF874023.1	EST_HUMAN	Drosophila heteronura fruitless (fru) gene, alternative splice products, 5' flanking region, exons 1 through 7 and complete cds
8840	17749		7.9	2.8E-01	D83329.1	NT	602137418F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4273853 5'
8852	17826	23905	4.34	2.8E-01	BE178698.1	EST_HUMAN	Mus musculus DNA for prostaglandin D2 synthase, complete cds
8980	17847	23915	1.23	2.8E-01	BE800118.1	EST_HUMAN	PM4-HT0606-030400-001-807 HT0606 Homo sapiens cDNA
9139	18268		2.15	2.8E-01	11433828	NT	601873020F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3955998 5'
483	8735	18868	3.37	2.7E-01	Y17324.1	NT	Homo sapiens CDC42-binding protein kinase beta (DMPK-like) (CDC42BPB), mRNA
619	8884	18984	3.09	2.7E-01	AA450061.1	EST_HUMAN	Rattus norvegicus CDK104 mRNA
1288	10483	19642	1.39	2.7E-01	AB004908.1	NT	z339b10.s1 Soares_fetal_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:788827 3' similar to contains Alu repetitive element
1598	10812		1.78	2.7E-01	X78815.1	NT	Ipomoea purpurea transposable element Tip100 gene for transposase, complete cds
1704	10916	20103	3.78	2.7E-01	W58087.1	EST_HUMAN	G. lamblia SR2 gene
1746	10958	20141	1.35	2.7E-01	P03341	SWISSPROT	z322h10.r1 Soares_fetal_heart_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:341443 5'
2105	12010		2.25	2.7E-01	AF047575.1	NT	GAG POLYPROTEIN [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]
2335	11528	20749	7.58	2.7E-01	Y13888.1	NT	Rattus norvegicus vesicular monoamine transporter type 2, promoter region and exon 1
						NT	Feline immunodeficiency virus env gene, isolate ITTO088PU (N88), partial

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2418	11809	20831	3.28	2.7E-01	A1310858.1	EST_HUMAN	ta43c11.x2 NCI_CGAP_Lu25 Homo sapiens cDNA clone IMAGE:2048836 3' similar to contains element L1 repetitive element ;
2941	12179		0.66	2.7E-01	BF088284.1	EST_HUMAN	CM1-HT0875-060800-385-e03 HT0875 Homo sapiens cDNA
3987	13201	22309	1.68	2.7E-01	A1928015.1	EST_HUMAN	wc92b11.x1 NCI_CGAP_Kld11 Homo sapiens cDNA clone IMAGE:2462828 3'
4001	13214	22318	0.77	2.7E-01	A1928015.1	NT	Drosophila buzzatii alpha-esterase 8 (ae8) gene, partial cds
4001	13214	22318	0.77	2.7E-01	AF216214.1	NT	Drosophila buzzatii alpha-esterase 8 (ae8) gene, partial cds
4007	13218	22322	2.21	2.7E-01	AF216214.1	NT	Homo sapiens D1George syndrome critical region, telomeric and
4914	14102	23185	1.12	2.7E-01	L77569.1	NT	Triticum aestivum (Wc688) gene, complete cds
5066	14246		2.97	2.7E-01	AW856131.1	EST_HUMAN	RC1-CT0286-230200-018-e03 CT0286 Homo sapiens cDNA
5308	14539	23544	2.45	2.7E-01	P17277	SWISSPROT	HOMEOBOX PROTEIN HOXA4 (CHOX-1.4)
6891	16273	24702	2.12	2.7E-01	Q61554	SWISSPROT	FIBRILLIN 1 PRECURSOR
8234	15415	24858	1.68	2.7E-01	Q11079	SWISSPROT	HYPOTHETICAL 20.9 KD PROTEIN B0563.3 IN CHROMOSOME X
6371	15551	25007	1.68	2.7E-01	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
6371	15551	25008	1.68	2.7E-01	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
6862	16052	25519	3.3	2.7E-01	O83809	SWISSPROT	THREONYL-TRNA SYNTHETASE (THREONINE-TRNA LIGASE) (THRRS)
6862	16052	25520	3.3	2.7E-01	O83809	SWISSPROT	THREONYL-TRNA SYNTHETASE (THREONINE-TRNA LIGASE) (THRRS)
7117	16284	25778	3.68	2.7E-01	AF087434.1	NT	Mus musculus transcription factor NF-ATc isoform a (NF-ATc) mRNA, complete cds
7389	16803	26091	2.21	2.7E-01	AV705043.1	EST_HUMAN	AV705043 ADB Homo sapiens cDNA clone ADBCOD05 5'
7389	16803	26092	2.21	2.7E-01	AV705043.1	EST_HUMAN	AV705043 ADB Homo sapiens cDNA clone ADBCOD05 5'
7399	16812	26102	4.34	2.7E-01	AJ133289.1	NT	Homo sapiens cavedin-1/-2 locus, Contig1, D7S522, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2)
8681	17638		1.41	2.7E-01	AJ012482.1	NT	Rattus norvegicus mRNA for phosphatidylinositol 3-kinase, catalytic subunit, beta isoform
9023	17874		1.5	2.7E-01	Q63827	SWISSPROT	CTD-BINDING SR-LIKE PROTEIN RA4
9122	17937		2.34	2.7E-01	AF217491.1	NT	Homo sapiens fragile 18D oxidoreductase (FOR) gene, exon 8
478	11868	18861	1.68	2.6E-01	P78411	SWISSPROT	IROQUOIS-CLASS HOMEODOMAIN PROTEIN IRX-2
487	9740		0.83	2.6E-01	D18459.1	NT	Bos taurus mRNA for mb-1, complete cds
1397	10611	19775	1.44	2.6E-01	BE885087.1	EST_HUMAN	601510338F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912345 5'
1438	10652	19826	0.97	2.6E-01	AB013290.1	NT	Glycine max pseudogene for Bd 30K
1881	11068	20258	6.36	2.6E-01	AL181472.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2
1881	11068	20258	6.36	2.6E-01	AL181472.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2082	11263		10.1	2.6E-01	AW733152.1	EST_HUMAN	b004d10.x1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2958451 3' similar to gb:M36072.60S RIBOSOMAL PROTEIN L7A (HUMAN); gb:M14889_cds1 Mouse surfact locus surfact 3 protein gene (MOUSE);
2121	11320	20538	1.03	2.6E-01	M11844.1	NT	Human prealbumin gene, complete cds
2436	11827		1.48	2.6E-01	Y12890.1	NT	B. maritimus rbcL gene
2511	11700		9.82	2.6E-01	BE272440.1	EST_HUMAN	601126016F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2890043 5'
3057	12283		1.03	2.6E-01	AW974531.1	EST_HUMAN	EST388635 IMAGE resequences, MAGM Homo sapiens cDNA
3557	12780	21910	1.04	2.6E-01	M22342.1	NT	Bacteriophage T2 DNA (adenine-N6)methyltransferase (dam) gene, complete cds
3622	12843	21963	1.94	2.6E-01	AF229118.1	NT	Homo sapiens acetylcholinesterase collagen-like tail subunit (COLO) gene, exons 1A, 2, 3, 4, and 5
3834	13150	22265	0.96	2.6E-01	AJ012174.2	NT	Chlamydomonas reinhardtii partial rpsB gene for RNase P RNA subunit
3834	13150	22266	0.96	2.6E-01	AJ012174.2	NT	Chlamydomonas reinhardtii partial rpsB gene for RNase P RNA subunit
4077	13287	22385	0.8	2.6E-01	AW959510.1	EST_HUMAN	EST371580 IMAGE resequences, MAGF Homo sapiens cDNA
4196	13342	22443	17.81	2.6E-01	BE080598.1	EST_HUMAN	QV1-BT0630-040400-132-603 BT0630 Homo sapiens cDNA
4350	13552	22847	1.15	2.6E-01	AF175293.1	NT	Enterococcus faecium strain N97-330 vanD glycopeptide resistance gene cluster, complete cds; and unknown gene
4494	13692	22785	0.83	2.6E-01	AB021180.1	NT	Gallus gallus mRNA for skeletal myosin heavy chain, complete cds
4494	13692	22786	0.83	2.6E-01	AB021180.1	NT	Gallus gallus mRNA for skeletal myosin heavy chain, complete cds
4545	13740	22840	1.51	2.6E-01	AA457617.1	EST_HUMAN	sa89d07.r1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:838477 5'
4848	13842	22832	1.45	2.6E-01	U01103.1	NT	Arabidopsis thaliana PSI type III chlorophyll a/b-binding protein (Lhca3*) mRNA, complete cds
4728	13917	23018	1.39	2.6E-01	AF142703.1	NT	Ophrestia radicata maturase-like protein (matK) gene, complete cds; chloroplast gene for chloroplast product
4991	14178	23269	4.02	2.6E-01	H04958.1	EST_HUMAN	Y51605.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:152286 5'
5068	14248		0.59	2.6E-01	AA884625.1	EST_HUMAN	am33b11.s1 Soares NFL_T_QBC_S1 Homo sapiens cDNA clone IMAGE:1488905 3'
5203	14378	23485	1.24	2.6E-01	AA985392.1	EST_HUMAN	am81g11.s1 Stratagene schizos brain S11 Homo sapiens cDNA clone IMAGE:1628572 3' similar to contains L1.12 L1 repetitive element;
5699	18398		2.32	2.6E-01	AE001811.1	NT	Thermotoga maritima section 123 of 138 of the complete genome
5754	14973	24371	2.17	2.6E-01	A1582557.1	EST_HUMAN	ts02a12.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2227438 3' similar to SW:NDP1_RAT Q64289 NEUROGENIC DIFFERENTIATION FACTOR 1 ;contains element LTR1 repetitive element;
5754	14973	24372	2.17	2.6E-01	A1582557.1	EST_HUMAN	ts02a12.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2227438 3' similar to SW:NDP1_RAT Q64289 NEUROGENIC DIFFERENTIATION FACTOR 1 ;contains element LTR1 repetitive element;
6575	15771	25233	2.72	2.6E-01	BF343588.1	EST_HUMAN	602014422F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4150398 5'

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6679	15874	25332	2.87	2.6E-01	BE830339.1	EST_HUMAN	RC5-ET0082-310500-021-F10 ET0082 Homo sapiens cDNA
6678	15874	25333	2.87	2.6E-01	BE830339.1	EST_HUMAN	RC5-ET0082-310500-021-F10 ET0082 Homo sapiens cDNA
7960	17099	26628	1.98	2.6E-01	P48280	SWISSPROT	CELL DIVISION PROTEIN FTSW HOMOLOG
8056	17101		25.08	2.6E-01	X51755.1	NT	Human lambda-Immunoglobulin constant region complex (germline)
8400	17478		2.5	2.6E-01	10180855	NT	Mus musculus jerky (Jrk), mRNA
8603	18269		2.25	2.6E-01	BE883491.1	EST_HUMAN	601511052F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912612 5'
8672	17847	23978	2.93	2.6E-01	AF316896.1	NT	Homo sapiens Na/K-ATPase gamma subunit (FXVD2) gene, complete cds, alternatively spliced
8017	17869		1.39	2.6E-01	D89425.1	NT	Cavia cobaya mRNA for serine/threonine kinase, complete cds
8145	17850		1.29	2.6E-01	AF141325.2	NT	Homo sapiens inositol polyphosphate 1-phosphatase (INPP1) gene, complete cds
9184	17975		1.27	2.6E-01	P47285	SWISSPROT	HYPOTHETICAL PROTEIN MG039
245	8523	18653	2.05	2.5E-01	4502298	NT	Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit (ATP5D), nuclear gene encoding mitochondrial protein, mRNA
246	9523	18653	2.52	2.5E-01	4502298	NT	Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit (ATP5D), nuclear gene encoding mitochondrial protein, mRNA
269	9535		7.15	2.5E-01	M26501.1	NT	Starfish (P. ochraceus) cytoplasmic actin gene, complete cds
842	10078	19237	1.27	2.5E-01	U09984.1	NT	Mus musculus ICR/Swiss glyceraldehyde 3-phosphate dehydrogenase (Gapd-S) gene, complete cds
1087	10293		0.95	2.5E-01	AE002156.1	NT	Ureaplasma urealyticum section 57 of 59 of the complete genome
1129	10353	19505	9.34	2.5E-01	T88837.1	EST_HUMAN	ye11g07.r1 Strategene lung (#837210) Homo sapiens cDNA clone IMAGE:117488 5'
1385	10569		2.16	2.5E-01	AB025343.1	NT	Olea europaea OEW mRNA for luped synthase, complete cds
1703	10916		5.2	2.5E-01	4885408	NT	Homo sapiens hyperpolarization activated cyclic nucleotide-gated potassium channel 4 (HCN4) mRNA
1848	12004	20248	1	2.5E-01	BE686804.1	EST_HUMAN	PM4-CT0400-310700-005-d08 CT0400 Homo sapiens cDNA
1848	12004	20247	1	2.5E-01	BE686804.1	EST_HUMAN	PM4-CT0400-310700-005-d08 CT0400 Homo sapiens cDNA
2371	11604		5.84	2.5E-01	AE000875.1	NT	Aquifer eolicus section 7 of 109 of the complete genome
2459	11650		1.02	2.5E-01	AA251887.1	EST_HUMAN	zs11a12.r1 NCJ_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:684882 5'
3390	12817		4.31	2.5E-01	AW973471.1	EST_HUMAN	EST385484 MAGE resequences, MAGM Homo sapiens cDNA
3508	12732	21870	0.77	2.5E-01	AF233875.1	NT	Danio rerio peptide YY precursor gene, complete cds
3524	12748	21879	6.77	2.5E-01	AL161517.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 29
4045	13255		0.9	2.5E-01	P32323	SWISSPROT	A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR
4309	13510		0.85	2.5E-01	Q03314	SWISSPROT	RHIB PROTEIN
4761	13952		1.18	2.5E-01	Q27225	SWISSPROT	MOLT-INHIBITING HORMONE PRECURSOR (MIH)
4767	13956	23057	4.65	2.5E-01	AF007768.1	NT	Charistoneura fumiferana diapause associated protein 2 (DAP2) mRNA, complete cds
4781	13980	23084	2.54	2.5E-01	AE004416.1	NT	Vibrio cholerae chromosome II, section 73 of 83 of the complete chromosome

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Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4816	14005		3.4	2.5E-01	AJ230113.1	NT	Mus musculus annexin V gene, intron 4 segment containing 5' LTR and gag portion of MuERV-L (murine endogenous retrovirus) element
5074	14254	23337	0.61	2.5E-01	AW873588.1	EST_HUMAN	hcd211.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3041897 3' similar to WP:Y71F8A_294.D CE22858 :
5349	14579	23656	12.94	2.5E-01	SB3390.1	NT	T3 receptor-associated cofactor-1 (human, fetal liver, mRNA, 2830 nt)
6349	15529	24979	4.91	2.5E-01	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
6536	15732	25196	3.18	2.5E-01	BF036595.1	EST_HUMAN	601459238F1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:3862609 5'
6666	15861	25320	4.29	2.5E-01	AF53238.1	EST_HUMAN	yq9407.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:202601 5'
6920	16113	25578	29.94	2.5E-01	U88651.2	NT	Homo sapiens matrix metalloproteinase MMP Rasi-1 gene, promoter region
6920	16113	25578	29.94	2.5E-01	U88651.2	NT	Homo sapiens matrix metalloproteinase MMP Rasi-1 gene, promoter region
7111	16288	25769	2.7	2.5E-01	AW581997.1	EST_HUMAN	RC3-ST0188-130100-015-407 ST0188 Homo sapiens cDNA
7217	16304	25878	2.22	2.5E-01	X58491.1	NT	Mouse L1Md LINE DNA
7843	16843	26341	3.62	2.5E-01	D50914.1	NT	Human mRNA for KIAA0124 gene, partial cds
8335	17433	26938	4.13	2.5E-01	AF200528.1	NT	Zea mays cellulose synthase-4 (Cesa-4) mRNA, complete cds.
8364	18350		6.92	2.6E-01	AL161641.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 41
8948	18192	23761	1.28	2.5E-01	AF170072.1	NT	Spodoptera frugiperda CALNUG mRNA, complete cds
8992	18113		1.37	2.5E-01	AV682543.1	EST_HUMAN	AV682543 GKC Homo sapiens cDNA clone GKCGZF10 5'
560	9810	18933	1.07	2.4E-01	AA836316.1	EST_HUMAN	on70d04.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1682023 3'
858	10094	19257	2.17	2.4E-01	BF576124.1	EST_HUMAN	602132442F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271578 5'
1311	10527	19687	11.61	2.4E-01	AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), X13 gene and LZTFL1 gene
1311	10527	19688	11.61	2.4E-01	AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), X13 gene and LZTFL1 gene
1818	11028		21.38	2.4E-01	AF267753.1	NT	Mesembryanthemum crystallinum putative potassium channel protein Mktip mRNA, complete cds
1884	11071	20262	1.38	2.4E-01	AF251708.1	NT	Zaccys dhumnades fructose-1,6-bisphosphatase mRNA, complete cds
2107	11308	20520	1.03	2.4E-01	AF111168.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
2134	11332		1.04	2.4E-01	P45384	SWISSPROT	IMMUNOGLOBULIN A1 PROTEASE PRECURSOR (IGA1 PROTEASE)
2227	11423	20649	1.67	2.4E-01	AE000880.1	NT	Aquifex aeolicus section 12 of 109 of the complete genome
2349	11642	20765	1.01	2.4E-01	BF002171.1	EST_HUMAN	7h23404.x1 NCJ_CGAP_Co16 Homo sapiens cDNA clone IMAGE:3316807 3' similar to SW:PRSB_XENLA
2502	11661	20811	1.68	2.4E-01	Z38534.1	NT	O42688 28S PROTEASE REGULATORY SUBUNIT 8A;
2717	11886	21113	5.18	2.4E-01	XT1783.1	NT	D discoideum (A33-K) ponA gene
2739	11918	21132	4.61	2.4E-01	AF030164.1	NT	S. pombe swi6 gene
							Bovine adenovirus 3 complete genome
3097	12333		3.32	2.4E-01	U72728.1	NT	Oriza longistaminata receptor kinase-like protein, family member D, and retrofit (gap/pd) genes, complete cds
3843	12864	21982	1	2.4E-01	AF169793.1	NT	Podospora anserina HET-C protein (Het-c) gene, complete cds

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3743	12663	22078	0.89	2.4E-01	AE000312.1	NT	Escherichia coli K-12 MG1655 section 202 of 400 of the complete genome
4008	13220		0.9	2.4E-01	D23880.1	NT	Rattus norvegicus mRNA for alphaB crystallin-related protein, complete cds
5512	14737	24101	9.26	2.4E-01	AF091216.1	NT	Mus musculus Wm protein (Wm) gene, complete cds
5512	14737	24102	9.26	2.4E-01	AF091216.1	NT	Mus musculus Wm protein (Wm) gene, complete cds
							7154404.x1 NCI_CGAP_B16 Homo sapiens cDNA clone IMAGE:3338503 3' similar to SW-SFR4_HUMAN
5612	14836	24211	2.4	2.4E-01	BF592338.1	EST_HUMAN	Q08170 SPLICING FACTOR, ARGININE/SERINE-RICH 4 ;contains element TAR1 TAR1 repetitive element
5648	14871	24258	2.63	2.4E-01	AF035546.1	NT	Drosophila melanogaster p38a MAP kinase gene, complete cds
5703	14922	24315	2.48	2.4E-01	766180.1	NT	Homo sapiens HSPC142 protein (HSPC142), mRNA
5894	15111	24523	1.92	2.4E-01	AI698089.1	EST_HUMAN	wc32x11.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2323220 3' similar to gb.J03464
6228	15409	24851	8.53	2.4E-01	L43001.1	NT	PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR (HUMAN);
6845	16089	25558	6.01	2.4E-01	AI693515.1	EST_HUMAN	Bos taurus guanylyl cyclase-activating protein 2 (guca2) mRNA, complete cds
7181	16368	25847	2.4	2.4E-01	Q03692	SWISSPROT	wc4302.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330908 3' similar to contains
7351	16507	26057	3.3	2.4E-01	AL161494.2	NT	Mus musculus type 1 sigma receptor gene, complete cds
7412	16824	28118	2.68	2.4E-01	AF030189.1	NT	P. asiatica mosaic virus genomic RNA
7764	16950		2.28	2.4E-01	Z21647.1	NT	Homo sapiens fragile 10D cDNA reductase (FOR) gene, exon 8
8281	17404	26831	1.22	2.4E-01	AF217491.1	NT	Arabidopsis thaliana ethylene-insensitive3-like1 (EIL1) mRNA, complete cds
8426	18136		1.93	2.4E-01	AF004213.1	NT	Mus musculus mRNA for putative mc7 protein (mc7 gene)
8492	17635		2.37	2.4E-01	AJ278191.1	NT	Gallus gallus gene coding for e-actin
8720	18120		2.21	2.4E-01	V01507.1	NT	Homo sapiens chromosome 21 segment HS21C081
9180	17972		3.79	2.4E-01	AL163281.2	NT	Human 14-3-3n protein mRNA, complete cds
9222	18001		2.34	2.4E-01	L20422.1	NT	aromatase [P. ocellularis guttatae=p. ocellularis finches, ovary, mRNA, 3188 nt]
394	9049	18784	1.02	2.3E-01	S75898.1	NT	Mycoplasma genitalium section 35 of 51 of the complete genome
643	8889		3.82	2.3E-01	U93713.1	NT	Methanococcus jannaschii section 138 of 150 of the complete genome
673	9018	19047	23.08	2.3E-01	U87598.1	NT	601142073F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3505818 5'
842	10175	19328	4.61	2.3E-01	BE311893.1	EST_HUMAN	Mus musculus vesicular protein sorting 4b (yeast) (Vps4b), mRNA
1489	10712	19884	0.92	2.3E-01	6677880	NT	Mus musculus cdh5 gene, exon 1, partial
1609	10822	19998	3.69	2.3E-01	Y10887.2	NT	Homo sapiens partial intron 3 of the wild type AF-4/FEL gene
2012	11214		1.15	2.3E-01	AJ235353.1	NT	60117562F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531015 5'
2408	11601	20821	1.57	2.3E-01	BE297718.1	EST_HUMAN	Marinibacteria agrovirens gyrB gene for DNA gyrase subunit B, partial cds, strain:IFO 14957
2778	10808	19770	2	2.3E-01	AB015033.1	NT	

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2918	12166	21291	0.98	2.3E-01	AA601379.1	EST_HUMAN	nt16d06.s1 NCI_CGAP_Pha1 Homo sapiens cDNA clone IMAGE:1100843 3' similar to contains Alu repetitive element; contains element THR repetitive element;
3049	12285		7	2.3E-01	R21732.1	EST_HUMAN	Yh21b07.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:130357 3'
3349	12577	21718	1.24	2.3E-01	H69836.1	EST_HUMAN	Yh87h10.r1 Soares fetal liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:213283 5'
3909	13125		5.19	2.3E-01	7682133	NT	Homo sapiens KIAA0450 gene product (KIAA0450), mRNA
4343	13545	22636	1.08	2.3E-01	R82252.1	EST_HUMAN	Y1701.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:148017 5'
4394	13595		1.97	2.3E-01	L78789.1	NT	Mus musculus renin (Ren-1c) gene, promoter region
4445	13844	22739	1.16	2.3E-01	D80899.1	NT	Synechocystis sp. PCC8803 complete genome, 1/27, 1-133859
4485	13893	22773	2.23	2.3E-01	AF082535.1	NT	Homo sapiens mitogen-activated protein kinase p38delta (PRKM13) mRNA, complete cds
4951	13746	22846	5.67	2.3E-01	5031894	NT	Homo sapiens nuclear transport factor 2 (placental protein 15) (PP15) mRNA
5076	14255	23338	0.64	2.3E-01	AB032400.1	NT	Mus musculus tulip 1 mRNA, complete cds
5252	14425		1.08	2.3E-01	AF080322.1	NT	Bos taurus NAD(+) isocitrate dehydrogenase subunit 1 IDH1-B precursor (IDH) mRNA, nuclear gene encoding mitochondrial protein, complete cds
5332	14663	23637	2.38	2.3E-01	AB040945.1	NT	Homo sapiens mRNA for KIAA1512 protein, partial cds
5407	14835	23763	2.13	2.3E-01	BF058381.1	EST_HUMAN	7a30b06.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3476699 3' similar to SW:GAG_SMSAV P03330 GAG POLYPROTEIN [CONTAINS: CORE PROTEIN P15; INNER COAT PROTEIN P12; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10];
5458	14882	24032	4.78	2.3E-01	X96587.1	NT	C.familiaris rom1 gene
5633	14857	24239	2.28	2.3E-01	A1708840.1	EST_HUMAN	as27e12.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2318446 3' similar to gb:X13238 CYTOCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);
5633	14857	24240	2.28	2.3E-01	A1708840.1	EST_HUMAN	as27e12.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2318446 3' similar to gb:X13238 CYTOCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);
6032	15240	24662	4.01	2.3E-01	A1718148.1	EST_HUMAN	as42f12.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2318887 3' similar to contains Alu repetitive element;
6267	15438	24878	2.77	2.3E-01	AF175389.1	NT	Glycine max resistance protein LM17 precursor RNA, partial cds
6339	15519		3.84	2.3E-01	8754779	NT	Mus musculus myosin XV (Myo15), mRNA
6398	15579		2.84	2.3E-01	N80983.1	EST_HUMAN	zai12e08.r1 Soares fetal liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:282358 5'
6482	15659	25131	2.45	2.3E-01	M88931.1	NT	Oxytricha nova macronuclear telomere-binding protein alpha subunit (tet-alpha alanine version) gene, complete cds
7049	16228	25701	3.31	2.3E-01	BE179060.1	EST_HUMAN	MIR0-H70559-240400-014-g11 HT0559 Homo sapiens cDNA
7199	16376		5.88	2.3E-01	BF133577.1	EST_HUMAN	601648155R2 NIH_MGC_59 Homo sapiens cDNA clone IMAGE:4102092 3'
7744	16840	26450	1.81	2.3E-01	AJ250189.1	NT	Mus musculus partial mRNA for muscle protein 534 (mg534 gene)
7744	16840	26451	1.81	2.3E-01	AJ250189.1	NT	Mus musculus partial mRNA for muscle protein 534 (mg534 gene)
7891	17107	26637	2.22	2.3E-01	AE092187.2	NT	Chlamydomonas reinhardtii AR39, section 4 of 94 of the complete genome

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Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8410	17485		3.18	2.3E-01	U45428.1	NT	Borrelia burgdorferi 2.9-6 locus, ORF-A-D genes, complete cds and REP+ gene, partial cds
8503	17542		25.49	2.3E-01	T27231.1	EST_HUMAN	HCOEST44 HT29M8 Homo sapiens cDNA clone HCOE44 5'
8527	18083		1.30	2.3E-01	AA089818.1	EST_HUMAN	chr1424.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'
8538	17561		1.46	2.3E-01	AW863940.1	EST_HUMAN	PM4-SN0012-030400-001-008 SN0012 Homo sapiens cDNA
8569	18281	23881	3.28	2.3E-01	AW303623.1	EST_HUMAN	xy21d07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813773 3' similar to TR:Q9Z175
8638	18331	23603	6.26	2.3E-01	BE882484.1	EST_HUMAN	Q9Z175 LYSYL OXIDASE-RELATED PROTEIN 2; contains PTR5.b2 TAR1 repetitive element;
8687	17656		1.79	2.3E-01	BF603318.1	EST_HUMAN	601607202F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3908689 5'
8739	17685		2.68	2.3E-01	AJ006518.1	NT	602144459F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4287718 5'
8834	17744		1.32	2.3E-01	U49845.1	NT	Rattus norvegicus mRNA for acid gated ion channel
9102	17925		3.77	2.3E-01	BF475811.1	EST_HUMAN	Pleurodeles waltl distal-less like protein PwOtk-3 (PwOtk-3) mRNA, complete cds
9261	18242	23708	1.28	2.3E-01	M60675.1	NT	nac3h12.x1 Lupski_sclatc_ nerve Homo sapiens cDNA clone IMAGE:3395950 3' similar to contains element MER38 repetitive element;
89	8382	18512	0.82	2.2E-01	A052180.1	EST_HUMAN	Human von Willebrand factor gene, exons 23 through 34
1547	10761	19835	2.55	2.2E-01	AF187850.1	NT	cc14a10.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1675280 3' similar to TR:Q13040 Q13040 ATP-BINDING CASSETTE PROTEIN;
1988	11189	20474	0.99	2.2E-01	AF171901.1	NT	Homo sapiens PPAR delta gene, promoter region
2058	11259	20474	2.57	2.2E-01	M34840.1	NT	Trimeresurus malabaricus cytb gene, partial cds; mitochondrial gene for mitochondrial product
2367	11560	20782	5.34	2.2E-01	BF677538.1	EST_HUMAN	Fresh-water sponge Emf1 alpha collagen (COLF1) gene
2548	11738	20863	1.67	2.2E-01	BE618258.1	EST_HUMAN	602085608F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249969 5'
2548	11738	20854	1.67	2.2E-01	BE618258.1	EST_HUMAN	601462628F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3868190 5'
2835	12074	21190	5.33	2.2E-01	BE155625.1	EST_HUMAN	601462628F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3868190 5'
2835	12074	21197	5.33	2.2E-01	BE155625.1	EST_HUMAN	PM2-HT0353-281289-003-a12 HT0353 Homo sapiens cDNA
2871	12109		1.67	2.2E-01	AF020503.1	NT	PM2-HT0353-281289-003-a12 HT0353 Homo sapiens cDNA
3369	12597		2.58	2.2E-01	AL161582.2	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
3735	12855	22071	0.61	2.2E-01	AL163285.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 62
3803	13021		1.89	2.2E-01	AF155728.1	NT	Homo sapiens chromosome 21 segment HS21C085
4073	13283	22382	0.59	2.2E-01	AF213391.1	NT	Xiphophorus maculatus truncated Rax1 retrotransposon reverse transcriptase (RT) pseudogene
4108	13313		0.61	2.2E-01	U68174.1	NT	Mus musculus ATP-binding cassette protein (Abcb8) mRNA, partial cds
4195	13399		1.05	2.2E-01	AF119102.1	NT	Mus musculus breast/ovarian cancer susceptibility protein (BRCA1) mRNA, complete cds
4203	13406	22501	6.45	2.2E-01	AF155142.1	NT	Drosophila melanogaster UNC-119 (unc-119) gene, complete cds Mus musculus mixed lineage kinase 3 (Mlk3) and two pore domain K+ channel subunit (Kcnk6) genes, complete cds

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4250	13453	22544	2.81	2.2E-01	AF117340.1	NT	Mus musculus MAP kinase kinase kinase 1 (Mekk1) mRNA, complete cds
4250	13453	22545	2.81	2.2E-01	AF117340.1	NT	Mus musculus MAP kinase kinase kinase 1 (Mekk1) mRNA, complete cds
4349	13551	22845	1.25	2.2E-01	U01307.1	NT	Human scRNA (BC200 beta) pseudogene
4349	13551	22846	1.25	2.2E-01	U01307.1	NT	Human scRNA (BC200 beta) pseudogene
4842	14031		1.18	2.2E-01	D50604.1	NT	Human beta-cytoplasmic actin (ACTBP8) pseudogene
4848	14037	23130	2.84	2.2E-01	AA211218.1	EST_HUMAN	z887c05.t1 Stratigene hNT neuron (#837233) Homo sapiens cDNA clone IMAGE:848968 5'
5068	14249		1.22	2.2E-01	L13288.1	NT	Mus musculus vinculin gene, exon 3
5549	14773	24141	1.98	2.2E-01	5803002	NT	Homo sapiens diaphanous (Drosophila, homolog) 2 (DIAPH2), transcript variant 156, mRNA
5553	14777		4.03	2.2E-01	D94000.1	NT	Synechocystis sp. PCC6803 complete genome, 1927, 2392726-2538999
6097	15287	24729	8.28	2.2E-01	AV756238.1	EST_HUMAN	AV756238 BM Homo sapiens cDNA clone BMFAHC08 5'
6204	15385	24827	1.82	2.2E-01	M24138.1	NT	Human glycoprotein B gene, exon 4
6204	15385	24828	1.82	2.2E-01	M24138.1	NT	Human glycoprotein B gene, exon 4
6470	15667		2.59	2.2E-01	AF155143.1	NT	Mus musculus nm23-M1 gene, promoter region
6742	15697	25398	2.32	2.2E-01	AE001713.1	NT	Thermotoga maritima section 25 of 138 of the complete genome
6771	15698		2.88	2.2E-01	AW855039.1	EST_HUMAN	PM3-CT0263-241299-009-b07 CT0263 Homo sapiens cDNA
6811	16006	25467	2.22	2.2E-01	8383247	NT	Mus musculus deformed epidermal autoregulatory factor 1 (Draef1), mRNA
6828	16022	25488	3.06	2.2E-01	BF376354.1	EST_HUMAN	MR1-TN0045-110800-006-c02 TN0045 Homo sapiens cDNA
6857	16109	25576	22.93	2.2E-01	P48834	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
7016	16183	25687	3.82	2.2E-01	AF197841.1	NT	Fusaria hygrometrica chloroplast-localized small heat shock protein (CP-shSP21) mRNA, complete cds;
7055	16232	25707	2.87	2.2E-01	BF208507.1	EST_HUMAN	nuclear gene for chloroplast product
7858	17088	26828	5.39	2.2E-01	X01918.1	NT	601869724F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4100189 5'
7898	16431	25918	2.66	2.2E-01	7708215	NT	Drosophila 68C glue gene cluster
8338	17436		2.06	2.2E-01	BE870858.1	EST_HUMAN	Homo sapiens H-2K binding factor-2 (LOC51560), mRNA
							601448957F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3850670 5'
8447	18342		3.56	2.2E-01	U82871.2	NT	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), cell surface (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and L1>
8539	17564		2.37	2.2E-01	AF188843.1	NT	Vitis vinifera cultivar Pinot Noir plasma membrane aquaporin (PIP1a) mRNA, complete cds
8858	14486	23584	3.17	2.2E-01	AW361088.1	EST_HUMAN	RC1-CT0249-141199-021-g04 CT0249 Homo sapiens cDNA
9192	18336		2.97	2.2E-01	AV694801.1	EST_HUMAN	AV694801 GKC Homo sapiens cDNA clone GKC4HB02 5'
9273	18036	23843	1.35	2.2E-01	BF243095.1	EST_HUMAN	601870452F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4104988 5'
9284	18283	23682	1.57	2.2E-01	AL161578.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 74
978	10210	19368	1.69	2.1E-01	AA59288.1	EST_HUMAN	nm31e11.a1 NCI_CGAP_Lip2 Homo sapiens cDNA clone IMAGE:1081804
981	10212	19368	1.99	2.1E-01	AL161504.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 18

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1132	10355		3.44	2.1E-01	AE002314.2	NT	Chlamydia muridarum, section 45 of 85 of the complete genome
1206	10425	19580	1.31	2.1E-01	6754299	NT	Mus musculus interferon (alpha and beta) receptor 2 (Ifnar2), mRNA
1208	10425	19581	1.31	2.1E-01	6754299	NT	Mus musculus interferon (alpha and beta) receptor 2 (Ifnar2), mRNA
1878	11085	20275	1.91	2.1E-01	AA908824.1	EST_HUMAN	ck73e02.a1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1519810 3' similar to gb:K02785
2124	11323	20541	4.13	2.1E-01	BF695073.1	EST_HUMAN	COMPLEMENT C3 PRECURSOR (HUMAN);
2875	12113	21241	2.07	2.1E-01	6912445	NT	602083129F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4247503 5'
2917	12155	21290	1.12	2.1E-01	U72145.1	NT	Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 4 (KCNH4), mRNA
3794	13012		6.81	2.1E-01	9838381	NT	Campylobacter acuminata 3-hydroxy-3-methylglutaryl coenzyme A reductase (hmrg3) mRNA, complete cds
4031	13241	22345	1.17	2.1E-01	P11976	SWISSPROT	Beta vulgaris mitochondrion, complete genome
4031	13241	22346	1.17	2.1E-01	P11976	SWISSPROT	IMMEDIATE-EARLY PROTEIN IE180
4238	13439		2.87	2.1E-01	AF124528.1	NT	IMMEDIATE-EARLY PROTEIN IE180
4370	13572		1.53	2.1E-01	AB033041.1	NT	Orchestria carmiana calcium-binding protein BP23 precursor (BP23) gene, complete cds
4574	13788	22863	1.99	2.1E-01	AB010273.1	NT	Homo sapiens pshap47 gene, complete cds
5290	14481	23528	1.2	2.1E-01	AE001173.1	NT	Borrelia burgdorferi (section 59 of 70) of the complete genome
5328	14561	23833	6	2.1E-01	BF672895.1	EST_HUMAN	602152001F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4283001 5'
6258	15439		2.04	2.1E-01	AE000972.1	NT	Archaeoglobus fulgidus section 135 of 172 of the complete genome
6378	15568	25014	1.92	2.1E-01	AF000949.1	NT	Canis familiaris keratin (KRT9) gene, complete cds
6770	15971	25427	5.83	2.1E-01	Z35786.1	NT	S. cerevisiae chromosome II reading frame ORF YBL025w
6918	16111	25577	4.87	2.1E-01	X97378.1	NT	A. thaliana mRNA for AFRBP1b protein
7182	16359	25838	2.49	2.1E-01	P52824	SWISSPROT	DIACYLGLYCEROL KINASE, DELTA (DIGLYCERIDE KINASE) (DGK-DELTA) (DAG KINASE DELTA)
8098	17232		2.2	2.1E-01	11038647	NT	(80 KD DIACYLGLYCEROL KINASE)
8108	17243	26784	2.2	2.1E-01	BE180422.1	EST_HUMAN	Homo sapiens pancreatic polypeptide 2 (PPY2), mRNA
8910	17731		1.54	2.1E-01	AF217490.1	NT	RC3-HT0622-040500-013-511 HT0622 Homo sapiens cDNA
9034	18247		1.28	2.1E-01	L32588.1	NT	Homo sapiens fragile 16D cDNA reductase (FOR) gene, exons 8, 9, and partial cds
9228	18004	23846	1.68	2.1E-01	BE672330.1	EST_HUMAN	Human granulosa gene
205	9485	18619	4.22	2.0E-01	AB017437.1	NT	7e69602.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:3223034 3'
540	9791		2.28	2.0E-01	7705601	NT	Gallus gallus mRNA for avena, complete cds
708	9948	19084	0.93	2.0E-01	M77085.1	NT	Homo sapiens CGI-18 protein (LOC31008), mRNA
820	10058	19211	1.88	2.0E-01	AF027885.1	NT	O. cuniculus germline IgH heavy chain V-H pseudogene, allotype VH42
1018	10247	18398	0.76	2.0E-01	D89305.1	NT	Mus musculus Major Histocompatibility Locus class II region
							Synechocystis sp. PCC6803 complete genome, 7127, 781449-920915

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1133	10358	19507	3.48	2.0E-01	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
1281	10478	19638	1.85	2.0E-01	AJ132895.5	NT	Homo sapiens rac1 gene
1315	10531	19693	1.37	2.0E-01	AW384837.1	EST_HUMAN	PM1-H70422-281289-002-c08 H70422 Homo sapiens cDNA
1480	10693	19888	12.02	2.0E-01	4503408	NT	Homo sapiens dystrobrevin, alpha (DTNA), mRNA
1537	10760	19923	4.33	2.0E-01	AB007974.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0505
1542	10765	19828	1.25	2.0E-01	AF260700.1	NT	Homo sapiens sodium/folate symporter mRNA, partial cds
1672	10885	20068	2.02	2.0E-01	U22346.1	NT	Human bradykinin B1 receptor (bradyb1) gene, complete cds
1692	10904		2.15	2.0E-01	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds, and unknown gene
1728	10841		3.16	2.0E-01	U67626.1	NT	Methanococcus jannaschii section 67 of 150 of the complete genome
1855	11082	20252	4.98	2.0E-01	BE871330.1	EST_HUMAN	801449441F1 NIH_MGC_85 Homo sapiens cDNA clone IMAGE:3853330 5'
1855	11082	20253	4.98	2.0E-01	BE871330.1	EST_HUMAN	801449441F1 NIH_MGC_85 Homo sapiens cDNA clone IMAGE:3853330 5'
2316	11510		1.87	2.0E-01	X82877.1	NT	H. sapiens Nat-D-glucose cotransport regulator gene
3462	12687	21823	1.8	2.0E-01	P46607	SWISSPROT	HOMEBOX PROTEIN GLABRA2 (HOMEBOX-LEUCINE ZIPPER PROTEIN ATHB-10) (HD-ZIP PROTEIN ATHB-10)
3644	12767		0.7	2.0E-01	AW238005.1	EST_HUMAN	xp15602.x1 NCI_CGAP_HN9 Homo sapiens cDNA clone IMAGE:2740395 3' similar to contains element
3688	12907	22027	0.88	2.0E-01	P34841	SWISSPROT	MER21 repetitive element;
3691	12912		0.85	2.0E-01	6680797	NT	CEB-11 PROTEIN
3831	13147	22264	0.71	2.0E-01	Z46906.1	NT	Mus musculus bone morphogenetic protein 6 (Bmp6), mRNA
4423	13623	22718	0.6	2.0E-01	AF242431.1	NT	Sus scrofa
4563	13757		9.02	2.0E-01	BE828165.1	EST_HUMAN	Mus musculus neuronal apoptosis inhibitory protein 6 (Nai6) gene, complete cds; and Nai6 gene, exons 2-9 and 11-16
5085	14245	23332	5.68	2.0E-01	8922080	NT	QV4-EN0032-180500-223-e03 EN0032 Homo sapiens cDNA
6135	14313	23405	1.02	2.0E-01	Y19216.1	NT	Homo sapiens hypothetical protein ASH1 (ASH1), mRNA
6232	14408	23489	1.4	2.0E-01	M59257.1	NT	Homo sapiens putative pshHbD pseudogene for hair keratin, exons 1 to 9
5415	14843	23775	2.42	2.0E-01	X56600.1	NT	Human carcinoembryonic antigen (CEA) gene, exon 4
6547	14771	24138	2.28	2.0E-01	11432540	NT	Rat SOD-2 gene for manganese-containing superoxide dismutase
5883	14913	24307	5.85	2.0E-01	U16300.1	NT	Homo sapiens dual oxidase-like domains 2 (DUOX2), mRNA
5842	15058	24467	3.26	2.0E-01	X61033.1	NT	Saccharomyces cerevisiae Hst5p (HAL5) mRNA, complete cds
5891	15108	24519	4.07	2.0E-01	AW360885.1	EST_HUMAN	Mauratus mu class glutathione transferase gene
6443	15840		8.48	2.0E-01	AF028028.1	NT	PM1-CT0247-141089-001-g08 CT0247 Homo sapiens cDNA
6529	15725	25180	4.35	2.0E-01	X91151.1	NT	Andes virus strain OI23133 glycoprotein G1 and G2 precursor, gene, partial cds
6839	16083		4.41	2.0E-01	AE001278.1	NT	M. musculus scp2 gene exon 14
7038	16215		2.78	2.0E-01	AF146892.1	NT	Chlamydia trachomatis section 5 of 87 of the complete genome
							Homo sapiens filamin 2 (FLN2) mRNA, complete cds

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Table 4
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7417	16828	28121	2.97	2.0E-01	D89088.1	NT	Salvelinus pluvius mRNA for transferrin, complete cds
7417	16829	28122	2.97	2.0E-01	D89088.1	NT	Salvelinus pluvius mRNA for transferrin, complete cds
9051	17823	23874	2.36	2.0E-01	A1023592.1	EST_HUMAN	ov60a10.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1843810 3'
9074	17800		7.52	2.0E-01	AF078184.2	NT	Homo sapiens Ku70-binding protein (KUB3) mRNA, partial cds
9218	17897	23868	1.9	2.0E-01	11528485	NT	Mus musculus fructosamine 3 kinase (Fn3k), mRNA
110	8398		9.7	1.9E-01	.7549743	NT	Rattus norvegicus Aryl hydrocarbon receptor nuclear translocator 1 (Ahr1), mRNA
367	9626	18755	7.17	1.9E-01	AF04353.1	NT	Mus musculus pale ear (ep) gene, wild type allele, 3' region, partial cds
982	9808	19038	1.12	1.9E-01	U32881.2	NT	Homo sapiens lambda/ota protein kinase C-interacting protein mRNA, complete cds
982	9808	19037	1.12	1.9E-01	U32881.2	NT	Homo sapiens lambda/ota protein kinase C-interacting protein mRNA, complete cds
989	9815	19044	5.78	1.9E-01	BE070801.1	EST_HUMAN	RC3-BT0502-251193-011-d01 BT0502 Homo sapiens cDNA
970	9815	19044	6.13	1.9E-01	BE070801.1	EST_HUMAN	RC3-BT0502-251193-011-d01 BT0502 Homo sapiens cDNA
983	10224		1.39	1.9E-01	7305180	NT	Mus musculus interleukin 2 receptor, gamma chain (Il2rg), mRNA
1112	10335	19487	13.08	1.9E-01	AA358813.1	EST_HUMAN	EST07764 Fetal lung II Homo sapiens cDNA 5' end
1378	10592	18758	2.31	1.9E-01	AF061282.1	NT	Sorghum bicolor 22 kDa kafirin cluster
1437	10851		3.35	1.9E-01	AF184623.1	NT	Plasmodium vivax reticulocyte binding protein-2 (rbp-2) gene, complete cds
2348	11541	20764	5.01	1.9E-01	8922533	NT	Homo sapiens hypothetical protein FLJ10581 (FLJ10581), mRNA
2873	12111	21239	4.06	1.9E-01	U68066.1	NT	Sigmodon hispidus p53 gene, partial cds
2886	12126		6.97	1.9E-01	J00822.1	NT	Gallus gallus ovalbumin (Y) gene, complete cds
2890	12198	21333	1.11	1.9E-01	U25148.1	NT	Rattus norvegicus brush border myosin-1 (BBM1) mRNA, partial cds
3373	12801	21737	4.46	1.9E-01	D13197.1	NT	Mouse gene for immunoglobulin diversity region D1
3455	12880	21815	5.59	1.9E-01	R18467.1	EST_HUMAN	y42f10.1 Soares fetal liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:129547 5'
3782	13010	22125	0.72	1.9E-01	AF264017.1	NT	Rattus norvegicus arylacetamide deacetylase gene, complete cds
3970	13185	22284	3.62	1.9E-01	AB006784.1	NT	Schistosoma mansoni DNA for cytoplasmic dynein heavy chain, complete cds
4058	13270	22372	1.63	1.9E-01	AW754108.1	EST_HUMAN	CM3-CT0315-271109-045-b11 CT0315 Homo sapiens cDNA
4210	13419	22514	1.02	1.9E-01	BE834943.1	EST_HUMAN	MR1-FN0010-280700-007-d04 FN0010 Homo sapiens cDNA
4465	13683	22756	0.59	1.9E-01	AL161493.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 6
4783	13972	23075	0.78	1.9E-01	Z83780.1	NT	Fugu rubripes genes encoding carbamoyl phosphate synthetase III, myosin light chain, MAP2
5039	14220		1.06	1.9E-01	AF223842.1	NT	Rattus norvegicus chemokine receptor CXCR3 mRNA, complete cds
6243	14480		3.78	1.9E-01	AE004564.1	NT	Pseudomonas aeruginosa PA01, section 155 of 528 of the complete genome
5492	14718		4.47	1.9E-01	AW130149.1	EST_HUMAN	x129a07.x1 NCI_CGAP_UH1 Homo sapiens cDNA clone IMAGE:2818444 3' similar to gb:M73779 RETINOIC ACID RECEPTOR ALPHA-1 (HUMAN);
5509	14734	24088	7.78	1.9E-01	AF127937.1	NT	Homo sapiens DNA polymerase epsilon catalytic subunit protein (POLE1) gene, exon 1a
5607	14831		2.29	1.9E-01	AU133118.1	EST_HUMAN	AU133118 NT2RP4 Homo sapiens cDNA clone NT2RP4001328 5'
6306	15487	24932	2.74	1.9E-01	AF072724.1	NT	Zea mays starch branching enzyme I (sbe1) gene, complete cds

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6676	15370	25329	15.9	1.9E-01	AB033024.1	NT	Homo sapiens mRNA for KIAA1198 protein, partial cds
7237	16458	25948	1.98	1.9E-01	AL161603.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 15
7237	16458	25947	1.98	1.9E-01	AL161503.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 15
7340	16558	26044	2.08	1.9E-01	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
8215	17346	26888	2.81	1.9E-01	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
9239	18176	28434	1.52	1.9E-01	7524759	NT	Chlorella vulgaris chloroplast, complete genome
33	8329	18434	3.28	1.8E-01	U73200.1	NT	Mus musculus p116Rip mRNA, complete cds
284	11864	18689	2.47	1.8E-01	AB022090.1	NT	Mus musculus Cctg gene for chaperonin containing TCP-1 gamma subunit, partial cds
375	9841	18778	1.41	1.8E-01	4502532	NT	Homo sapiens calcium channel, voltage-dependent, beta 2 subunit (CACNB2) mRNA, and translated products
754	9895	18140	0.76	1.8E-01	AB021490.2	NT	Oryzias latipes gene for membrane guanylyl cyclase OIGC1, complete cds
989	10220	19374	0.88	1.8E-01	AB17212.1	EST_HUMAN	wc71f02.2.1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2337051 3'
1089	10322	19473	3.09	1.8E-01	AF000580.1	NT	Dictyostellium discoideum plasmid Ddp5, complete genome
1295	10510	19670	8.42	1.8E-01	AL117188.1	NT	Yersinia pestis plasmid pCD1
1814	11022		1.71	1.8E-01	4505038	NT	Homo sapiens latent transforming growth factor beta binding protein 4 (LTBP4) mRNA
1832	11040		1.82	1.8E-01	AI733708.1	EST_HUMAN	qg22d10.55 NCL CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1761811 3' similar to TR:O75938 O75938 GAMMA BUTYROBETAINE HYDROXYLASE
1890	11087	20277	1.62	1.9E-01	AB051897.1	NT	Mus musculus Scys6, Scys9, Scys16-ps, Scys5 genes for small inducible cytokine A8 precursor, small inducible cytokine A9 precursor, Scys18 pseudogene, small inducible cytokine A5 precursor, complete cds
2652	11835		2.24	1.9E-01	AW935728.1	EST_HUMAN	QV3-DT0018-081299-038-g04 DT0018 Homo sapiens cDNA
2850	12089		1.85	1.8E-01	AF184589.1	NT	Jonopodium acule LEAFY protein (LEAFY2) gene, partial cds
2855	12093	21223	1.11	1.8E-01	AW182300.1	EST_HUMAN	x41e03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2669758 3'
3088	12324	21446	1.89	1.8E-01	AW985178.1	EST_HUMAN	QV0-BN0041-070300-147-c04 BN0041 Homo sapiens cDNA
3344	12572	21711	0.8	1.8E-01	BF183592.1	EST_HUMAN	601809723R1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040621 3'
3600	12821	21942	0.97	1.8E-01	H03389.1	EST_HUMAN	y45601.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:151704 3' similar to contains Alu repetitive element
3600	12821	21943	0.97	1.8E-01	H03389.1	EST_HUMAN	y45601.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:151704 3' similar to contains Alu repetitive element
4325	13526		1.2	1.8E-01	D37954.1	NT	Bovine NB25 mRNA for MHC class II (BdLA-DQB), complete cds
4553	13748	22847	5.71	1.8E-01	AL181556.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 58

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4784	13973	23078	2.53	1.8E-01	AB051897.1	NT	Mus musculus Scya8, Scya8, Scya16-ps, Scya5 genes for small inducible cytokine A8 precursor, small inducible cytokine A8 precursor, Scya16 pseudogene, small inducible cytokine A5 precursor, complete cds
5072	14252	23335	2.38	1.8E-01	AW814270.1	EST_HUMAN	MR3-ST0203-151289-112-g06 ST0203 Homo sapiens cDNA
5081	14271	23355	4.94	1.8E-01	AI782382.1	EST_HUMAN	en28g07.y5 Gassler Wilms tumor Homo sapiens cDNA clone IMAGE:1700028 5'
5128	14305	23395	7.48	1.8E-01	AF181258.1	NT	Mesocricetus auratus Na-taurocholate cotransporting polypeptide mRNA, partial cds
5143	14322	23414	1.28	1.8E-01	AK39881.1	EST_HUMAN	t57c04.x1 NCJ CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2134580 3'
5254	14427	23503	11.75	1.8E-01	AW809402.1	EST_HUMAN	MR4-ST0121-041189-018-b01 ST0121 Homo sapiens cDNA
5904	15121		2.11	1.8E-01	N84853.1	EST_HUMAN	Y92H02.f1 Soares_multiple sclerosis_2NIBHMS Homo sapiens cDNA clone IMAGE:278163 5'
7231	16452	25942	2.83	1.8E-01	X77338.1	NT	A.thaliana mRNA for ribonucleotide reductase R2
7270	16489	25979	7.41	1.8E-01	U98906.1	NT	Bacteriophage r11 Integrase, repressor protein (ro), dUTPase, hollin and lysin genes, complete cds
7322	16289	24721	2.94	1.8E-01	AB018591.1	NT	Citrus latifolius mRNA for wscs, complete cds
7322	16289	24722	2.94	1.8E-01	AB018581.1	NT	Citrus latifolius mRNA for wscs, complete cds
7323	16339	26028	4.55	1.8E-01	AF019107.1	NT	Dicystosellum discoidium unknown (DG1041) gene, complete cds
7588	16792	28284	1.89	1.8E-01	M59257.1	NT	Human carcinoembryonic antigen (CEA) gene, exon 4
7888	18433	26921	4.57	1.8E-01	X57033.1	NT	B.taurus mRNA for potassium channel
8238	17365	26903	2.48	1.8E-01	8394421	NT	Rattus norvegicus Thromboxane receptor (Tbx2r), mRNA
8371	17458		1.24	1.8E-01	10080591	NT	Bovine ephemeral fever virus, complete genome
8433	17489	24014	1.38	1.8E-01	BF348623.1	EST_HUMAN	602019928F1 NCJ CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4155318 5'
8919	17805		2.59	1.8E-01	Q98882	SWISSPROT	DNA TERMINAL PROTEIN (BELLETT PROTEIN) (PTP PROTEIN)
9042	17884		9.36	1.8E-01	R24494.1	EST_HUMAN	YH48h10.f1 Soares placenta N22HP Homo sapiens cDNA clone IMAGE:133027 5'
9084	17806		1.98	1.8E-01	Y11114.1	NT	E.diaper mRNA for hexokinase (hck1)
984	9833	18951	1.41	1.7E-01	BE385184.1	EST_HUMAN	601274804F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3815788 5'
815	10053	19207	2.22	1.7E-01	X53330.1	NT	P.dumerilii histone gene cluster for core histones H2A, H2B, H3 and H4
988	10201		1.93	1.7E-01	P35818	SWISSPROT	NEUROFILAMENT TRIPLET L PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE) (NF-L)
1085	10281	19441	0.82	1.7E-01	AF081810.1	NT	Lymantia dispar nucleopolydnavirus, complete genome
1085	10281	19442	0.82	1.7E-01	AF081810.1	NT	Lymantia dispar nucleopolydnavirus, complete genome
1788	10886	20192	1.31	1.7E-01	AL161573.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 69
1950	11154		3.02	1.7E-01	AF255051.1	NT	Homo sapiens BNIP3H (BNIP3H) gene, complete cds; nuclear gene for mitochondrial product
2812	12052	21173	1.9	1.7E-01	AF000716.1	NT	Vibrio cholerae hypoxanthine phosphoribosyltransferase (hpt) gene, partial cds, hemagglutinin/protease regulatory protein (hapR) gene, complete cds, and YRAL VIBCO gene, partial cds

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2812	12052	21174	1.8	1.7E-01	AF000718.1	NT	Vibrio cholerae hypoxanthine phosphoribosyltransferase (hpt) gene, partial cds, hemagglutinin/protease regulatory protein (hapt) gene, complete cds, and YRAL VIBCO gene, partial cds
2877	12115	21244	1.75	1.7E-01	AA336908.1	EST_HUMAN	EST41651 Endometrial tumor Homo sapiens cDNA 5' end
2854	12182	21326	1.34	1.7E-01	AJ238736.1	NT	Naja naja atra cbc-1 gene, exons 1-3
2854	12182	21327	1.34	1.7E-01	AJ238736.1	NT	Naja naja atra cbc-1 gene, exons 1-3
3088	12305	21427	1.82	1.7E-01	AF081514.1	NT	Taous caradenalis geranylgeranyl diphosphate synthase mRNA, complete cds
3343	12671	21710	0.87	1.7E-01	N55763.1	EST_HUMAN	J2346F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J2346 5'
3423	12848	21778	1.51	1.7E-01	AJ288505.1	NT	Anabaena sp. ORF4 (partial), ORF3, ORF2, ORF1, adpA gene, adpB gene, adpC gene, adpD gene, adpE gene and adpF gene
3605	12826		0.88	1.7E-01	5031886	NT	Homo sapiens LIM domain-containing preferred translocation partner in lipoma (LPP) mRNA
3912	13128	22245	5.85	1.7E-01	AJ295377.1	NT	Homo sapiens derivative 11 breakpoint fragment: partial intron 10 of the ALL-1/MLL/HRX gene fused to intron 5 of the AF-4/FEL gene
4453	12052	21173	3.09	1.7E-01	AF000718.1	NT	Vibrio cholerae hypoxanthine phosphoribosyltransferase (hpt) gene, partial cds, hemagglutinin/protease regulatory protein (hapt) gene, complete cds, and YRAL VIBCO gene, partial cds
4453	12052	21174	3.09	1.7E-01	AF000718.1	NT	Vibrio cholerae hypoxanthine phosphoribosyltransferase (hpt) gene, partial cds, hemagglutinin/protease regulatory protein (hapt) gene, complete cds, and YRAL VIBCO gene, partial cds
4558	13782		1.93	1.7E-01	X52836.1	NT	Schistosoma gregaria alpha repetitive DNA
4773	13962	23084	0.73	1.7E-01	AF217490.1	NT	Homo sapiens fragile 180 cdkc reductase (FOR) gene, exons 8, 9, and partial cds
4857	14045	23138	1.13	1.7E-01	AJ247635.1	EST_HUMAN	qh57c08.x1 Soares fetal liver spleen_1N1FLS_S1 Homo sapiens cDNA clone IMAGE:1848808 3' similar to contains ORF.b1 OFR repetitive element;
5154	14333		1.49	1.7E-01	AF072725.1	NT	Zea mays starch branching enzyme 1b (ae) gene, complete cds
5801	15018	24420	11.05	1.7E-01	H72118.1	EST_HUMAN	ys02g08.s1 Soares fetal liver spleen_1N1FLS Homo sapiens cDNA clone IMAGE:213658 3'
6033	15241		2.08	1.7E-01	AF026552.3	NT	Mesocricetus auratus oroktulin precursor (OVI) gene, complete cds
6205	15386	24828	8.82	1.7E-01	BE734178.1	EST_HUMAN	601689022F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3843984 5'
6551	15747	25207	5.8	1.7E-01	7706428	NT	Homo sapiens cleavage and polyadenylation specificity factor 3, 73kD subunit (CPSF3), mRNA
6551	15747	25208	5.8	1.7E-01	7706428	NT	Homo sapiens cleavage and polyadenylation specificity factor 3, 73kD subunit (CPSF3), mRNA
6889	15894	25344	3.97	1.7E-01	D00384.1	NT	Rat (SHR strain) SX1 gene
6858	16134	25804	11.14	1.7E-01	AP001508.1	NT	Bacillus halodurans genomic DNA, section 2/14
6895	16173	25644	2.61	1.7E-01	U16288.1	NT	Human class IV alcohol dehydrogenase (ADH7) gene, exon 3
7143	16320		3.39	1.7E-01	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
7272	16491	25982	9.77	1.7E-01	BE390835.1	EST_HUMAN	601286547F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3813258 5'

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7384	16588	26086	3.22	1.7E-01	AA814617.1	EST_HUMAN	of43a03.a1 NCI_CGAP_CNS1 Homo sapiens cDNA clone IMAGE:1426924 3'
7673	16872	26375	8.77	1.7E-01	7106300	NT	Mus musculus adenomatosis polyposis coli binding protein Eb1 (Eb1), mRNA
7673	16872	26376	8.77	1.7E-01	7106300	NT	Mus musculus adenomatosis polyposis coli binding protein Eb1 (Eb1), mRNA
8202	17334		1.64	1.7E-01	P15272	SWISSPROT	AMP NUCLEOSIDASE
8270	17618		1.34	1.7E-01	AJ272584.1	NT	Bifidobacterium lactis mitochondrial partial COII gene for cytochrome c oxidase subunit II
8274	17395	26929	3.62	1.7E-01	11418157	NT	Homo sapiens calcium channel, voltage-dependent, alpha 1I subunit (CACNA1I), mRNA
8404	18282		1.48	1.7E-01	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
8701	18124		1.59	1.7E-01	AI824404.1	EST_HUMAN	bc8905.x1 NCI_CGAP_UH1 Homo sapiens cDNA clone IMAGE:2274872 3' similar to gb:M73779 RETINOIC ACID RECEPTOR ALPHA-1 (HUMAN);
9005	17663	23889	9.13	1.7E-01	U01317.1	NT	Human beta globin region on chromosome 11
124	9409	18543	1.74	1.6E-01	AF217532.1	NT	Homo sapiens mevalonate kinase gene, exon 6 and 7
688	11941	19060	1.2	1.6E-01	R31497.1	EST_HUMAN	yh75f12.f1 Soares placenta NB2HP Homo sapiens cDNA clone IMAGE:135589 5'
1509	10722	18694	3.18	1.6E-01	AF298117.1	NT	Homo sapiens homeobox protein OTX2 gene, complete cds
1892	11099	20280	1.84	1.6E-01	P22063	SWISSPROT	AXONIN-1 PRECURSOR (AXONAL GLYCOPROTEIN TAG-1)
1953	11167		1.12	1.6E-01	U10034.1	NT	Craosostrea glabra RNA polymerase II largest subunit mRNA, partial cds
2456	11847	20968	1.25	1.6E-01	AB037729.1	NT	Homo sapiens mRNA for KIAA1308 protein, partial cds
2844	12083	21209	11.43	1.6E-01	AF185588.1	NT	Homo sapiens cytochrome P450 3A4 (CYP3A4) gene, promoter region
2844	12083	21210	11.43	1.6E-01	AF185588.1	NT	Homo sapiens cytochrome P450 3A4 (CYP3A4) gene, promoter region
2988	12206	21342	1.77	1.6E-01	AE001862.1	NT	Deinococcus radiodurans R1 section 1 of 2 of the complete chromosome 2
3611	12832	21952	1.23	1.6E-01	AJ003165.1	NT	Populus trichocarpa cv. Trichobol ABIS gene
3611	12832	21953	1.23	1.6E-01	AJ003165.1	NT	Populus trichocarpa cv. Trichobol ABIS gene
3754	12973	22089	0.73	1.6E-01	AE000862.1	NT	Archaeoglobus fulgidus section 145 of 172 of the complete genome
3977	13181		2.81	1.6E-01	AE004413.1	NT	Vibrio cholerae chromosome II, section 70 of 93 of the complete chromosome
4320	13521	22616	11.43	1.6E-01	AF170880.1	NT	Homo sapiens apelin gene, complete cds
4450	13849		3.4	1.6E-01	AW968601.1	EST_HUMAN	EST380677 MAGE resequences, MAGJ Homo sapiens cDNA
4459	13637		4.67	1.6E-01	6753319	NT	Mus musculus chaperonin subunit 3 (gamma) (Cct3), mRNA
4945	14132	23227	0.79	1.6E-01	P40631	SWISSPROT	MICRONUCLEAR LINKER HISTONE POLYPROTEIN (MIC LH) [CONTAINS: LINKER HISTONE PROTEINS ALPHA, BETA, DELTA AND GAMMA]
4984	14151	23242	1.37	1.6E-01	AA088343.1	EST_HUMAN	z84h09.a1 Strategene colon (#837204) Homo sapiens cDNA clone IMAGE:511361 3' similar to TR:E221855
4988	14176	23265	1.3	1.6E-01	AJ008358.1	NT	E221855 38,855 BP SEGMENT OF CHROMOSOME XIV ;
4988	14175	23266	1.3	1.6E-01	AJ008358.1	NT	Lycopodium obscurum Real fragment 2, satellite region
							Lycopodium obscurum Real fragment 2, satellite region
5451	14677	23838	3	1.6E-01	AW197496.1	EST_HUMAN	xm43f01.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2686569 3' similar to TR:O75984 O75984 HYPOTHETICAL 127.6 KD PROTEIN ;

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5451	14877	23837	3	1.6E-01	AW197498.1	EST_HUMAN	hm43101.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2688089 3' similar to TR:O75084 O75084
5459	14885	24035	2.4	1.6E-01	AF034718.1	NT	HYPOTHETICAL 127.6 KD PROTEIN:
5841	15058	24465	2	1.6E-01	AL161588.2	NT	Rattus norvegicus CCAAT/enhancer binding protein epsilon (cebpε) gene, complete cds
5841	15058	24468	2	1.6E-01	AL161588.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84
6089	14518	23558	4.34	1.6E-01	AW291215.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84
6417	15614	25078	2.81	1.6E-01	L49349.1	NT	UH-B12-egl-b-08-Q-U1.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724418 3'
6979	16157	25629	3.08	1.6E-01	Z49501.1	NT	Gorilla gorilla androgen receptor gene, partial exon
7250	18470	25862	3.11	1.6E-01	AW850893.1	EST_HUMAN	S. cerevisiae chromosome X reading frame ORF YJR001w
7876	16876		8.9	1.6E-01	AF106084.1	NT	IL3-CT0220-111188-028-G01 CT0220 Homo sapiens cDNA
7850	17089	26619	11.94	1.6E-01	6871552	NT	Plasmodium falciparum calcium-dependent protein kinase-3 (cdpk3) gene, complete cds
8286	18288		1.58	1.6E-01	6878468	NT	Mus musculus adaptor-related protein complex AP-1, beta 1 subunit (Aptb1), mRNA
8406	17482	26598	3.89	1.6E-01	AV719585.1	EST_HUMAN	Mus musculus protein kinase, cGMP-dependent, type II (Prkg2), mRNA
8854	18100		8.77	1.6E-01	AB045310.1	NT	AV719585 GLC Homo sapiens cDNA clone GLCEMF07 5'
9028	17877		3.64	1.6E-01	AK024486.1	NT	Cucumis sativus KS mRNA for anti-leukemia synthase, complete cds
9117	17835		2.51	1.6E-01	AF287344.1	NT	Homo sapiens mRNA for FLJ00104 protein, partial cds
9141	17947	23882	1.7	1.6E-01	9506522	NT	Fuchelia hybrid cultivar Qiu 94208 ribosomal protein S10 gene, partial cds; nuclear gene for mitochondrial product
262	9528	18658	1.25	1.5E-01	BE710087.1	EST_HUMAN	Rattus norvegicus chondroitin sulfate proteoglycan 5 (neuroglycan C) (Cspg5), mRNA
252	9528	18659	1.25	1.5E-01	BE710087.1	EST_HUMAN	IL3-HT0619-040700-197-E05 HT0619 Homo sapiens cDNA
584	11940		1.58	1.5E-01	AV711698.1	EST_HUMAN	IL3-HT0619-040700-197-E05 HT0619 Homo sapiens cDNA
792	10032	19181	1.17	1.5E-01	AL163284.2	NT	AV711698 DCA Homo sapiens cDNA clone DCAADH08 5'
1100	10324	19475	0.79	1.5E-01	AJ009735.1	NT	Homo sapiens chromosome 21 segment HS21C084
1105	10329	19479	2.27	1.5E-01	AJ251885.1	NT	Cyprinus carpio mRNA for EGG522 myosin heavy chain, 3'UTR
1121	10345		1.4	1.5E-01	L36125.1	NT	Homo sapiens partial SLC22A2 gene for organic cation transporter (OCT2), exon 1
1224	10442	19597	0.77	1.5E-01	AW195518.1	EST_HUMAN	Rattus norvegicus insulin-responsive glucose transporter (GLUT4) gene, 5' end
1282	10497	19658	3.74	1.5E-01	D26835.1	NT	hm38d11.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2688085 3'
1282	10497	19657	3.74	1.5E-01	D26835.1	NT	Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-15)
1475	10888	19805	1.28	1.5E-01	AF117340.1	NT	Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-15)
1872	11079	20289	1.34	1.5E-01	AW444451.1	EST_HUMAN	Mus musculus MAP kinase kinase 1 (Mek1) mRNA, complete cds
2831	12189	21301	1.28	1.6E-01	AF208088.1	NT	UH-B13-abb-b-09-Q-U1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733841 3'
2831	12189	21302	1.28	1.6E-01	AF208088.1	NT	Murine hepatitis virus strain Penn 97-1, complete genome
3328	12555	21892	4.94	1.5E-01	AA935049.1	EST_HUMAN	Murine hepatitis virus strain Penn 97-1, complete genome
							oc88d05.s1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1571337 3' similar to gb:M11433
							RETINOL-BINDING PROTEIN I, CELLULAR (HUMAN);

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Table 4
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3347	12575	21715	0.77	1.5E-01	Z23104.1	NT	L.stagnalis mRNA for G protein-coupled receptor
3347	12575	21718	0.77	1.5E-01	Z23104.1	NT	L.stagnalis mRNA for G protein-coupled receptor
3738	12958	22073	1.62	1.5E-01	U09984.1	NT	Mus musculus ICR/ Swiss glyceroldehyde 3-phosphate dehydrogenase (Gapd-S) gene, complete cds
3751	12970	22085	0.59	1.5E-01			Homo sapiens pyruvate dehydrogenase kinase, isoenzyme 1 (PDK1), nuclear gene encoding mitochondrial protein, mRNA
3764	12982	22086	0.63	1.5E-01	M97882.1	NT	XYN4; Thermosaccharobacterium; xynA; 4182 base-pairs
3848	13065	22178	2.72	1.5E-01	AW685883.1	EST_HUMAN	h10068.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2881411 3'
4027	13238	22343	0.92	1.5E-01	AW366359.1	EST_HUMAN	RC2-HT0149-101089-012-c08 HT0149 Homo sapiens cDNA
4164	13368	22467	10.65	1.5E-01	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4484	13682	22771	0.77	1.5E-01	BE781253.1	EST_HUMAN	601583988F1 NIH_MGC 7 Homo sapiens cDNA clone IMAGE:3938345 5'
4484	13682	22772	0.77	1.5E-01	BE781253.1	EST_HUMAN	601583988F1 NIH_MGC 7 Homo sapiens cDNA clone IMAGE:3938345 5'
4737	13928	23032	1.55	1.5E-01	BF687665.1	EST_HUMAN	602067192F1 NIH_MGC 57 Homo sapiens cDNA clone IMAGE:4060223 5'
4762	11853	21069	2.25	1.5E-01	BF695381.1	EST_HUMAN	602068326F1 NIH_MGC 81 Homo sapiens cDNA clone IMAGE:4247537 5'
4800	13989	23098	0.97	1.5E-01	BE173786.1	EST_HUMAN	CNM-HT0565-280200-245-b10 HT0565 Homo sapiens cDNA
4800	13989	23097	0.97	1.5E-01	BE173786.1	EST_HUMAN	CNM-HT0565-280200-245-b10 HT0565 Homo sapiens cDNA
5023	14210	23283	1.25	1.5E-01	AL161580.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 60
5304	14538	23540	2.13	1.5E-01	P07998	SWISSPROT	THROMBOSPONDIN 1 PRECURSOR
5351	14581						SEX HORMONE-BINDING GLOBULIN PRECURSOR (SHBG) (SEX STEROID-BINDING PROTEIN)
5461	14687	24038	7.98	1.5E-01	P15196	SWISSPROT	(SBP) (TESTIS-SPECIFIC ANDROGEN-BINDING PROTEIN) (ABP)
5480	14707	24061	4.08	1.5E-01	AW850754.1	EST_HUMAN	IL3-CT0219-160200-064-F10 CT0219 Homo sapiens cDNA
5490	14707	24062	6.6	1.5E-01	U85018.1	NT	Mus musculus transforming growth factor alpha (TGFa) mRNA, complete cds
5655	14878	24267	6.6	1.5E-01	U85018.1	NT	Mus musculus transforming growth factor alpha (TGFa) mRNA, complete cds
5655	14878	24267	1.86	1.5E-01	6753659	NT	Mus musculus DNA methyltransferase 2 (Dnmt2), mRNA
5655	14878	24268	1.86	1.5E-01	6753659	NT	Mus musculus DNA methyltransferase 2 (Dnmt2), mRNA
5683	14803	24268	2.11	1.5E-01	AJ278505.1	NT	Mus musculus genomic fragment, 278 Kb, chromosome 7
5752	14971	24369	27.85	1.5E-01	BE727658.1	EST_HUMAN	601584322F1 NIH_MGC 20 Homo sapiens cDNA clone IMAGE:3833981 5'
5771	14989		1.88	1.5E-01	4506396	NT	Homo sapiens RAD54 (S.cerevisiae)-like (RAD54L) mRNA
5808	15025	24425	1.73	1.5E-01	AF134907.1	NT	Influenza B virus (BN/anchang/480/94) NB protein gene, complete cds; and neuraminidase gene, partial cds
5878	18065	24507	2.13	1.5E-01	AE001039.1	NT	Archaeoglobus fulgidus section 68 of 172 of the complete genome
5882	15109	24520	5.01	1.5E-01	11417236	NT	Homo sapiens chromosome 5 open reading frame 3 (C5ORF3), mRNA
5899	15116	24528	1.64	1.5E-01	P48508	SWISSPROT	GLUTAMATE-CYSTEINE LIGASE REGULATORY SUBUNIT (GAMMA-GLUTAMYL-CYSTEINE SYNTHETASE) (GAMMA-ECS) (GCS LIGHT CHAIN)

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Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5826	15142	24553	2.25	1.5E-01	Q28462	SWISSPROT	AMELOGENIN
5970	15185	24602	1.71	1.5E-01	P30143	SWISSPROT	HYPOTHETICAL 51.7 KD PROTEIN IN THRC-TALB INTERGENIC REGION (ORF8)
6078	14524	23588	5.82	1.5E-01	AW870295.1	EST_HUMAN	EST382378 MAGE resequences, MAGK Homo sapiens cDNA
6172	15354		2.42	1.5E-01	AF210842.1	NT	Homo sapiens HARP (HARP) gene, exon 17 and complete cds
6252	15433	24872	1.72	1.5E-01	AI973157.1	EST_HUMAN	wf52c08.x1 NCI CGAP_U11 Homo sapiens cDNA clone IMAGE:2491310 3'
6332	15513	24859	1.92	1.5E-01	AW500811.1	EST_HUMAN	UI-HF-BNO-alk-4-05-0-UI.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077409 5'
6332	15513	24860	1.92	1.5E-01	AW500811.1	EST_HUMAN	UI-HF-BNO-alk-4-05-0-UI.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077409 5'
6800	15788		19.61	1.5E-01	C16800.1	EST_HUMAN	C16800 Clontech human esorta polyA+ mRNA (#6572) Homo sapiens cDNA clone IMAGE:286868 3' similar to
6808	16003	25463	2.48	1.5E-01	N74228.1	EST_HUMAN	z559e06.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:286868 3' similar to
6828	16023		3.09	1.5E-01	AV754819.1	EST_HUMAN	PIR-S44443 S44443 RAD23 protein homolog2 - human ;
6896	16601	25067	7.82	1.5E-01	U00455.1	NT	AV754819 TP Homo sapiens cDNA clone TPAAHB12 5'
7044	16221	25686	6.88	1.5E-01	AF007570.1	NT	Acipenser transmontano vitellogenin mRNA, partial cds
7044	16221	25687	6.88	1.5E-01	AF007570.1	NT	Aplysia californica carboxypeptidase D mRNA, complete cds
7135	16312	25793	4.58	1.5E-01	X98852.1	NT	P. lentusculum mRNA for Integrin beta subunit
7168	16346	25826	4.07	1.5E-01	AI814046.1	EST_HUMAN	wk53h12.x1 NCI CGAP_P122 Homo sapiens cDNA clone IMAGE:2416175 3' similar to gb:M27508 BETA
7168	16346	25827	4.07	1.5E-01	AI814046.1	EST_HUMAN	GALACTOSIDASE-RELATED PROTEIN PRECURSOR (HUMAN);
7401	16814	26103	6.47	1.5E-01	AL163280.2	NT	wk53h12.x1 NCI CGAP_P122 Homo sapiens cDNA clone IMAGE:2416175 3' similar to gb:M27508 BETA
7401	16814	26104	6.47	1.5E-01	AL163280.2	NT	GALACTOSIDASE-RELATED PROTEIN PRECURSOR (HUMAN);
7646	16763		1.84	1.5E-01	AB042975.1	NT	Homo sapiens chromosome 21 segment HS21C080
7646	16763		1.84	1.5E-01	AB042975.1	NT	Homo sapiens chromosome 21 segment HS21C080
7646	16763		1.84	1.5E-01	AB042975.1	NT	Sua scrofa CYP51 gene for lanosterol 14 alpha-demethylase, exon 1
7942	16842	26340	1.8	1.5E-01	AW841915.1	EST_HUMAN	IL5-CN0024-030300-025-D04 CN0024 Homo sapiens cDNA
7725	15433	24872	2.9	1.5E-01	AI973157.1	EST_HUMAN	wf52c08.x1 NCI CGAP_U11 Homo sapiens cDNA clone IMAGE:2491310 3'
8363	18157		31.79	1.5E-01	BF700582.1	EST_HUMAN	602128753F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:2491310 3'
8755	17696		1.5	1.5E-01	AF030358.2	NT	Rattus norvegicus chemokine CX3C mRNA, complete cds
8758	17698		1.22	1.5E-01	AJ236332.1	NT	Mus musculus mRNA for death inducer-inhibitor-1 (Dio-1)
8819	18177		6.75	1.5E-01	R83077.1	EST_HUMAN	yp87e04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:194430 5'
8918	18200		2.3	1.5E-01	AV741272.1	EST_HUMAN	AV741272 CB Homo sapiens cDNA clone CBDAGD04 5'
9027	18103	23808	6.2	1.5E-01	AL139074.2	NT	Campylobacter jejuni NC1C1168 complete genome; segment 1/8
9251	18020	23851	3.72	1.5E-01	AJ278242.1	NT	Sus scrofa mRNA for sodium iodide symporter
304	9577		1.45	1.4E-01	AF008683.1	NT	Homo sapiens T cell receptor beta locus, TCRBV85P to TCRBV21S2A2 region
920	10155		3.95	1.4E-01	D78638.1	NT	Xenopus laevis mRNA for DNA (cytosine-5)-methyltransferase, complete cds
1268	10481		2.73	1.4E-01	T81864.1	EST_HUMAN	y554c01.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:112032 3'

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1720	10332		1.43	1.4E-01	6878980	NT	Mus musculus growth differentiation factor 5 (Gdf5), mRNA
1723	10335	20118	1.65	1.4E-01	AE001710.1	NT	Thermotoga maritima section 22 of 138 of the complete genome
1869	11078		0.82	1.4E-01	AW135741.1	EST_HUMAN	UI-H-B11-act-e-09-Q-U1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2714009 3'
1854	11158		10.51	1.4E-01	AA720815.1	EST_HUMAN	ny72007.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1283821 3'
2745	11824	21139	4.09	1.4E-01	AB33498.1	EST_HUMAN	wm74d01.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2441665 3'
4155	13361	22481	11.2	1.4E-01	AB99094.1	EST_HUMAN	b56c02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2273570 3'
4155	13361	22482	11.2	1.4E-01	AB99094.1	EST_HUMAN	b56c02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2273570 3'
4222	13426	22518	3.52	1.4E-01	AE001710.1	NT	Thermotoga maritima section 22 of 138 of the complete genome
4680	13973	22873	0.81	1.4E-01	6453881	NT	Homo sapiens phosphodiesterase 4A, cAMP-specific (dunce (Drosophila)-homolog phosphodiesterase E2) (PDE4A), mRNA
5334	14565	23639	4.95	1.4E-01	T80877.1	EST_HUMAN	ye15c11.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:117812 3'
5352	14582	23657	4.24	1.4E-01	AB004558.1	NT	Candida tropicalis DNA for mitochondrial NADP-linked isocitrate dehydrogenase, complete cds
5352	14582	23658	4.24	1.4E-01	AB004558.1	NT	Candida tropicalis DNA for mitochondrial NADP-linked isocitrate dehydrogenase, complete cds
5787	15004	24408	2.98	1.4E-01	BE326891.1	EST_HUMAN	hr67c02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3133538 3'
5885	15083	24486	4.8	1.4E-01	AU117147.1	EST_HUMAN	AU117147 HEMBA1 Homo sapiens cDNA clone HEMBA1000769 5'
5885	15083	24487	4.8	1.4E-01	AU117147.1	EST_HUMAN	AU117147 HEMBA1 Homo sapiens cDNA clone HEMBA1000769 5'
5811	15128	24537	3.7	1.4E-01	AW082798.1	EST_HUMAN	xb71d12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2581751 3'
5923	15140		1.85	1.4E-01	BE266536.1	EST_HUMAN	601183523F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3537581 5'
5835	15151	24661	2.2	1.4E-01	BF378533.1	EST_HUMAN	QV1-JM0036-080300-103-009 UM0038 Homo sapiens cDNA
6250	15431		1.76	1.4E-01	AW015373.1	EST_HUMAN	UI-H-B10-eat-e-09-Q-U1.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2710289 3'
8749	15944	25404	7.58	1.4E-01	AA307073.1	EST_HUMAN	EST178192 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
6825	16019	26484	6.29	1.4E-01	BF310959.1	EST_HUMAN	601895465F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124824 5'
6867	16057	25524	2.65	1.4E-01	Y10186.1	NT	Homo sapiens PHEX gene
6867	16057	25525	2.65	1.4E-01	Y10186.1	NT	Homo sapiens PHEX gene
7297	16518		1.91	1.4E-01	AA811480.1	EST_HUMAN	oa89a03.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1320384 3'
7419	16631	26123	3.5	1.4E-01	R53400.1	EST_HUMAN	Y70c05.r1 Soares breast 2NBHst Homo sapiens cDNA clone IMAGE:154088 5'
7840	17032	26547	2.07	1.4E-01	X66082.1	NT	C.perfringens ORF for putative membrane transport protein
7874	15431		1.74	1.4E-01	AW015373.1	EST_HUMAN	UI-H-B10-eat-e-09-Q-U1.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2710289 3'
8005	16440	25928	2.41	1.4E-01	U28760.1	NT	Borrelia burgdorferi glyceraldehyde-3-phosphate dehydrogenase (GAPDH), phosphoglycerate kinase (PGK),
8057	17192		1.63	1.4E-01	X52102.1	NT	triosephosphate isomerase (TPI) genes, complete cds
8842	18128	23814	1.28	1.4E-01	AB000890.1	NT	M.musculus p10K gene for 18 kDa protein
8894	17682	23848	2.39	1.4E-01	X74773.1	NT	Ephydrata fluviatilis mRNA for aldolase, partial cds
8708	17670		2.27	1.4E-01	11988117	NT	P.salina plastid gene secY
							Rattus norvegicus desmin (Des), mRNA

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Table 4
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8753	18355		1.85	1.4E-01	BE513802.1	EST_HUMAN	601315638F1 NIH_MGC 8 Homo sapiens cDNA clone IMAGE:3834328 5'
8849	17758		3.74	1.4E-01	AF083221.1	NT	Fugu rubripes putative neurotransmitter receptors, YDR140w homolog, and glycylamide ribonucleotide transformylase (GART) genes, complete cds
8881	17764		2.08	1.4E-01	D84004.1	NT	Synechocystis sp. PCC6803 complete genome, 23127, 2868787-3002865
8943	18374		3.7	1.4E-01	P10447	SWISSPROT	TYROSINE-PROTEIN KINASE TRANSFORMING PROTEIN ABL
9196	18178		3.78	1.4E-01	D82983.1	NT	Mus musculus mRNA for prolidase, complete cds
9245	18018		1.74	1.4E-01	AW377988.1	EST_HUMAN	MRO-HT0208-221289-204-c08 HT0208 Homo sapiens cDNA
327	9598	18727	5.19	1.3E-01	4758467	NT	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA
327	9598	18728	5.19	1.3E-01	4758467	NT	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA
535	9788	18909	1.81	1.3E-01	AB013139.1	NT	Homo sapiens gene for NBS1, complete cds
842	9888	19013	1.32	1.3E-01	AJ277808.1	NT	Human calicivirus HUNLV/Girlington/83/UK RNA for capsid protein (ORF2), strain HUNLV/Girlington/83/UK
842	9888	19014	1.32	1.3E-01	AJ277808.1	NT	Human calicivirus HUNLV/Girlington/83/UK RNA for capsid protein (ORF2), strain HUNLV/Girlington/83/UK
884	10080	18252	0.8	1.3E-01	X53330.1	NT	P. diemerilli histone gene cluster for core histones H2A, H2B, H3 and H4
904	10139	19301	1.77	1.3E-01	AF138518.1	NT	Rattus norvegicus A-kinase anchor protein mRNA, complete cds
1034	10280	19410	1.42	1.3E-01	AL117078.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
1135	10358		2.11	1.3E-01	AL115285.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
1223	10441	19596	1.48	1.3E-01	AV712487.1	EST_HUMAN	AV712487 DCA Homo sapiens cDNA clone DCAAFF05 5'
1445	10558		0.93	1.3E-01	AF148277.1	NT	Homo sapiens adapter protein CMS mRNA, complete cds
1825	11033	20228	7.72	1.3E-01	6880957	NT	Mus musculus procollagen, type XI, alpha 1 (Col11a1), mRNA
1828	11133	20328	2.16	1.3E-01	AL117078.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
2138	11334		0.97	1.3E-01	AJ243578.1	NT	Rhodospirillum rubrum acidothiobacillus pucB5, pucA5, pucB6, pucA6, pucB7, pucA7, pucB8, pucA8 and pucC genes and ORF151
2254	11449		0.97	1.3E-01	AW812104.1	EST_HUMAN	RC4-ST0173-191098-032-d12 ST0173 Homo sapiens cDNA
2347	11540		2.94	1.3E-01	AE001016.1	NT	Archaeoglobus fulgidus section 91 of 172 of the complete genome
2547	11735	20852	2.11	1.3E-01	M88918.1	NT	Cerastium auriculatum keratin type I mRNA, complete cds
3034	12270	21397	0.59	1.3E-01	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
3332	12581	21699	0.93	1.3E-01	AF198778.1	NT	Homo sapiens transcription factor IGEM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synapophycin genes, complete cds; and L-type calcium channel a2
3428	12653	21783	1.07	1.3E-01	M21572.1	NT	Bovine branched chain alpha-keto acid dihydriolipoyl transacylase mRNA, complete cds
3702	12922	22040	0.81	1.3E-01	AP000001.1	NT	Pyrococcus horikoshii OT3 genome DNA, 1-287000 nt. position (177)
3702	12922	22041	0.81	1.3E-01	AP000001.1	NT	Pyrococcus horikoshii OT3 genome DNA, 1-287000 nt. position (177)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3709	12829	22047	0.63	1.3E-01	AB032159.1	NT	Homo sapiens DD4 gene for dihydrolid dehydrogenase 4 [AKR 1C4], exon 2
3763	12822	22040	0.66	1.3E-01	AF000001.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt position (1/7)
3763	12822	22041	0.66	1.3E-01	AF000001.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt position (1/7)
3769	13007	22122	0.89	1.3E-01	6878940	NT	Rattus norvegicus Fibrinogen, gamma polypeptide (Fgg), mRNA
3968	13181		1.52	1.3E-01	AL161581.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 77
4028	9888	19013	0.9	1.3E-01	AJ277608.1	NT	Human calicivirus HUNLV/Girlington/83/UK RNA for capsid protein (ORF2), strain HUNLV/Girlington/83/UK
4028	9888	19014	0.9	1.3E-01	AJ277608.1	NT	Human calicivirus HUNLV/Girlington/83/UK RNA for capsid protein (ORF2), strain HUNLV/Girlington/83/UK
4120	13326		1.03	1.3E-01	AF020713.1	NT	Bacteriophage SPBc2 complete genome
4140	13346		3.88	1.3E-01	AW364341.1	EST_HUMAN	QV3-DT0018-081288-038-a03 DT0018 Homo sapiens cDNA
4148	13364	22466	2.2	1.3E-01	AF026805.1	NT	Schistosoma mansoni fructose biphosphate aldolase mRNA, complete cds
4167	13371	22470	21.57	1.3E-01	AW273741.1	EST_HUMAN	x23710.x1 Soares NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:2813985 3'
4275	13478	22575	0.94	1.3E-01	AV752278.1	EST_HUMAN	AV752279 NP4 Homo sapiens cDNA clone NPDAZE02 5'
4275	13478	22578	0.94	1.3E-01	AV752278.1	EST_HUMAN	AV752279 NP4 Homo sapiens cDNA clone NPDAZE02 5'
4304	13505		1.33	1.3E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
4475	13673	22763	0.68	1.3E-01	M21572.1	NT	Bovine branched chain alpha-keto acid dihydrolipoyl transacylase mRNA, complete cds
4531	13727	22824	2.2	1.3E-01	BE272339.1	EST_HUMAN	601126086F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2890063 5'
6141	14320	23412	1.04	1.3E-01	AJ432531.1	EST_HUMAN	th38c10.x1 NC1_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2120562 3'
6281	14432		1.03	1.3E-01	D82818.1	NT	Gallus gallus domesticus mitochondrial DNA, D-loop region, strain:Ayem Kakok Balenggek
6376	14604	23713	1.94	1.3E-01	AW804417.1	EST_HUMAN	QV0-UM0083-100400-168-a08 UM0083 Homo sapiens cDNA
5966	15084	24468	14.81	1.3E-01	AB031328.1	NT	Schizosaccharomyces pombe gene for Alp41, complete cds
5909	15126	24535	2.17	1.3E-01	X89891.1	NT	C.jacchus intron 4 of visual pigment gene (red allele)
6191	15373		1.84	1.3E-01	H49684.1	EST_HUMAN	y33402.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:207075 5'
6452	15848	26117	2.19	1.3E-01	11423284	NT	Homo sapiens PRO0811 protein (PRO0811), mRNA
6578	15775		4.84	1.3E-01	Z74102.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL054c
6594	15790		3.41	1.3E-01	8923918	NT	Homo sapiens core histone macroH2A2.2 (MACROH2A2), mRNA
7227	16448		3.33	1.3E-01	BF330999.1	EST_HUMAN	MR4-BT0358-130700-010-h08 BT0358 Homo sapiens cDNA
7442	16650	26142	1.64	1.3E-01	H01893.1	EST_HUMAN	y32809.r1 Soares placenta Nb2IP Homo sapiens cDNA clone IMAGE:150449 5'
7661	16861	26363	1.67	1.3E-01	AF119117.1	NT	Homo sapiens dopamine transporter (SLC6A3) gene, complete cds
7803	16966		8.14	1.3E-01	8871745	NT	Mus musculus cofilin 2, muscle (Cif2), mRNA
8123	17267	26789	4.07	1.3E-01	BE279449.1	EST_HUMAN	601158052F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3504804 5'
8531	17557	23989	1.31	1.3E-01	BE018346.1	EST_HUMAN	601482741F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3966003 5'
8678	17648		3.75	1.3E-01	AJ242780.1	NT	Gallus gallus scyl1 gene for lymphotactin, exons 1-3

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8082	17891		2.08	1.3E-01	AB028829.1	NT	Ephratalia fluvialis mRNA for eALK-8, complete cds
8090	17809		1.63	1.3E-01	AW001114.1	EST_HUMAN	wu24009.x1 Soares_Dieckgraebe_colon_NHCD Homo sapiens cDNA clone IMAGE:2520977 3' similar to TR:O60287 O60287 KIAA0539 PROTEIN. ;
388	8882	18819	10.48	1.2E-01	AI421744.1	EST_HUMAN	U39402.x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2088539 3' similar to gb:U05780_mna1 ANNEXIN V (HUMAN);
430	9285		1.32	1.2E-01	U68912.1	NT	Dictyostelium discoideum ORF DG1016 gene, partial cds
554	8804		2.81	1.2E-01	AF039442.1	NT	Homo sapiens colon cancer antigen NY-CO-45 mRNA, partial cds
1383	10597	19763	2.4	1.2E-01	AU149148.1	EST_HUMAN	AU149148 NT2RM4 Homo sapiens cDNA clone NT2RM4001691 3'
1383	10597	19764	2.4	1.2E-01	AU149148.1	EST_HUMAN	AU149148 NT2RM4 Homo sapiens cDNA clone NT2RM4001691 3'
1390	10604		3.4	1.2E-01	AV735249.1	EST_HUMAN	AV735249 cda Homo sapiens cDNA clone cdaAJB11 5'
1608	10821	19897	5.44	1.2E-01	Q14834	SWISSPROT	NUCLEAR FACTOR OF ACTIVATED T-CELLS, CYTOPLASMIC 4 (T CELL TRANSCRIPTION FACTOR NFAT3) (NF-ATC4) (NF-AT3)
1628	10841	20018	2.84	1.2E-01	AI285402.1	EST_HUMAN	q168709.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:1980553 3'
1739	10851		20.58	1.2E-01	X89211.1	NT	Hi.sapiens DNA for endogenous retroviral like element
1888	11093		2.95	1.2E-01	AW449388.1	EST_HUMAN	U1-H-B13-akt-e-10-0-U1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2734554 3'
2148	11346	20563	2.6	1.2E-01	BF248480.1	EST_HUMAN	601821567F1 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:4048224 5'
2551	11739	20856	1.17	1.2E-01	AW986558.1	EST_HUMAN	QV3-BN0048-220300-129-110 BN0048 Homo sapiens cDNA
2785	12035	21159	1.4	1.2E-01	U18018.1	NT	Human E1A enhancer binding protein (E1A-F) mRNA, partial cds
2854	12092	21222	2.39	1.2E-01	AI720470.1	EST_HUMAN	es80cd09.x1 Barstead cdon HPLRB7 Homo sapiens cDNA clone IMAGE:2335024 3' similar to gb:U05095 80S RIBOSOMAL PROTEIN L30 (HUMAN);
2885	12123	21289	3.54	1.2E-01	M16364.1	NT	Human creatine kinase-B mRNA, complete cds
2884	12202	21337	0.81	1.2E-01	X58882.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3188	12431	21567	2.17	1.2E-01	AW370688.1	EST_HUMAN	QV1-BT0259-261099-021-c05 BT0259 Homo sapiens cDNA
3224	12458		1.01	1.2E-01	U67600.1	NT	Methanococcus jannaschii section 142 of 160 of the complete genome
3329	12558	21898	1.01	1.2E-01	AW503374.1	EST_HUMAN	U1-HF-BNO-akw-a-10-0-U1.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078427 5'
3454	12678		0.71	1.2E-01	Z89118.1	NT	Bacillus subtilis complete genome (section 15 of 21); from 2785131 to 3013540
3484	12718	21854	0.8	1.2E-01	X56882.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3484	12718	21855	0.8	1.2E-01	X56882.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3584	12879		0.78	1.2E-01	Z89118.1	NT	Bacillus subtilis complete genome (section 15 of 21); from 2785131 to 3013540
4163	13367	22465	2.35	1.2E-01	Z54255.1	NT	P.clarkii mRNA; repeat region (ID 2MRT7)
4163	13367	22468	2.35	1.2E-01	Z54255.1	NT	P.clarkii mRNA; repeat region (ID 2MRT7)
4300	13501	22687	0.81	1.2E-01	M15881.1	NT	Chicken neural cell-adhesion molecule (N-CAM) gene, exon 19
4843	14130	23225	15.91	1.2E-01	AF134904.1	NT	Schistosoma gregaria semaphorin 2a mRNA, complete cds
5078	14258	23342	2.21	1.2E-01	BE173168.1	EST_HUMAN	MRO-HT0559-240400-016-c09 HT0559 Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5078	14258	23343	2.21	1.2E-01	BE173168.1	EST_HUMAN	MRO-HT0558-240400-018-c09 HT0559 Homo sapiens cDNA
5284	14455	23524	0.73	1.2E-01	AW892582.1	EST_HUMAN	CM3-NIN004-100300-111-408 NN0004 Homo sapiens cDNA
5337	14568	23642	2.63	1.2E-01	W33035.1	EST_HUMAN	zc08d02.r1 Scarsa_papillary_tumor_NbHPA Homo sapiens cDNA IMAGE:321688 5'
5380	14609	23721	3.16	1.2E-01	Z88266.1	NT	Homo sapiens gene encoding plakophilin (exons 1-13)
5763	14972	24370	2.02	1.2E-01	BE620945.1	EST_HUMAN	601493518F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3885613 5'
5788	15005	24409	2.3	1.2E-01	AW845275.1	EST_HUMAN	IL0-C10031-221089-113-404 CT0031 Homo sapiens cDNA
6448	15843	25110	4.78	1.2E-01	AI913753.1	EST_HUMAN	wc38q03.x1 NCI_CGAP_Cc3 Homo sapiens cDNA clone IMAGE:2328804 3' similar to SW:GST2_HUMAN
6599	15785		4.99	1.2E-01	AW083852.1	EST_HUMAN	Q88735 MICROSOMAL GLUTATHIONE S-TRANSFERASE II;
6608	15802		3.94	1.2E-01	AF053772.1	NT	Staphylococcus aureus plasmid pSK23 putative recombinase Sin (sin) gene, partial cds; and transcriptional
6877	15872		2.87	1.2E-01	U32714.1	NT	regulator QacR (qacR) and multidrug efflux protein QacB (qacB) genes, complete cds
6848	16106	25573	4.01	1.2E-01	X77961.1	NT	Haemophilus influenzae Rd section 20 of 163 of the complete genome
7075	16252	25725	2.29	1.2E-01	AV710857.1	EST_HUMAN	S.cerevisiae HXT5 gene
7463	16671		3.81	1.2E-01	D26184.1	NT	AV710857 Cu Homo sapiens cDNA clone CuAAKE08 5'
7833	16834		3.64	1.2E-01	BE862324.2	EST_HUMAN	Yeast MPT5 gene for suppressor protein, complete cds
7707	16808		1.79	1.2E-01	BF314481.1	EST_HUMAN	601655578R1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3846283 3'
7807	17000	28512	2.82	1.2E-01	AF190493.1	NT	601800783F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130103 5'
8041	17177		1.98	1.2E-01	M95109.1	NT	Homo sapiens dynein intermediate chain DNAL1 (DNAL1) gene, exon 17
8263	17405		2.6	1.2E-01	AV658033.1	EST_HUMAN	Rabbit glycogen-associated protein phosphatase regulatory subunit (RG1) mRNA, complete cds
8659	17636		2.36	1.2E-01	AJ271738.1	NT	AV658033 GLC Homo sapiens cDNA clone GLCFB12 3'
8741	18317	23594	3.89	1.2E-01	Q04912	SWISSPROT	Homo sapiens Xq pseudautosomal region; segment 2/2
8853	17758		1.79	1.2E-01	AF188892.1	NT	MACROPHAGE-STIMULATING PROTEIN RECEPTOR PRECURSOR (MSP RECEPTOR) (P186-RON)
8855	9804		8.49	1.2E-01	AF039442.1	NT	(CDW138) (CD138 ANTIGEN)
8969	17839		2.13	1.2E-01	X53981.1	NT	Drosophila melanogaster strain Oregon R potential RNA-binding protein gene, complete cds, and syntactin
9043	18328	23601	1.55	1.2E-01	BE061418.1	EST_HUMAN	Homo sapiens colon cancer antigen NY-CO-45 mRNA, partial cds
9088	17893	23900	8.08	1.2E-01	AI295903.1	EST_HUMAN	R.novogigicus NF88 gene for 68kDa neurofilament
9088	17907		2.44	1.2E-01	L10187.1	NT	QV4-BT0234-111199-031-g10 BT0234 Homo sapiens cDNA
9082	18249		5.45	1.2E-01	O88433	SWISSPROT	qz20g05.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1899840 3'
9120	17836	23878	1.47	1.2E-01	AE004428.1	NT	Xenopus laevis integrin alpha 3 subunit mRNA, partial cds
							CYCLIN T
							Vibrio cholerae chromosome II, section 85 of 93 of the complete chromosome

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Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9274	18038		1.35	1.2E-01	BF314481.1	EST_HUMAN	601800763F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130103 5'
571	9821	18942	1.05	1.1E-01	AI561003.1	EST_HUMAN	bt18089.x1 NCI_CGAP_Bim25 Homo sapiens cDNA clone IMAGE:2167883 3'
621	9868	18987	2.28	1.1E-01	AA569008.1	EST_HUMAN	nm08g11.s1 NCI_CGAP_Cot10 Homo sapiens cDNA clone IMAGE:4286771 5'
1061	10287	19438	1.48	1.1E-01	BF697308.1	EST_HUMAN	HEME OXYGENASE 1 (HUMAN);
1063	10317		1.63	1.1E-01	AL161560.2	NT	602128847F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:1059620 3' similar to gb:X06985_ma1
1187	11887	18540	3.89	1.1E-01	AW672188.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 60
1256	10472	18635	3.8	1.1E-01	D64004.1	NT	EST384142 IMAGE resequences, MAGL Homo sapiens cDNA
1508	10721	18893	2.15	1.1E-01	AU140363.1	EST_HUMAN	Synechocystis sp. PCC6803 complete genome, 23/27, 2868787-3002865
2280	11475		2.2	1.1E-01	8755215	NT	AU140363 PLACE2 Homo sapiens cDNA clone IMAGE:2000403 5'
2503	11853		1.9	1.1E-01	6878876	NT	Mus musculus pre T-cell antigen receptor alpha (Pitra), mRNA
2807	12047	21168	1.04	1.1E-01	S62418.1	NT	Rattus norvegicus Procollagen II alpha 1 (Col2a1), mRNA
2899	12235	21365	0.81	1.1E-01	F03265.1	EST_HUMAN	Interleukin-12 p35 subunit [Homo sapiens, Genomic, 700 nt, segment 4 of 5]
3315	12845		1.76	1.1E-01	6763231	NT	HSC1RF022 normalized infant brain cDNA Homo sapiens cDNA clone c-1f02 3'
3398	12026	21757	2.28	1.1E-01	BE393186.1	EST_HUMAN	Mus musculus calcium channel, voltage-dependent, T type, alpha 1G subunit (Ca _v 1g), mRNA
3429	12654	21784	1.56	1.1E-01	X62135.1	NT	601308878F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3927068 5'
3490	12691	21828	0.7	1.1E-01	R68946.1	EST_HUMAN	C. reinhardtii nuclear gene on linkage group XIX
3559	12782	21911	0.94	1.1E-01	Y07695.1	NT	yq92g08.s1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:200414 3' similar to contains
3681	12802		0.76	1.1E-01	P67384	SWISSPROT	Alu repetitive element
3688	12910	22028	1.91	1.1E-01	X52708.1	NT	A. immsenus gene for transposase
4088	13267	22393	1.04	1.1E-01	AW818412.1	EST_HUMAN	ANNEXIN XI (CALCYCLIN-ASSOCIATED ANNEXIN 50) (CAP-50)
4088	13297	22394	1.04	1.1E-01	AW818412.1	EST_HUMAN	G.gallus gene encoding non-histone chromosomal protein HMG-14b, exons 4 and 5
							MR3-ST0280-280100-025-g07 ST0280 Homo sapiens cDNA
							MR3-ST0280-280100-025-g07 ST0280 Homo sapiens cDNA
							Mus musculus major histocompatibility locus class III region: butyrophilin-like protein gene, partial cds;
4095	13303		0.88	1.1E-01	AF030001.1	NT	Notch4, PBX2, RAGE, lysophosphatidic acid acyl transferase-alpha, palmitoyl-protein thioesterase 2 (PPT2),
4240	13443		10.22	1.1E-01	AF167068.1	NT	CREB-RP, and tenascin X (TNX) genes, complete>
4272	13475	22572	0.63	1.1E-01	AW802058.1	EST_HUMAN	Drosophila melanogaster kirschstein protein (klar) mRNA, complete cds
							IL5-UM0070-020500-068-a08 UM0070 Homo sapiens cDNA
							Tape-1=Integral membrane protein TAPA-1 [Homo sapiens, B cell lymphoma line 38C13, Genomic, 1973 nt, segment 1 of 7]
4641	13835	22624	1.09	1.1E-01	S44957.1	NT	A. immsenus gene for transposase
4849	14038	23131	1.24	1.1E-01	Y07695.1	NT	A. immsenus gene for transposase
							Mus musculus major histocompatibility locus class III region: butyrophilin-like protein gene, partial cds;
5045	13303		0.87	1.1E-01	AF030001.1	NT	Notch4, PBX2, RAGE, lysophosphatidic acid acyl transferase-alpha, palmitoyl-protein thioesterase 2 (PPT2),
							CREB-RP, and tenascin X (TNX) genes, complete>

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5224	14398		0.82	1.1E-01	8923317	NT	Homo sapiens hypothetical protein FLJ20342 (FLJ20342), mRNA
5396	14810	24184	1.79	1.1E-01	X6851.1	NT	S. pombe sbf8 gene encoding protein kinase
5601	14825	24201	4.71	1.1E-01	M88533.1	NT	Providencia rettgeri penicillin G amidase gene
5698	14908	24269	1.72	1.1E-01	BE769152.1	EST_HUMAN	PM3-FT0024-130800-004-412 FT0024 Homo sapiens cDNA
5698	14918	24310	7.89	1.1E-01	AW853699.1	EST_HUMAN	RC3-CT0254-280989-011-a01 CT0254 Homo sapiens cDNA
5837	15153	24584	3.86	1.1E-01	O89635	SWISSPROT	ACETYL-COENZYME A SYNTHETASE (ACETATE-COA LIGASE) (ACYL-ACTIVATING ENZYME)
5968	15181		2.87	1.1E-01	AF032922.1	NT	Homo sapiens syntaxin 4 binding protein UNC-18c (UNC-18c) mRNA, complete cds
5965	15278	24708	2.49	1.1E-01	11432372	NT	Homo sapiens phosphatidylinositol glycan, class B (PIGB), mRNA
6305	15488	24830	7.65	1.1E-01	BF884628.1	EST_HUMAN	602140976F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4302019 5'
6305	15488	24831	7.65	1.1E-01	BF884628.1	EST_HUMAN	602140976F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4302019 5'
6361	15541	24936	1.77	1.1E-01	P41067	SWISSPROT	TRAB PROTEIN
6375	15555	25012	2.92	1.1E-01	AA798784.1	EST_HUMAN	ah31b06.s1 Soares parathyroid tumor NbrHPA Homo sapiens cDNA clone 1240403 3' similar to gb:J03483
6561	15777	25237	3.04	1.1E-01	AL134349.1	EST_HUMAN	CHROMOGRAIN A PRECURSOR (HUMAN);
6760	15975	25432	3.04	1.1E-01	AA192153.1	EST_HUMAN	DKFZp547P184_r1 547 (synonym: hbrt) Homo sapiens cDNA clone DKFZp547P184 5'
6760	15975	25433	3.04	1.1E-01	AA192153.1	EST_HUMAN	zp83b12.r1 Stratagene muscle 837209 Homo sapiens cDNA clone IMAGE:627743 5'
6821	16015	25480	4.18	1.1E-01	T72675.1	EST_HUMAN	zp83b12.r1 Stratagene muscle 837209 Homo sapiens cDNA clone IMAGE:627743 5'
6910	16098		3.01	1.1E-01	BF085149.1	EST_HUMAN	yd18H03.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:108725 3' similar to gb:M81181 SODIUMPOTASSIUM-TRANSPORTING ATPASE BETA-2 (HUMAN);
7383	12235	21365	2.34	1.1E-01	F03265.1	EST_HUMAN	MF2-GN0027-040800-005-a08 GN0027 Homo sapiens cDNA
7486	16703		3.49	1.1E-01	AF169032.1	NT	HSC1RF022 normalized infant brain cDNA Homo sapiens cDNA clone c-1h02 3'
7614	16817	26313	3.37	1.1E-01	R23708.1	EST_HUMAN	Carassius auratus activin beta A precursor, mRNA, complete cds
7620	16823	26319	1.88	1.1E-01	6981351	NT	yk35f12.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:131759 5' similar to contains Alu repetitive element; contains TAR1 repetitive element;
7638	14788	24157	1.98	1.1E-01	AL110985.1	NT	Rattus norvegicus Phosphofructokinase, liver, B-type (Pfkfb), mRNA
7738	16933	26441	1.83	1.1E-01	X70058.1	NT	Bovis chinea strain T4 cDNA library under conditions of nitrogen deprivation
7780	16956	26464	3.14	1.1E-01	Z11910.1	NT	M.musculus cytokine gene
7780	16956	26465	3.14	1.1E-01	Z11910.1	NT	Z.mobilis tgf and lig genes encoding RNA guanine transglycosylase and DNA ligase
7854	17044	26561	3.45	1.1E-01	P17437	SWISSPROT	Z.mobilis tgf and lig genes encoding RNA guanine transglycosylase and DNA ligase
8511	17547		2.88	1.1E-01	BE767023.1	EST_HUMAN	SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN)
8772	18117		2.2	1.1E-01	BE767023.1	EST_HUMAN	RC2-NT0112-120600-014-r03 NT0112 Homo sapiens cDNA
9212	17983	23865	5.88	1.1E-01	BF239753.1	EST_HUMAN	RC2-NT0112-120600-014-r03 NT0112 Homo sapiens cDNA
9283	18287		1.42	1.1E-01	Y08172.1	NT	601680551R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3850804 3'
1209	10428		2.84	1.0E-01	O82855	SWISSPROT	601680551R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4134085 5'
							R.norvegicus mRNA for 2-oxopropionyl-CoA epimerase
							DEOXYRIBONUCLEASE II PRECURSOR (DNASE II) (ACID DNASE) (LYSOSOMAL DNASE II)

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1279	10484	18653	1.87	1.0E-01	AI085499.1	EST_HUMAN	ws08401.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2498577 3' similar to contains MER7.13 MER7 repetitive element;
1398	10810	19774	1.78	1.0E-01	AL181504.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 18
3487	12711	21847	1.08	1.0E-01	BF033991.1	EST_HUMAN	601466301F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3859849 5'
3700	12820	22038	1.03	1.0E-01	BF239818.1	EST_HUMAN	601908489F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4134071 5'
3850	13148	22283	2.78	1.0E-01	BF388703.1	EST_HUMAN	QV2-NT0048-180800-318-e05 NT0048 Homo sapiens cDNA
4401	13801	22701	1.86	1.0E-01	AE002265.2	NT	Chlamydomonas reinhardtii AR309, section 91 of 94 of the complete genome
4552	13747		0.89	1.0E-01	AI782348.1	EST_HUMAN	en32c04.y5 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1700358 5'
4723	13814	23015	1.51	1.0E-01	U50450.1	NT	Drosophila melanogaster tyrosine kinase p45 lscform (fer) mRNA, complete cds
4942	14129	23224	2.15	1.0E-01	AW952344.1	EST_HUMAN	EST384414 MAGE resequencing, MAGB Homo sapiens cDNA
5181	14357	23443	0.86	1.0E-01	BE389100.1	EST_HUMAN	601286989F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3813552 5'
5265	14438		0.83	1.0E-01	AV783980.1	EST_HUMAN	AV783980 MDS Homo sapiens cDNA clone MDSBQB11 5'
5345	14575		9.19	1.0E-01	W86490.1	EST_HUMAN	zh62h04.e1 Scores_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:416885 3'
5670	14891	24283	11.88	1.0E-01	AF274875.1	NT	Homo sapiens growth factor receptor-bound protein 7 (GRB7) gene, complete cds
6086	15286		1.97	1.0E-01	R23821.1	EST_HUMAN	yk34h06.l1 Scores placenta Nb2HP Homo sapiens cDNA clone IMAGE:131875 5' similar to contains Alu repetitive element;
6391	15571		2.51	1.0E-01	Y12488.1	NT	M.musculus wfm gene
6913	16101		2.59	1.0E-01	M78729.1	NT	Human pro-alpha-1 (V) collagen mRNA, complete cds
7050	16227	25702	12.87	1.0E-01	AB048789.1	NT	Homo sapiens mRNA for KIAA1579 protein, partial cds
7050	16227	25703	12.87	1.0E-01	AB046788.1	NT	Homo sapiens mRNA for KIAA1579 protein, partial cds
7261	16471		2.48	1.0E-01	AU159127.1	EST_HUMAN	AU159127 THYRO1 Homo sapiens cDNA clone THYRO1000895 3'
7600	16803	26287	3.47	1.0E-01	BF242948.1	EST_HUMAN	601877703F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4108089 5'
7600	16803	26288	3.47	1.0E-01	BF242948.1	EST_HUMAN	601877703F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4108089 5'
7838	17078	26908	4.88	1.0E-01	BE790543.1	EST_HUMAN	601582559F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3838734 5'
8497	17897		3.22	1.0E-01	BE537718.1	EST_HUMAN	601085554F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451833 5'
8738	17882		2.74	1.0E-01	7682185	NT	Homo sapiens KIAA0514 gene product (KIAA0514), mRNA
8752	17895		1.78	1.0E-01	X00854.1	NT	Drosophila melanogaster f1z gene
9039	18308		2.64	1.0E-01	U52691.1	NT	Gonyaulax polyedra putative type-1 serine/threonine phosphatase (PP-1) mRNA, complete cds
9070	17897		2.48	1.0E-01	BE537719.1	EST_HUMAN	601085554F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451833 5'
9132	18280		12.74	1.0E-01	U68834.1	NT	Saccharomyces cerevisiae suppressor of ABF1 (SAB2) gene, complete cds
9184	17981		8.43	1.0E-01	AP001507.1	NT	Bacillus halodurans genomic DNA, section 1/14
2733	11912	21125	0.86	9.9E-02	AF274008.1	NT	Drosophila melanogaster cAMP-dependent protein kinase type II regulatory subunit (pka-RII) mRNA, complete cds
2740	11919	21133	1.16	9.9E-02	BE545554.1	EST_HUMAN	601070219F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456365 5'

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2740	11919	21134	1.16	9.8E-02	BE545554.1	EST_HUMAN	601070219F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3458365 5'
3233	12467	21598	1.43	9.8E-02	AF098810.1	NT	Homo sapiens neuraxin III-alpha gene, partial cds
3928	13144	22281	0.79	9.8E-02	AI821637.1	EST_HUMAN	zu45603.x5 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:740932 3'
6074	14520	23563	8.08	9.8E-02	D83710.1	NT	Aspergillus terreus BSD mRNA for blastidin S deaminase, complete cds
6840	16045	25510	2.52	9.8E-02	6755111	NT	Mus musculus phospholipid transfer protein (Pltp), mRNA
570	9820		1.04	9.8E-02	X56338.1	NT	O. sativa RAmYGc gene for alpha-amylase
3110	12345	21472	3.7	9.8E-02	AF184274.1	NT	Daucus carota leucoanthocyanidin dioxygenase 2 (LDOX) mRNA, LDOX-2 allele, complete cds
4209	13412	22506	8.37	9.8E-02	AF257326.1	NT	Leptospira maculans beta-tubulin mRNA, complete cds
4209	13412	22507	8.37	9.8E-02	AF257326.1	NT	Leptospira maculans beta-tubulin mRNA, complete cds
7695	16430	25917	2.22	9.8E-02	BF037421.1	EST_HUMAN	601460783F1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:3884287 5'
8480	17516		1.34	9.8E-02	8393751	NT	Rattus norvegicus microtubule-associated protein tau (Mapt), mRNA
1358	10573	19738	1.29	9.7E-02	AB005808.1	NT	Alcea arborescens mRNA for NADP-malic enzyme, complete cds
1565	10778		3.75	9.7E-02	4503710	NT	Homo sapiens fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism) (FGFR3) mRNA
2228	11422	20848	1.89	9.7E-02	BE168680.1	EST_HUMAN	QV1-HT0516-070300-095-a04 HT0516 Homo sapiens cDNA
3961	13176		4.12	9.7E-02	Q89785	SWISSPROT	CELL SURFACE A33 ANTIGEN PRECURSOR (GLYCOPROTEIN A33)
6208	15387	24630	2.95	9.7E-02	Z99119.1	NT	Bacillus subtilis complete genome (section 16 of 21): from 2897771 to 3213410
6732	15927	25396	2.42	9.7E-02	A853984.1	EST_HUMAN	wx78b06.x1 NCI_CGAP_Oy38 Homo sapiens cDNA clone IMAGE:2549747 3' similar to gb:X52851_ma1
7751	16947		2.37	9.7E-02	U58337.1	NT	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE A (HUMAN);
1983	11186	20395	3.52	9.6E-02	A080721.1	EST_HUMAN	Mus musculus ligatin (Lgtn) mRNA, partial cds
1983	11186	20396	3.52	9.6E-02	A080721.1	EST_HUMAN	oz47d11.x1 Soares NhlMIPu_S1 Homo sapiens cDNA clone IMAGE:1678485 3'
4338	13539	22630	7.92	9.6E-02	Z32686.2	NT	oz47d11.x1 Soares NhlMIPu_S1 Homo sapiens cDNA clone IMAGE:1678485 3'
4695	13896	22687	0.86	9.6E-02	U37056.1	NT	Proteus mirabilis fibrinolytic operon, strain H4320
5025	14211	23284	0.99	9.6E-02	AW968230.1	EST_HUMAN	Glossidium cellulosum endo-1,4-beta glucanase EngF (engF) gene, complete cds
6710	14928		3.07	9.6E-02	BE910039.1	EST_HUMAN	EST378303 IMAGE resequences, MAGI Homo sapiens cDNA
7153	16330	25813	4.32	9.6E-02	P08174	SWISSPROT	601498088F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3900185 5'
7328	16644	26033	7.1	9.6E-02	Z79702.1	NT	COMPLEMENT DECAY-ACCELERATING FACTOR PRECURSOR (CD55)
8210	17341	26680	1.89	9.6E-02	AA625755.1	EST_HUMAN	Mycobacterium tuberculosis H37Rv complete genome, segment 102/162
9103	17928		1.58	9.6E-02	H14599.1	EST_HUMAN	zu91g01.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:745392 3'
4079	13289	22388	2.65	9.5E-02	AW992395.1	EST_HUMAN	ym19h03.s1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:48853 3'
6208	15369	24833	4.88	9.5E-02	AB003473.1	NT	CM2-BN0023-050200-087-112 BN0023 Homo sapiens cDNA
6321	15503	24949	8.19	9.5E-02	AL161538.2	NT	Trimeresurus flavoviridis DNA for phospholipase A2 inhibitor, complete cds
6420	15617	25080	4.43	9.5E-02	BF035861.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 38
							601453042F1 NIH_MGC_86 Homo sapiens cDNA clone IMAGE:3857243 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6420	15617	25081	4.43	9.5E-02	BF035861.1	EST_HUMAN	601453842F1 NIH_MGC 68 Homo sapiens cDNA clone IMAGE:3857243 5'
7271	16490	25980	4.04	9.5E-02	BF035861.1	EST_HUMAN	601453842F1 NIH_MGC 68 Homo sapiens cDNA clone IMAGE:3857243 5'
7271	16490	25981	4.04	9.5E-02	BF035861.1	EST_HUMAN	601453842F1 NIH_MGC 68 Homo sapiens cDNA clone IMAGE:3857243 5'
1801	11010	20202	3.84	9.4E-02	BF671063.1	EST_HUMAN	602150882F1 NIH_MGC 81 Homo sapiens cDNA clone IMAGE:4281917 5'
3861	13077	22193	5.59	9.4E-02	Z33059.1	NT	M. capricorn DNA for CONTIG MC073
5081	14261	23346	0.7	9.4E-02	6753517	NT	Mus musculus coding region determinant-binding protein (Crbp), mRNA
6855	15650		2.23	9.4E-02	Z46983.1	NT	Acinetobacter sp. cysD, cobQ, sodM, lysS, rubA, rubB, estB, oxyR, ppk, mtgA, ORF2 and ORF3 genes
7507	15511	24957	2.82	9.4E-02	L78833.1	NT	Human BRCA1, Rho7 and vail genes, complete cds, and lpr35 gene, partial cds
8345	18213		3.85	9.4E-02	U31815.1	NT	Rattus norvegicus calcium channel alpha-1C subunit (ROB2) mRNA, partial cds
2948	12184		2.07	9.3E-02	4908280	NT	Homo sapiens BAI1-associated protein 3 (BAIAP3) mRNA
2894	12231		8.38	9.3E-02	6912625	NT	Homo sapiens nasopharyngeal epithelium specific protein 1 (NESG1), mRNA
3223	12457	21591	1.95	9.3E-02	BF575511.1	EST_HUMAN	602133086F1 NIH_MGC 81 Homo sapiens cDNA clone IMAGE:4288269 5'
4134	13340	22439	4.02	9.3E-02	BE391843.1	EST_HUMAN	601286082F1 NIH_MGC 44 Homo sapiens cDNA clone IMAGE:3607653 6'
4134	13340	22440	4.02	9.3E-02	BE391843.1	EST_HUMAN	601286082F1 NIH_MGC 44 Homo sapiens cDNA clone IMAGE:3607653 5'
4748	13937		2.16	9.3E-02	AV732224.1	EST_HUMAN	AV732224 HTF Homo sapiens cDNA clone HTFAUA06 5'
5038	14221	23305	1	9.3E-02	AF115443.1	NT	HIV-1 isolate BR112 from Brazil gag protein (gag) gene, partial cds
5238	14413	23482	0.87	9.3E-02	D16583.1	NT	Human gene for L-histidine decarboxylase, complete cds
5238	14413	23483	0.87	9.3E-02	D16583.1	NT	Human gene for L-histidine decarboxylase, complete cds
7131	16308	25786	4.97	9.3E-02	Q15034	SWISSPROT	HYPOTHETICAL PROTEIN KIAA0032
7131	16308	25789	4.97	9.3E-02	Q15034	SWISSPROT	HYPOTHETICAL PROTEIN KIAA0032
7174	16351		4.06	9.3E-02	AW208117.1	EST_HUMAN	U1-H-B11-af-h-05-0-J1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2723553 3'
8619	18137		2.83	9.3E-02	AJ249850.1	NT	Photobacterium damsela subsp. damsela partial gyrB gene for DNA gyrase B subunit
8003	18166		13.31	9.3E-02	AW468850.1	EST_HUMAN	hd28h12.k1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2810887 3'
9216	18212		1.48	9.3E-02	AF100956.1	NT	Mus musculus major histocompatibility locus class II region; Fac-binding protein Daxx (DAXX) gene, partial cds; Bln1 (BING1), tapasin (tapasin), RalGDS-like factor (RLF), KE2 (KE2), BING4 (BING4), beta1, 3-galactosyl transferase (beta1,3-galactosyl tr>
234	9513	18839	8.2	9.2E-02	U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome
234	9513	18840	8.2	9.2E-02	U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome
234	9513	18841	8.2	9.2E-02	U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome
2184	11391		1.48	9.2E-02	R54156.1	EST_HUMAN	y988107.r1 Soares Infant brain 1NIB Homo sapiens cDNA clone IMAGE:41618 5'
3144	12378	21510	3.99	9.2E-02	Q28631	SWISSPROT	MAJOR EPIDIDYMIS-SPECIFIC PROTEIN E4 (EPIDIDYMAL PROTEIN BE-20)
3278	12509	21639	0.68	9.2E-02	AAS34354.1	EST_HUMAN	n79601.s1 NCI_CGAP_C03 Homo sapiens cDNA clone IMAGE:928136 3'
3563	12786		1.46	9.2E-02	6755215	NT	Mus musculus pre T-cell antigen receptor alpha (Ptrca), mRNA

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4223	13428		1.12	9.2E-02	U92048.1	NT	Human herpesvirus 1 strain KOS-63, latency-associated transcript, promoter region
4295	13498		0.74	9.2E-02	BE299722.1	EST_HUMAN	600944385F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2860178 5'
4840	13834	22823	1.21	9.2E-02	X88402.1	NT	G.gallus Mia-CK gene
6518	15714	25179	2.57	9.2E-02	X95298.1	NT	H. vulgare xylose isomerase gene
429	6284	18397	2.98	9.1E-02	X77885.1	NT	O. cuniculus K12 keratin gene
2378	11571	20781	1.02	9.1E-02	P78985	SWISSPROT	6-PHOSPHOFRUCTOKINASE (PHOSPHOFRUCTOKINASE) (PHOSPHOHEXOKINASE)
4481	13679	22769	1.85	9.1E-02	AL161554.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 54
6251	15432	24871	13.12	9.1E-02	AW160658.1	EST_HUMAN	eu74a05.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781988 5'
8526	18315		1.51	9.1E-02	AA179801.1	EST_HUMAN	zp38h12.s1 Strabagene muscle 637209 Homo sapiens cDNA clone IMAGE:611783 3' similar to SW:TRT3_HUMAN P45378 TROPONIN T, FAST SKELETAL MUSCLE, ISOFORM BETA ;
8607	17605		1.53	9.1E-02	AF032886.1	NT	Rattus norvegicus cell cycle protein p55CDC gene, complete cds
9091	18169		6.56	9.1E-02	AL291300.1	NT	Homo sapiens partial MUC3B gene for MUC3B mucin, exons 1-11
762	9863	18137	3.57	9.0E-02	P15328	SWISSPROT	FOLATE RECEPTOR ALPHA PRECURSOR (FR-ALPHA) (FOLATE RECEPTOR 1) (FOLATE RECEPTOR, ADULT) (ADULT FOLATE-BINDING PROTEIN) (FBP) (OVARIAN TUMOR-ASSOCIATED ANTIGEN MOV18) (KB CELLS FBP)
1611	10824	18999	6.83	9.0E-02	BE220482.1	EST_HUMAN	h938g10.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3175842 3' similar to contains Alu repetitive element
2755	11834	21150	3.82	9.0E-02	AF138522.1	NT	HIV-1 p8c095-08 from USA envelope glycoprotein (env) gene, partial cds
2755	11834	21151	3.82	9.0E-02	AF138522.1	NT	HIV-1 p8c095-08 from USA envelope glycoprotein (env) gene, partial cds
3310	12540	21875	0.75	9.0E-02	AF278135.1	NT	Dicystidium discoidium spore coat structural protein SP85 (cotE) gene, complete cds
4871	13865	22968	1.98	9.0E-02	X65740.2	NT	Plasmodium falciparum P-type ATPase 3 gene
5238	14410		0.98	9.0E-02	AJ132368.1	NT	Helicobacter pylori (strain P1) comB and pilA/pilQ (partial) genes, and partial ORF1 and ORF2
5652	14875	24262	12.37	9.0E-02	W56037.1	EST_HUMAN	za68a12.r1 Soares_fetal_lung_NbHL10W Homo sapiens cDNA clone IMAGE:297894 5' similar to PIR:352171 S52171 small G protein - human ;
8929	17811		1.35	9.0E-02	AF022236.1	NT	Escherichia coli strain E2348/89 pathogenicity island, rOrf1 (rOrf1), rOrf2 (rOrf2), EscR (escR), EscS (escS) (escS), EscT (escT), EscU (escU), CesD (cesD), EscC (escC), EscJ (escJ), SepZ (sepZ), EscV (escV), EscN (escN), SepQ (sepQ), Tir (tir), OrfU (orfU), >
1439	10653	19828	1.23	8.9E-02	BF701593.1	EST_HUMAN	602128030F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285851 5'
1439	10653	19827	1.23	8.9E-02	BF701593.1	EST_HUMAN	602128030F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285851 5'
4181	13385		1.78	8.9E-02	AF286055.1	NT	Atichium angustatum AtranFla2 protein (AtranFla2) gene, partial cds
6234	14408		0.95	8.9E-02	AB025922.1	NT	Mus musculus Gif1 mRNA, complete cds
5583	14817	24182	2.61	8.9E-02	AW452122.1	EST_HUMAN	U1-H-B13-elo-f-08-0-U1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068284 3'
5583	14817	24183	2.61	8.9E-02	AW452122.1	EST_HUMAN	U1-H-B13-elo-f-08-0-U1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068284 3'
5598	14822	24189	3.12	8.9E-02	11433478	NT	Homo sapiens similar to endoglycan (H. sapiens) (LOC63107), mRNA

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Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6316	15496		2	8.9E-02	Z78021.1	NT	H.sapiens flow-sorted chromosome 6 HindIII fragment, SC8pA20F8
6854	16949	26308	7.54	8.9E-02	AA309319.1	EST_HUMAN	EST180187 Liver, hepatocellular carcinoma Homo sapiens cDNA 5' end
8344	18164		1.33	8.9E-02	P18524	SWISSPROT	MYOSIN-2 ISOFORM
8409	17540		4.1	8.9E-02	BF696818.1	EST_HUMAN	602128682F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286180 5'
1380	10584	19780	1.39	8.8E-02	Q27474	SWISSPROT	PROBABLE DNA LIGASE (POLYDEOXYRIBONUCLEOTIDE SYNTHASE [ATP])
4012	13224		4.05	8.8E-02	O00268	SWISSPROT	TRANSCRIPTION INITIATION FACTOR TFIID 135 KDA SUBUNIT (TAFII135) (TAFII130)
4224	13427		1.03	8.8E-02	4502804	NT	Homo sapiens chromogranin A (parathyroid secretory protein 1) (CHGA) mRNA
4288	13480		0.65	8.8E-02	4580423	NT	Homo sapiens paired box gene 6 (amrtdia, keratilis) (PAX6), isoform b, mRNA
7678	16877	26382	3.02	8.8E-02	BE264455.1	EST_HUMAN	601191770F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535848 5'
7878	16877	26383	3.02	8.8E-02	BE264455.1	EST_HUMAN	601191770F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535848 5'
7813	17006	26519	11.51	8.8E-02	AL040126.1	EST_HUMAN	DKFZp434D1313_1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434D1313 5'
8577	17593	24001	1.59	8.8E-02	Z71561.1	NT	S.cerevisiae chromosome XIV reading frame ORF YNL285W
1624	10837	20014	2.52	8.7E-02	A167261.1	EST_HUMAN	ox85b01.s1 Soares_NHHMPu_S1 Homo sapiens cDNA clone IMAGE:1681161 3'
3872	12863	22014	5.01	8.7E-02	U82685.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
3872	12893	22015	5.01	8.7E-02	U82685.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
4717	13908	23010	1.41	8.7E-02	AF178636.1	NT	Mus musculus JNK interacting protein-3a (Jip3) mRNA, complete cds
6341	14571	23648	5.63	8.7E-02	AA296876.1	EST_HUMAN	zs55g08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701438 3'
6341	14571	23647	5.63	8.7E-02	AA296875.1	EST_HUMAN	zs55g08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701438 3'
7300	16519		2.75	8.7E-02	L04758.1	NT	Oryctolagus cuniculus cytochrome P-450 (CYP4A4) gene, 5' end
7445	16853	26144	1.71	8.7E-02	A1823393.1	EST_HUMAN	wh53e07.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2384484 3'
7659	17049	26568	2.23	8.7E-02	AJ007763.1	NT	Glucobacter oxydans tRNA-ile and tRNA-Ala genes
8568	17598		1.74	8.7E-02	X17116.1	NT	Human DNA for immunoglobulin alpha heavy chain from a case of alpha heavy chain disease
8771	17705		1.7	8.7E-02	6878057	NT	Mus musculus nidogen 2 (Nid2), mRNA
1259	10474	19638	5.5	8.6E-02	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
2208	11405	20629	2.12	8.6E-02	BE408667.1	EST_HUMAN	601304016F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638643 5'
3161	12398	21518	2.48	8.6E-02	L05488.1	NT	Trichomonas vaginalis beta-tubulin (btub1) gene, complete cds
3623	12844		3.32	8.6E-02	AF153362.1	NT	Dicystotellum discoideum adenyl cyclase (acaA) gene, complete cds
3762	12981		0.65	8.6E-02	U29187.1	NT	Mus musculus long incubation prion protein (Prnp) and prion-like protein (Prnd) genes, complete cds

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6269	14442		0.7	8.6E-02	BF570296.1	EST_HUMAN	602185710T1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310250 3'
5706	14925	24319	4.11	8.6E-02	Y10826.1	NT	Homo sapiens LCN1b gene
7519	16724	26214	1.93	8.6E-02	AF206551.1	NT	Lacerta media cytochrome c oxidase subunit 1 gene, partial cds; mitochondrial gene for mitochondrial product
7519	16724	26215	1.93	8.6E-02	AF206551.1	NT	Lacerta media cytochrome c oxidase subunit 1 gene, partial cds; mitochondrial gene for mitochondrial product
7801	16894	26507	3.96	8.6E-02	BF305606.1	EST_HUMAN	601893437F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139216 5'
7801	16894	26508	3.96	8.6E-02	BF305606.1	EST_HUMAN	601893437F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139216 5'
7976	16411	25897	6.33	8.6E-02	AE001073.1	NT	Archaeoglobus fulgidus section 34 of 172 of the complete genome
2361	11554	20776	2.26	8.5E-02	AE000652.1	NT	Helicobacter pylori 26895 section 130 of 134 of the complete genome
5540	14784		1.93	8.6E-02	P08089	SWISSPROT	M PROTEIN, SEROTYPE 6 PRECURSOR
5681	14884	24272	6.72	8.5E-02	AF233885.1	NT	Mus musculus phospholipase C-like protein mRNA, partial cds.
6657	15852	25311	3.4	8.5E-02	6754778	NT	Mus musculus myosin XV (Myo16), mRNA
7022	16189	25676	4.07	8.6E-02	BE833054.1	EST_HUMAN	RC4-OT0037-200700-014-e05 OT0037 Homo sapiens cDNA
7022	16189	25677	4.07	8.6E-02	BE833054.1	EST_HUMAN	RC4-OT0037-200700-014-e05 OT0037 Homo sapiens cDNA
7716	16815		12.86	8.5E-02	AF15510.1	NT	Homo sapiens heparanase precursor, mRNA, complete cds
7730	16828	26436	4.49	8.5E-02	AB001562.1	NT	Streptococcus mutans gene for glucose-1-phosphate uridylyltransferase, complete cds
8978	18094		2.18	8.5E-02	AJ005586.1	NT	Antirrhinum majus mRNA for MYB-related transcription factor
9166	17957		2.25	8.5E-02	AA362834.1	EST_HUMAN	EST72736 Ovary II Homo sapiens cDNA 5' end
2627	12022	21027	2.95	8.4E-02	W86330.1	EST_HUMAN	zd44e11.1 Soares_fetal_heart_NbHH16W Homo sapiens cDNA clone IMAGE:343532 5'
4347	13549	22641	1.01	8.4E-02	AF257213.1	NT	Cavia porcellus glycoprotein alpha-subunit mRNA, complete cds
4347	13549	22642	1.01	8.4E-02	AF257213.1	NT	Cavia porcellus glycoprotein alpha-subunit mRNA, complete cds
6218	14392	23477	1.41	8.4E-02	5453817	NT	Homo sapiens nucleobindin 1 (NUCB1), mRNA
5339	14589	23844	9.48	8.4E-02	BE267153.1	EST_HUMAN	601190436F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3534393 5'
5962	15177	24594	1.76	8.4E-02	AK024456.1	NT	Homo sapiens mRNA for FLJ005050 protein, partial cds
6474	16671	25142	2.87	8.4E-02	BE095074.1	EST_HUMAN	OM3-BT0780-260400-182-d05 BT0780 Homo sapiens cDNA
8482	17531	24026	1.53	8.4E-02	R78408.1	EST_HUMAN	y83h12.1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:145895 5'
3570	12783	21820	6.45	8.3E-02	P75534	SWISSPROT	HYPOTHETICAL LIPOPROTEIN MG308 HOMOLOG PRECURSOR
3568	12819	21839	0.67	8.3E-02	AI436797.1	EST_HUMAN	th82g06.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:2125210 3'
3598	12819	21940	0.67	8.3E-02	AI436797.1	EST_HUMAN	th82g06.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:2125210 3'
4708	13669	22688	0.69	8.3E-02	AB038490.1	NT	Homo sapiens gene for fukutin, complete cds
5818	15035	24438	2.53	8.3E-02	AF032683.1	NT	Homo sapiens protocadherin 43 gene, exon 1
6456	15653	25122	3.77	8.3E-02	AF195787.1	NT	Rattus norvegicus dystrophin-related protein 2 A-form splice variant (Dnp2) mRNA, complete cds
8562	18318		1.98	8.3E-02	BE858458.1	EST_HUMAN	601644770F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3928663 5'

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1386	10600		6.88	8.2E-02	Y08170.2	NT	Gallus gallus mRNA for OBCAM protein gamma isoform
1488	10889	19873	1.71	8.2E-02	AF167077.2	NT	Canis familiaris glutamate transporter (EAAT4) mRNA, complete cds
3038	12275		1.94	8.2E-02	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C008
3788	13006		1.65	8.2E-02	AL161498.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 10
3884	13198	22308	1.27	8.2E-02	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C008
4269	13472	22565	6.55	8.2E-02	P48960	SWISSPROT	LEUCOCYTE ANTIGEN CD97 PRECURSOR
4269	13472	22566	6.55	8.2E-02	P48960	SWISSPROT	LEUCOCYTE ANTIGEN CD97 PRECURSOR
4269	13472	22567	6.55	8.2E-02	P48960	SWISSPROT	LEUCOCYTE ANTIGEN CD97 PRECURSOR
5111	14291	23378	3.05	8.2E-02	U78008.1	NT	Mus musculus zinc transporter (ZnT-3) gene, complete cds
6098	15288	24728	3.38	8.2E-02	AF308555.1	NT	Bos taurus connective tissue growth factor precursor (CTGF) gene, complete cds
6981	16139	25609	8.44	8.2E-02	X04197.1	NT	Beet necrotic yellow vein virus RNA-2
8588	17588	24005	4.79	8.2E-02	AE002246.2	NT	Chlamydia pneumoniae AF39, section 73 of 94 of the complete genome
9007	18086		2.57	8.2E-02	AF275386.1	NT	Mus musculus epidermal growth factor receptor (Egfr) gene, exons 5 through 28, and complete cds, alternatively spliced
5	11857	18405	5.12	8.0E-02	AW954853.1	EST_HUMAN	EST368723 MAGE resequences, MAGC Homo sapiens cDNA
944	10177	18331	0.81	8.0E-02	U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome
1673	12000	20070	12.38	8.0E-02	D26535.1	NT	Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-15)
1673	12000	20071	12.38	8.0E-02	D26535.1	NT	Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-15)
1887	11074	20265	3.81	8.0E-02	BE087218.1	EST_HUMAN	PM3-BT0347-170200-001-b08 BT0347 Homo sapiens cDNA
2433	11824		2.31	8.0E-02	BF246744.1	EST_HUMAN	PM3-BT0347-170200-001-b08 BT0347 Homo sapiens cDNA
2772	10323	19474	2.25	8.0E-02	M23449.1	NT	Human gene for dihydrolipoamide succinyltransferase, complete cds
2852	12080	21219	0.59	8.0E-02	AL445067.1	EST_HUMAN	EST378191 MAGE resequences, MAGC Homo sapiens cDNA
3808	13024	22135	0.84	8.0E-02	AW968118.1	EST_HUMAN	EST378191 MAGE resequences, MAGC Homo sapiens cDNA
4829	14018		6.62	8.0E-02	X72794.1	NT	M. musculus gene for gelatinase B
5217	14391		1.38	8.0E-02	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
5277	10177	18331	0.75	8.0E-02	U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome
5610	14834	24209	3.45	8.0E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
6158	14834	24208	1.69	8.0E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
6502	15699	25165	3.26	8.0E-02	AL114983.1	NT	Baby's chere strain T4 cDNA library under conditions of nitrogen deprivation
7373	16589	26078	3.74	8.0E-02	AF217786.1	NT	Homo sapiens SCG10 like-protein, helicase-like protein NHL, M88, and ADP-ribosylation factor related protein 1 (ARFRP1) genes, complete cds
8620	17616	23870	3.35	8.0E-02	AJ005375.1	NT	Drosophila arene hunchback region
9210	14495		1.7	8.0E-02	4503034	NT	Homo sapiens cAMP responsive element binding protein-like 2 (CREBL2) mRNA
2140	11338	20556	3.19	7.9E-02	BE250008.1	EST_HUMAN	600943191F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2859510 5'

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Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2836	12174	21308	13.43	7.9E-02	AI582028.1	EST_HUMAN	ar98c08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2173846 3' similar to gb:Z28876
3834	13061	22181	3.02	7.9E-02	6881044	NT	60S RIBOSOMAL PROTEIN L38 (HUMAN);
3834	13061	22182	3.02	7.9E-02	6881044	NT	Mus musculus colony stimulating factor 1 receptor (Csfr1), mRNA
4826	14015		1.28	7.9E-02	AB008019.1	NT	Mus musculus colony stimulating factor 1 receptor (Csfr1), mRNA
4830	14118	23213	1.12	7.9E-02	L24757.1	NT	Arabidopsis thaliana RXW24L mRNA, partial cds
6475	15072	25143	4.71	7.9E-02	U27832.1	NT	Human bone sialoprotein (BNSP) gene, exons 2, 3 and 4
7083	16260	25736	7.68	7.9E-02	AI081844.1	EST_HUMAN	Saccharomyces cerevisiae suppressor of MIF2 Sm4p (SMT4) gene, complete cds
7083	16260	25737	7.68	7.9E-02	AI081844.1	EST_HUMAN	ou63b05.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1632465 3' similar to WP:C37A2.2
1218	10438	18501	1.27	7.8E-02	AI793275.1	EST_HUMAN	CE08811;
1218	10438	18592	1.27	7.8E-02	AI793275.1	EST_HUMAN	ou63b05.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1632465 3' similar to WP:C37A2.2
2360	11563	20774	1.02	7.8E-02	AF221942.1	NT	CE08811;
2360	11563	20775	1.02	7.8E-02	AF221942.1	NT	ou58d02.y5 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1570467 5' similar to contains L1.13 L1
4806	13865	23103	0.59	7.8E-02	BE834331.1	EST_HUMAN	repetitive element;
5118	12860		2.33	7.9E-02	BE250048.1	EST_HUMAN	ou58d02.y5 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1570467 5' similar to contains L1.13 L1
7257	10477	25868	2	7.8E-02	U32323.1	NT	repetitive element;
8219	17888		3.82	7.8E-02	AF098349.1	NT	Sus scrofa telomerase RNA pseudogene
1403	11894	18782	1.27	7.7E-02	AF181897.1	NT	Sus scrofa telomerase RNA pseudogene
3594	12787		2.81	7.7E-02	AJ238083.1	NT	PM3-FN0058-140700-005-f09 FN0058 Homo sapiens cDNA
5013	14200	23287	10.43	7.7E-02	AL161501.2	NT	600943055F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2859083 5'
6426	15625	25080	3.91	7.7E-02	AA402949.1	EST_HUMAN	Human Interleukin-11 receptor alpha chain gene, complete cds
7021	16186	25675	4.03	7.7E-02	P38080	SWISSPROT	HIV-1 strain 87USNG30 from USA, envelope glycoprotein (env) gene, partial cds
7681	16788	26280	6.03	7.7E-02		NT	Homo sapiens WRN (WRN) gene, complete cds
8823	18172		2.35	7.7E-02	11422757	NT	Homo sapiens partial AF-4 gene, exons 2 to 7 and Alu repeat elements
3365	12363	21732	1.98	7.6E-02	BE514432.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 13
3386	12613	21746	1.09	7.6E-02	AA296447.1	EST_HUMAN	zu53d11.1 Soares ovary tumor N8HOT Homo sapiens cDNA clone IMAGE:741717 5' similar to
3534	12757	21889	0.68	7.6E-02	AJ400877.1	NT	TR:G1173905 G1173905 SPLICEOSOME ASSOCIATED PROTEIN.;
7039	16216		2.98	7.6E-02	AL138078.2	NT	PROBABLE SERINE/THREONINE-PROTEIN KINASE YBR058C
							Homo sapiens KIAA0628 gene product (KIAA0628), mRNA
							Homo sapiens interferon regulatory factor 7 (IRF7), mRNA
							601318428F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3634903 5'
							EST112214 Cerebellum II Homo sapiens cDNA 5' end similar to similar to protocadherin 43
							Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
							Campylobacter jejuni NCTC11168 complete genome; segment 5/6

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8177	17309	28852	2.52	7.6E-02	AW966845.1	EST_HUMAN	QV3-BN0048-150400-151-e04 BN0048 Homo sapiens cDNA
794	10034	19183	1.35	7.5E-02	5902083	NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter, glycine), member 9 (SLC8A9), mRNA
794	10034	19184	1.35	7.5E-02	5902083	NT	Homo sapiens solute carrier family 9 (neurotransmitter transporter, glycine), member 9 (SLC8A9), mRNA
1887	11084	20284	1.13	7.5E-02	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
4509	13705	22789	0.73	7.5E-02	AB015881.1	NT	Homo sapiens IL-18 gene for interleukin-18, intron 1 and exon 2
484	9738	18869	1.55	7.4E-02	AW838547.1	EST_HUMAN	RC5-LT0054-280100-011-H09 LT0054 Homo sapiens cDNA
3572	12785	21821	0.77	7.4E-02	AI807885.1	EST_HUMAN	W43M01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2358385 3'
4715	13908	23007	1.83	7.4E-02	L78810.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
4805	13984	23102	2.72	7.4E-02	6978442	NT	Rattus norvegicus Activin receptor like kinase 1 (Acvrl1), mRNA
4960	14147	23239	1.79	7.4E-02	6978492	NT	Mus musculus ubiquitin C-terminal hydrolase related polypeptide (Uchrrp), mRNA
5873	15091		1.94	7.4E-02	R17477.1	EST_HUMAN	yg14g08.r1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:32339 5'
8541	17568		1.41	7.4E-02	11525883	NT	Homo sapiens histone deacetylase 5 (NY-CO-9), mRNA
8815	18294		3.13	7.4E-02	AW378431.1	EST_HUMAN	CN44-HT0243-081189-037-d11 HT0243 Homo sapiens cDNA
8975	17844	23814	1.32	7.4E-02	BF036096.1	EST_HUMAN	601453813F1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:3857738 5'
8175	17868		1.77	7.4E-02	4828887	NT	Homo sapiens receptor tyrosine kinase-like orphan receptor 1 (ROR1), mRNA
476	9728	18859	1.45	7.3E-02	BE964861.2	EST_HUMAN	601658738R1 NIH_MGC_89 Homo sapiens cDNA clone IMAGE:3888209 3'
475	9728	18860	1.45	7.3E-02	BE964861.2	EST_HUMAN	601658738R1 NIH_MGC_89 Homo sapiens cDNA clone IMAGE:3888209 3'
681	9834	18084	5.5	7.3E-02	AE001788.1	NT	Thermotoga maritima section 101 of 138 of the complete genome
1474	11898	18884	2.54	7.3E-02	AW900281.1	EST_HUMAN	CN40-NN1004-130300-284-g08 NN1004 Homo sapiens cDNA
1812	12003		17.52	7.3E-02	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
5021	14208		1.28	7.3E-02	U12283.1	NT	Mus musculus transcription factor USF2 (USF2) gene, exons 8-10 and complete cds
6280	15480	24901	2.17	7.3E-02	P05143	SWISSPROT	PROLINE-RICH PROTEIN MP-3
6280	15480	24902	2.17	7.3E-02	P05143	SWISSPROT	PROLINE-RICH PROTEIN MP-3
7770	15087	24477	2.81	7.3E-02	AA78977.1	EST_HUMAN	z124402.81 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:451178 3' similar to gb102428.26S PROTEASE SUBUNIT 4 (HUMAN);
120	9408	18538	1.42	7.2E-02	AED00882.1	NT	Methanobacterium thermoautotrophicum from bases 1028155 to 1038834 (section 88 of 148) of the complete genome
120	9408	18539	1.42	7.2E-02	AED00882.1	NT	Methanobacterium thermoautotrophicum from bases 1028155 to 1038834 (section 88 of 148) of the complete genome
1470	10883	18857	2.33	7.2E-02	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
1470	10883	18858	2.33	7.2E-02	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101

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Table 4
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2514	11703		2.78	7.2E-02	U14794.1	NT	Human immunodeficiency virus type 1 isolate 28 reverse transcriptase (pol) gene, internal fragment, partial cds
2832	12170	21303	1.39	7.2E-02	AF065133.1	NT	Drosophila melanogaster CLOCK (Clk) mRNA, complete cds
3884	13080	22196	0.69	7.2E-02	AW288322.1	EST_HUMAN	U1-H-BW0-aj-e-05-0-U1.s1 NCL_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:2732049 3'
4339	13540	22831	4.22	7.2E-02	BF572307.1	EST_HUMAN	602077757F1 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:4251950 5'
4703	13894	22863	0.59	7.2E-02	11468583	NT	Rhodomonas salina mitochondrion, complete genome
5317	14549	23619	3	7.2E-02	U67531.1	NT	Methanococcus jannaschii section 73 of 150 of the complete genome
5318	14550	23620	8.39	7.2E-02	P11120	SWISSPROT	CALMODULIN
6970	16148	25819	2.59	7.2E-02	AV712452.1	EST_HUMAN	AV712452 DCA Homo sapiens cDNA clone DCAAUG01 5'
7074	16251	25724	2.4	7.2E-02	AW873187.1	EST_HUMAN	h24H11.x1 NCL_CGAP_Adr1 Homo sapiens cDNA clone IMAGE:3120333 3' similar to TR:Q9Z340 Q9Z340 ATYPICAL PKC SPECIFIC BINDING PROTEIN.:
7181	16358	25837	2.63	7.2E-02	U62895.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
7207	16384	25865	6.09	7.2E-02	BE565003.1	EST_HUMAN	601343926F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3885951 5'
7213	16390		3.32	7.2E-02	BE53214.1	EST_HUMAN	601065194F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451559 5'
7487	16894	28178	4.78	7.2E-02	AFO49874.1	NT	Rattus norvegicus BHLH transcription factor Mist1 (Mist1) gene, complete cds
8481	17630		2.88	7.2E-02	AJ230798.1	EST_HUMAN	AJ230798 Homo sapiens library (Seranski P) Homo sapiens cDNA clone PS13D5 3'
8543	17689		1.84	7.2E-02	AA594465.1	EST_HUMAN	nc05908.s1 NCL_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1098838 3'
8608	17806		2.42	7.2E-02	U82828.1	NT	Homo sapiens ataxia telangiectasia (ATM) gene, complete cds
8622	18141		4.94	7.2E-02	AW800962.1	EST_HUMAN	CM4-NN1009-200300-118-c11 NN1009 Homo sapiens cDNA
9134	17843		1.42	7.2E-02	AA401779.1	EST_HUMAN	z57c12.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728454 5'
1868	11075	20268	1.76	7.1E-02	L02290.1	NT	Human immunodeficiency virus type 1 (D9) proviral structural capsid protein (gag) gene, partial cds
2258	11451	20670	6.31	7.1E-02	BF208802.1	EST_HUMAN	801872281F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:4092981 5'
8328	17427		6.31	7.1E-02	BE304764.1	EST_HUMAN	801143974F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3051234 5'
534	9785	18908	0.74	7.0E-02	Q07092	SWISSPROT	COLLAGEN ALPHA 1(XVI) CHAIN PRECURSOR
1491	10704		1.12	7.0E-02	X06677.1	NT	Martellia Mrcut-1 gene
1732	10944	20127	1.13	7.0E-02	AA056343.1	EST_HUMAN	z66104.s1 Stratagene colon (#837204) Homo sapiens cDNA clone IMAGE:509589 3'
2995	12232	21363	2.07	7.0E-02	AW138152.1	EST_HUMAN	U1-H-B11-acy-c-07-0-U1.s1 NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2716020 3'
3875	13081	22207	0.87	7.0E-02	AA815438.1	EST_HUMAN	af65a12.s1 Soares_testis_NHT Homo sapiens cDNA clone 1375878 3' similar to gb:K03002 60S
4021	13233	22338	1.24	7.0E-02	BE070264.1	EST_HUMAN	RIBOSOMAL PROTEIN L32 (HUMAN);
4121	13327		1.01	7.0E-02	AW792962.1	EST_HUMAN	QV4-BT0407-280100-090-e10 BT0407 Homo sapiens cDNA
							CM0-UM0001-060300-270-e12 UM0001 Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4197	13401	22499	11.13	7.0E-02	AF077821.1	NT	Canis familiaris inducible nitric oxide synthase mRNA, complete cds
4950	14137	23231	8.23	7.0E-02	BF381987.1	EST_HUMAN	601816291F1 NIH_MGC 56 Homo sapiens cDNA clone IMAGE:4050071 5'
6959	16137	25608	2.22	7.0E-02	K02901.1	NT	Rat Ig germline epsilon H-chain gene C-region, 3' end
7912	17127	26857	2.69	7.0E-02	AA724295.1	EST_HUMAN	af98a05.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1327184 3' similar to gb:L14837
520	9771	18894	16.86	6.8E-02	AL163210.2	NT	TIGHT JUNCTION PROTEIN ZO-1 (HUMAN);
520	9771	18895	16.86	6.8E-02	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1341	10555		1.3	6.8E-02	4507988	NT	Homo sapiens chromosome 21 segment HS21C010
3775	12993	22108	1.48	6.8E-02	Q06394	SWISSPROT	Homo sapiens regulator of Gz-selective protein signaling (ZGAP1) mRNA, and translated products
3775	12993	22109	1.48	6.8E-02	Q06394	SWISSPROT	26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)
5182	14358		0.91	6.8E-02	AF079906.1	NT	26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)
8474	17527		3.36	6.8E-02	X74315.1	NT	Rabies virus isolate b815 glycoprotein gene, partial cds
8682	17639		1.32	6.8E-02	P44621	SWISSPROT	X laevis XFD2 mRNA for fork head protein
8687	17782		2.42	6.8E-02	AF195953.1	NT	PROTEIN TRANSPORT PROTEIN HOF C HOMOLOG
1847	11055	20244	1.09	6.8E-02	AA496759.1	EST_HUMAN	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds
1847	11055	20245	1.09	6.8E-02	AA496759.1	EST_HUMAN	ae30f02.r1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897339 5' similar to gb:M22362
1871	11078	20268	3.81	6.8E-02	AF156673.1	NT	MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (HUMAN);
4650	13745		0.72	6.8E-02	BE141076.1	EST_HUMAN	ae30f02.r1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897339 5' similar to gb:M22362
6200	15381	24822	7.45	6.8E-02	AL163268.2	NT	MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (HUMAN);
6555	15751	25212	7.23	6.8E-02	AJ248287.1	NT	Homo sapiens putative hepatic transcription factor (WBSOR14) gene, complete cds
6555	15751	25213	7.23	6.8E-02	AJ248287.1	NT	MRO-HT0069-071089-001-c05 HT0069 Homo sapiens cDNA
8273	18341		1.76	6.8E-02	T03214.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C088
8405	17481		2.35	6.8E-02	AA756014.1	EST_HUMAN	Pyrococcus abyssi complete genome; segment 5/8
9004	17862		2.51	6.8E-02	AW975539.1	EST_HUMAN	Pyrococcus abyssi complete genome; segment 5/8
9068	17896		2.42	6.8E-02	9910595	NT	FB448 Fetal brain, Stratiogene Homo sapiens cDNA clone FB448 3'end similar to LINE-1
9270	18287	23685	1.75	6.8E-02	6978895	NT	af67f05.s1 Soares testis_NHT Homo sapiens cDNA clone 1320705 3'
9714	10728		2.09	6.7E-02	AF115536.1	NT	EST387948 MAGN Homo sapiens cDNA
1858	11065	20258	1.82	6.7E-02	AJ20285.1	EST_HUMAN	EST387948 MAGN Homo sapiens cDNA
3698	12918	22035	5.07	6.7E-02	P12726	SWISSPROT	Mus musculus latent TGF beta binding protein (Tgfb), mRNA
1358	10571	19738	1.07	6.6E-02	AJ735509.1	EST_HUMAN	Rattus norvegicus Growth factor independent-1 (Gfi1), mRNA
							Oncorhynchus mykiss TAP1 protein (OnmyTAP1) mRNA, OnmyTAP1'01 allele, complete cds
							qg79e04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1841406 3'
							HOMEBOX PROTEIN HOXD4 (CHDX-A)
							af12e09.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2354820 3' similar to
							SW:LIN1_NYOCO P08548 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.;

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1377	10361	19757	1.01	6.6E-02	AF245118.1	NT	Drosophila melanogaster cactin mRNA, complete cds
2147	11345	20562	11.31	6.6E-02	AJ289241.1	NT	Mus musculus Capn12 gene (for calpain 12, exons 1-21, three alternative transcripts
3440	12665	21769	10.35	6.6E-02	R84306.1	EST_HUMAN	y118b10.s1 Soares placenta Nb2H-P Homo sapiens cDNA clone IMAGE:139578 3'
3453	12678	21813	2.75	6.6E-02	7108357	NT	Homo sapiens mesothelin (MSLN), transcript variant 1, mRNA
3453	12678	21814	2.75	6.6E-02	7108357	NT	Homo sapiens mesothelin (MSLN), transcript variant 1, mRNA
4056	13268	22369	1.94	6.6E-02	AF260226.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
4868	14185	23273	12.34	6.6E-02	Q61703	SWISSPROT	INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2)
4908	14185	23274	12.34	6.6E-02	Q61703	SWISSPROT	INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2)
5922	15139	24651	3.91	6.6E-02	X06411.1	NT	P. vulgaris mRNA for chalcone synthase
6441	15638	25105	2.34	6.6E-02	AF052572.1	NT	Homo sapiens chemokine receptor CXCR4 gene, promoter region and complete cds
7534	16739	26230	7.23	6.6E-02	BF374248.1	EST_HUMAN	NR1-SND0094-010600-008-a12 SND0084 Homo sapiens cDNA
8882	17777		2.4	6.6E-02	9937991	NT	Mus musculus DIPB gene (Dipb), mRNA
8201	17868		1.32	6.6E-02	AF167430.1	NT	Rattus norvegicus cytochrome P450 2E1 (CYP2E1) gene, 5' flanking region
589	9837	18956	1.86	6.6E-02	BF027638.1	EST_HUMAN	601671046F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954178 5'
904	10226	19382	2.88	6.6E-02	7708088	NT	Homo sapiens E2F-like protein (LOC51270), mRNA
1395	10609	19773	3.06	6.6E-02	U47624.1	NT	Xenopus laevis alpha(E)-catenin mRNA, complete cds
1708	10920	20105	1.9	6.6E-02	AE000784.1	NT	Aquifex aeolicus section 98 of 108 of the complete genome
4967	14154	23246	3.91	6.6E-02	7661863	NT	Homo sapiens KIAA0019 gene product (KIAA0019), mRNA
5472	14688	24051	1.87	6.6E-02	AA443991.1	EST_HUMAN	z46f112.s1 Soares ovary tumor NBH0T Homo sapiens cDNA clone IMAGE:756743 3' similar to gb:M26038
7233	16454	25943	6.3	6.6E-02	AA195848.1	EST_HUMAN	HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR-5 BETA CHAIN (HUMAN);
8295	17408		3.32	6.6E-02	M21498.1	NT	z32g05.s1 Soares NIH-MP, S1 Homo sapiens cDNA clone IMAGE:665144 3'
8670	17645		4.71	6.6E-02	AF102883.1	NT	Rabbit microsomal epoxide hydrolase
582	9831	18949	2.37	6.6E-02	X94548.1	NT	Nectria haematococca kinase related protein 2 (KRP2) gene, complete cds
6714	14932	24327	3.98	6.6E-02	AF052733.1	NT	A. carterae precursor of peridinin-chlorophyll-protein (PCP) gene
6714	14932	24328	3.98	6.6E-02	AF052733.1	NT	Heterodera glycines beta-1,4-endoglucanase-1 precursor (HG-eng-1) gene, complete cds
6005	15287	24718	4.78	6.6E-02	BE974448.1	EST_HUMAN	Heterodera glycines beta-1,4-endoglucanase-1 precursor (HG-eng-1) gene, complete cds
6678	15772		2.71	6.6E-02	6753323	NT	601680425R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950503 3'
6673	15868	25327	4.73	6.6E-02	AA063305.1	EST_HUMAN	Mus musculus chaperonin subunit 6a (zeta) (Cct6a), mRNA
6887	16175	25646	2.29	6.6E-02	AB011126.1	NT	K1419.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'
							Homo sapiens mRNA for KIAA0554 protein, partial cds
8189	17331	26873	2.12	6.6E-02	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8189	17331	26874	2.12	6.4E-02	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Refet gene, and sodium phosphate transporter (NPT3) gene, complete cds
8582	18248		3.84	6.4E-02	AF107890.1	NT	Homo sapiens mucin 6B (MUC6B) gene, partial cds
8813	17610	23985	2.47	6.4E-02	AJ277174.1	NT	Drosophila melanogaster mRNA for mod(mdg4)51.4 protein
1726	10638	20121	2.34	6.3E-02	AF109805.1	NT	Mus musculus major histocompatibility locus class III regiona Hec701 gene, partial cds; emRNP, G7A, NG23, Muts homolog, CLCP, NG24, NG25, and NG28 genes, complete cds; and unknown genes
3582	12804		2.89	6.3E-02	P37082	SWISSPROT	HEAT SHOCK PROTEIN 70 HOMOLOG
7077	18254	25727	5.25	6.3E-02	AB010182.1	NT	Hepatitis G virus RNA for polyprotein (NS5A region), partial cds, strain: CMR-152
7303	14948	24343	3.42	6.3E-02	BF210738.1	EST_HUMAN	601873318F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4097499 5'
8849	17632		1.46	6.3E-02	P15276	SWISSPROT	TRANSCRIPTIONAL REGULATORY PROTEIN ALGP (ALGINATE REGULATORY PROTEIN ALGR3)
4237	13440	22532	3.53	6.2E-02	AL161572.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 68
4331	13532		1.31	6.2E-02	AF271235.1	NT	Rattus norvegicus differentiation-associated Na-dependent inorganic phosphate cotransporter (DNPI) mRNA, complete cds
4581	13778		7.85	6.2E-02	Q82191	SWISSPROT	52 KD RO PROTEIN (SJOEGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)) (RO52)
7888	17104	26634	1.97	6.2E-02	AJ242735.1	NT	Metarhizium anisopliae mRNA for Chymotrypsin (chyl gene)
8383	18372		6.97	6.2E-02	AE000750.1	NT	Aquifex aeolicus section 82 of 108 of the complete genome
8828	17741	23932	2.62	6.2E-02	BF112038.1	EST_HUMAN	737808.X1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3523815 3' similar to TR:Q9Y436 Q9Y436 HYPOTHETICAL 30.3 KD PROTEIN. [1];
260	9536	18898	5.6	6.1E-02	D18471.1	NT	Human mRNA, Xq terminal portion
3868	13184		2.44	6.1E-02	U73325.1	NT	Arabidopsis thaliana K+ inward rectifying channel protein (AKCT) gene, complete cds
4657	13851	22846	0.95	6.1E-02	AF119413.1	NT	Lupinus albus 1-aminocyclopropane-1-carboxylate synthase 3 (ACS3) gene, complete cds
4657	13851	22947	0.95	6.1E-02	AF119413.1	NT	Lupinus albus 1-aminocyclopropane-1-carboxylate synthase 3 (ACS3) gene, complete cds
6549	15745	26205	4.27	6.1E-02	X89288.1	NT	H. sapiens mRNA for B-HLH DNA binding protein
7317	16535	26023	6.21	6.1E-02	BE179543.1	EST_HUMAN	IL3-HT0818-110500-138-C08 HT0818 Homo sapiens cDNA
8349	18289		7.82	6.1E-02	X70969.1	NT	S. japonicum mRNA for serine-enzyme
9089	17808		4.49	6.1E-02	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
1269	10484	19643	1.24	6.0E-02	AE001777.1	NT	Thermoboga maritima section 89 of 136 of the complete genome
2635	11818	21035	1.2	6.0E-02	AW968948.1	EST_HUMAN	EST390924 MAGE resequences, MAGJ Homo sapiens cDNA
2728	11907		1.34	6.0E-02	AB031286.1	NT	Mesocistoides corti mitochondrial DNA, NADH dehydrogenase subunit 4, tRNA-Gln, tRNA-Phe, tRNA-Met, ATPase subunit 6, and NADH dehydrogenase subunit 2
2887	8390	18519	0.97	6.0E-02	AA188730.1	EST_HUMAN	zp78c04.r1 Stragene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:928310 5'
2887	8390	18520	0.97	6.0E-02	AA188730.1	EST_HUMAN	zp78c04.r1 Stragene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:928310 5'

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Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3195	12430	21565	1.53	6.0E-02	AA372376.1	EST_HUMAN	EST84286 Colon adenocarcinoma IV Homo sapiens cDNA 5' end similar to tissue-specific protein
3195	12430	21566	1.53	6.0E-02	AA372376.1	EST_HUMAN	EST84286 Colon adenocarcinoma IV Homo sapiens cDNA 5' end similar to tissue-specific protein
3613	12834		1.01	6.0E-02	BE964443.2	EST_HUMAN	601658150R1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3876060 3'
6083	14529	23553	2.83	6.0E-02	5174688	NT	Homo sapiens stimulated trans-acting factor (50 kDa) (STAF50) mRNA
6083	14529	23554	2.83	6.0E-02	5174688	NT	Homo sapiens stimulated trans-acting factor (50 kDa) (STAF50) mRNA
6180	15343	24780	2.16	6.0E-02	BF382349.1	EST_HUMAN	601815274F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4049226 5'
6368	15548	25004	1.79	6.0E-02	AJ204275.1	EST_HUMAN	qf58b08.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1754198 3'
6878	16069	25538	3.1	6.0E-02	AJ245395.1	NT	Acipenser baeri partial IGLV gene for Immunoglobulin light chain variable region, exons 1-2
6878	16069	25539	3.1	6.0E-02	AJ245395.1	NT	Acipenser baeri partial IGLV gene for Immunoglobulin light chain variable region, exons 1-2
7878	17066		2.05	6.0E-02	AA128389.1	EST_HUMAN	zn87c08.r1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:565168 5' similar to
8612	17609	23984	1.52	6.0E-02	11431702	NT	gb:X69181 60S RIBOSOMAL PROTEIN L31 (HUMAN); Homo sapiens DNA-dependent protein kinase catalytic subunit-interacting protein 2 (KIP2), mRNA
8016	17668		2.41	6.0E-02	AI809273.1	EST_HUMAN	wf68h03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2360885 3' similar to TR:O60288
235	9514	18842	5.1	5.9E-02	AW834719.1	EST_HUMAN	O60288 KIAA0551 PROTEIN;
2940	12178	21313	2.36	5.9E-02	AF190266.1	NT	RC1-DT0001-290100-012-e10 DT0001 Homo sapiens cDNA
5249	14422	23498	0.87	5.9E-02	AW028748.1	EST_HUMAN	Mus musculus p53 tumor suppressor gene, exon 10 and 11, partial cds; alternatively spliced
5249	14422	23498	0.87	5.9E-02	AW028748.1	EST_HUMAN	wv34e02.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:2631450 3' similar to TR:O65388
6860	15855	25314	2.7	5.9E-02	9055249	NT	wv34e02.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:2531450 3' similar to TR:O65388
7366	16582		3.4	5.9E-02	6879870	NT	O65388 F12F1.20 PROTEIN.;
7560	16794	26288	2.73	5.9E-02	11433356	NT	Mus musculus trophoblast related homeobox 5 (Drosophila) (lrx5), mRNA
8075	17210		1.66	5.9E-02	BF572539.1	EST_HUMAN	Mus musculus follistatin-like (Fstl), mRNA
8089	17224		1.97	5.9E-02	AJ240733.1	EST_HUMAN	Homo sapiens ninein (LOC51189), mRNA
941	10174		6.49	6.8E-02	D90110.1	NT	602078548F1 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:4243834 5'
3044	12865	21863	13.92	5.8E-02	AE001775.1	NT	Gallus gallus HKC9 telomere junction
4348	13550	22843	5.33	5.8E-02	AW051927.1	EST_HUMAN	Thibacillus ferrooxidans merC, merA genes and URF-1
4348	13550	22844	5.33	5.8E-02	AW051927.1	EST_HUMAN	Thermotoga maritima section 87 of 136 of the complete genome
4544	13738	22838	5.2	5.8E-02	AJ247505.1	EST_HUMAN	wv24c02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2544578 3'
4544	13738	22839	5.2	5.8E-02	AJ247505.1	EST_HUMAN	wv24c02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2544578 3'
4571	13765		2.44	5.8E-02	AF096264.1	NT	qf56f01.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1848687 3' similar to
							gb:M13142 COAGULATION FACTOR XI PRECURSOR (HUMAN);
							qf56f01.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1848687 3' similar to
							gb:M13142 COAGULATION FACTOR XI PRECURSOR (HUMAN);
							Gallus gallus tyrosine kinase JAK1 (JAK1) mRNA, complete cds

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Table 4
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5161	14330	23421	0.8	5.8E-02	AF275366.1	NT	Mus musculus epidermal growth factor receptor (Egfr) gene, exons 5 through 28, and complete cds, alternatively spliced
5161	14330	23422	0.8	5.8E-02	AF275366.1	NT	Mus musculus epidermal growth factor receptor (Egfr) gene, exons 5 through 28, and complete cds, alternatively spliced
6233	14407		0.94	5.8E-02	L78978.1	NT	Schizosaccharomyces pombe HMG-CoA reductase (hmg1+) gene, complete cds
6367	16547	25002	2.63	5.8E-02	M88150.1	NT	Human polymorphic microsatellite DNA
6367	16547	25003	2.53	5.8E-02	M88150.1	NT	Human polymorphic microsatellite DNA
8408	17539		2.41	5.8E-02	AF220177.1	NT	Drosophila melanogaster male fruitless type-A (fru) mRNA, complete cds
8805	18358		6.22	5.8E-02	AA604289.1	EST_HUMAN	no75e11.s1 NCL_CGAP_AA1 Homo sapiens cDNA clone IMAGE:1112894.3'
3022	12258	21386	1.34	5.7E-02	AI081644.1	EST_HUMAN	ou63b05.s1 NCL_CGAP_Bir2 Homo sapiens cDNA clone IMAGE:1632465.3' similar to WP:C37A2.2
3036	12272	21400	1.43	5.7E-02	AF119117.1	NT	CE08611 ; Homo sapiens dopamine transporter (SLC6A3) gene, complete cds
3687	12808		0.93	5.7E-02	AF001292.1	NT	Chironomus thummi thummi globin VIIA.1 (ctt-7A.1), globin II-beta (ctt-2beta), non-functional globin XIII (ctt-13RT), globin XII (ctt-12) and globin XI (ctt-11) genes, complete cds
3768	13004	22119	2.32	5.7E-02	AW868791.1	EST_HUMAN	EST378865 MAGIE resequences, MAGI Homo sapiens cDNA
4691	13882		1.01	5.7E-02	M95099.1	NT	Bos taurus lysozyme gene (cow 3), complete cds
7743	16839	26448	4.13	5.7E-02	AI752685.1	EST_HUMAN	cn18b09.y1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NH-TBC_cn18b09 random
7743	16839	26449	4.13	5.7E-02	AI752685.1	EST_HUMAN	cn18b09.y1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NH-TBC_cn18b09 random
8718	18169		7	5.7E-02	D50320.1	NT	Pig DNA for SPAL-2, complete cds
8959	18244		2.46	5.7E-02	AF217490.1	NT	Homo sapiens fragile 16D oddo reductase (FOR) gene, exons 8, 9, and partial cds
9105	18349		4.1	5.7E-02	AF261280.1	NT	Pan troglodytes apolipoprotein-E gene, complete cds
4942	13836	22925	1.34	5.6E-02	AB013100.1	NT	Lyoparsicon esculentum LE-ACS8 mRNA for 1-aminocyclopropane-1-carboxylate synthase, complete cds
4708	13897	22968	1.32	5.6E-02	AA280599.1	EST_HUMAN	zb45c01.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:700418.3'
5956	15172	24587	4.45	5.6E-02	AW172708.1	EST_HUMAN	x02a10.x1 NCL_CGAP_U2 Homo sapiens cDNA clone IMAGE:2656050.3' similar to TR:O94979 O94979 KIAA0905 PROTEIN. ;
6140	16324	24769	3.23	5.6E-02	BE008001.1	EST_HUMAN	QV0-BN0147-280400-214-g07 BN0147 Homo sapiens cDNA
6717	15912	25370	3.92	5.6E-02	BE542893.1	EST_HUMAN	601067158F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453279.5'
6717	15912	25371	3.92	5.6E-02	BE542893.1	EST_HUMAN	601067159F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453279.5'
8069	17233		2.72	5.6E-02	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
2016	11800	21018	5.48	5.5E-02	X97869.1	NT	H.sapiens gene encoding La autoantigen
3181	12416	21551	3.96	5.5E-02	6755501	NT	Mus musculus SH3 domain protein 1B (Sh3d1B), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4199	13403	22500	1.12	5.5E-02	L41581.1	NT	Gallid herpesvirus mRNA fragment
5158	14337		1.07	5.5E-02	U67518.1	NT	Methanococcus jannaschii section 60 of 150 of the complete genome
5516	14741	24107	3.4	5.5E-02	Q01174	SWISSPROT	TROPOMYOSIN ALPHA CHAIN, NON MUSCLE
5671	14741	24107	4.13	5.5E-02	Q01174	SWISSPROT	TROPOMYOSIN ALPHA CHAIN, NON MUSCLE
7589	16793	26285	14.31	5.5E-02	U09771.1	NT	Citrobacter freundii DSM 30040 cyclopropane fatty acid synthase (cfa) gene, partial cds, dihydroxyacetone kinase (dhak), glycerol dehydrogenase (dhad), transcriptional activator (dhaR), 1,3-propanediol dehydrogenase (dhaT), glycerol dehydratase (dhaB)>
1288	10511		0.6	5.4E-02	AF157823.1	NT	Homo sapiens HTRA serine protease (PRSS11) gene, complete cds
2884	12221		1.01	5.4E-02	AJ277488.1	NT	Oryza sativa rbb3-1 gene for putative Bowman Birk trypsin inhibitor
3400	14477		7.28	5.4E-02	BE073468.1	EST_HUMAN	RC5-BT0559-140200-012-C03 BT0559 Homo sapiens cDNA
3889	13105	22223	0.72	5.4E-02	U85808.1	NT	Hinudo medicinalis SNAP-25 homolog mRNA, complete cds
7289	16508	25898	2.68	5.4E-02	U20780.1	NT	Neurospora crassa ubiquitin-cytochrome c oxidoreductase subunit VIII (QCR8) mRNA, complete cds
8598	18163		1.71	5.4E-02	U44894.1	NT	Rana catesbeiana heat shock protein 30 (HSP30) mRNA, complete cds
1090	10288	18436	1.14	5.3E-02	AW391248.1	EST_HUMAN	QV0-ST0213-021299-062-608 ST0213 Homo sapiens cDNA
1090	10288	18437	1.14	5.3E-02	AW391248.1	EST_HUMAN	QV0-ST0213-021299-062-609 ST0213 Homo sapiens cDNA
1498	10709	19882	11.81	5.3E-02	T94759.1	EST_HUMAN	ye37f12.1 Stratagene lung (#837210) Homo sapiens cDNA clone IMAGE:118951 5' similar to gb:K01508
2460	11651	20872	2.39	5.3E-02	AJ278408.1	NT	HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DP(1) ALPHA CHAIN (HUMAN);
2883	12131	21268	0.92	5.3E-02	M58417.1	NT	Pseudomonas putida tlgS gene
2883	12131	21267	0.92	5.3E-02	M58417.1	NT	Drosophila melanogaster laminin B2 gene, complete cds
3115	12350	21478	3.95	5.3E-02	AJ278408.1	NT	Drosophila melanogaster laminin B2 gene, complete cds
5120	14289	23387	8.22	5.3E-02	M80463.1	NT	Pseudomonas putida tlgS gene
6343	14573	23849	1.95	5.3E-02	AE000527.1	NT	Mus musculus caudal type homeobox-1 (Cbx-1) gene, complete cds
6343	14573	23850	1.95	5.3E-02	AE000527.1	NT	Helicobacter pylori 26695 section 5 of 134 of the complete genome
6034	15242	24863	4.21	5.3E-02	9895413	NT	Helicobacter pylori 26695 section 5 of 134 of the complete genome
6238	15417		2.31	5.3E-02	S78221.1	NT	Lymphocystis disease virus 1, complete genome
8242	18013	23850	1.36	5.3E-02	AF276815.1	NT	nuclear protein TIF1 isoform [mice, mRNA, 4053 nt]
2249	11444		91.88	5.2E-02	5031808	NT	Branchiostoma floridae homeodomain-containing protein Hox13 (Hox13) gene, exon 2 and partial cds
3078	12314	21435	2.27	5.2E-02	AJ277681.1	NT	Homo sapiens meprin A, alpha (PABA peptide hydrolase) (MEP1A) mRNA
3078	12314	21436	2.27	5.2E-02	AJ277681.1	NT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
3913	13129	22248	0.7	5.2E-02	AF236101.1	NT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
4263	13466	22557	2.98	5.2E-02	U07132.1	NT	Arabidopsis thaliana putative dicarboxylate diiron protein (Cyd1) mRNA, complete cds
						NT	Human steroid hormone receptor Nsr-1 mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5199	14375	23482	0.72	5.2E-02	AB035201.1	NT	Rattus norvegicus mRNA for thyroglobulin, complete cds
2332	11525		1.1	5.1E-02	AL134071.1	EST_HUMAN	DKFZp547D073_r1 547 (synonym: hfrb1) Homo sapiens cDNA clone DKFZp547D073 5'
4186	13390	22489	0.81	5.1E-02	AE001301.1	NT	Chlamydia trachomatis section 28 of 87 of the complete genome
5080	14280	23345	1.07	5.1E-02	BE957423.2	EST_HUMAN	601653565R2 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3838361 3'
5235	14409	23490	0.71	5.1E-02	P01785	SWISSPROT	IG HEAVY CHAIN V REGION MOO
6021	14511	23569	1.77	5.1E-02	BF378625.1	EST_HUMAN	QV0-UM0051-250800-350-508 UM0051 Homo sapiens cDNA
7016	16192	25668	6.18	5.1E-02	AF012698.1	NT	Candida albicans protein phosphatase Sed1 homolog (SSD1) gene, complete cds
7406	16618	26108	2.98	5.1E-02	AF083930.1	NT	Homo sapiens ES18 mRNA, partial cds
7408	16618	26108	2.88	5.1E-02	AF083930.1	NT	Homo sapiens ES18 mRNA, partial cds
8856	17759		1.7	5.1E-02	AF062487.1	NT	Cucumis melo polygalacturonase precursor (MPC3) mRNA, complete cds
489	9742	18872	1	5.0E-02	AF088004.1	NT	Mus musculus fatty acid amide hydrolase gene, exon 10
1212	10430	19585	10.56	5.0E-02	Z99104.1	NT	Bacillus subtilis complete genome (section 1 of 21): from 1 to 213080
1959	11163	20398	6.31	5.0E-02	P02810	SWISSPROT	SALVARY ACIDIC PROLINE-RICH PHOSPHOPROTEIN 1/2 PRECURSOR (PRP-1/PRP-3) (PRP-2/PRP-4) (PIF-FPIF-S) (PROTEIN A/PROTEIN C) (CONTAINS: PEPTIDE P-C)
2770	10225	19381	1.08	5.0E-02	U72742.1	NT	Oryctolagus cuniculus UDP-glucuronosyltransferase (UGT2B13) mRNA, complete cds
3311	12541		1.45	5.0E-02	7305610	NT	Mus musculus Unc-51 like kinase 2 (C. elegans) (Ulk2), mRNA
3573	12798		0.94	5.0E-02	U32782.1	NT	Haemophilus influenzae Rd section 87 of 163 of the complete genome
3684	12885	22008	4.54	5.0E-02	U12769.2	NT	Antheraea pernyi period clock protein homolog mRNA, complete cds
4837	14026		0.98	5.0E-02	P40232	SWISSPROT	CASEIN KINASE II BETA CHAIN (CK II)
6307	15488	24933	11.19	5.0E-02	P35616	SWISSPROT	NEUROFILAMENT TRIPLET L PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE)(NF-L)
8025	17162	26698	2.76	5.0E-02	U67600.1	NT	Methanococcus jannaschii section 142 of 150 of the complete genome
8360	18205		4.81	5.0E-02	Q04047	SWISSPROT	NO-ON-TRANSIENT A PROTEIN
229	9507		34.14	4.9E-02	M14230.1	NT	Chicken 28-kDa vitamin D-dependent calcium-binding protein (CaBP-28) mRNA, complete cds
374	9840	18774	2.22	4.9E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
374	9840	18775	2.22	4.9E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
2828	12065	21186	0.77	4.9E-02	U32638.1	NT	Zea mays phytoene synthase (Y1) gene, complete cds
3257	12490	21621	1.72	4.9E-02	P54258	SWISSPROT	ATROPHIN-1 (DENTATORUBRAL-PALLIDOLYSIAN ATROPHY PROTEIN)
3545	12766		0.76	4.9E-02	AA188940.1	EST_HUMAN	zr48a12.s1 Striatogene hNT neuron (#837233) Homo sapiens cDNA clone IMAGE:632828 3' similar to contains Alu repetitive element; contains element MSR1 repetitive element ;
3569	12792	21618	1.13	4.9E-02	AA400914.1	EST_HUMAN	Z178a03.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:728428 3'
3569	12792	21919	1.13	4.9E-02	AA400914.1	EST_HUMAN	Z178a03.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:728428 3'
4858	14046	23140	1.62	4.9E-02	AW167821.1	EST_HUMAN	xg56g10.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2632386 3'
4858	14046	23141	1.62	4.9E-02	AW167821.1	EST_HUMAN	xg56g10.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2632386 3'
5382	14611	23723	1.8	4.9E-02	L00122.1	NT	Rat elastase II gene, exon 6

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Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5382	14611	23724	1.8	4.8E-02	L00122.1	NT	Rat elastase II gene, exon 6
7840	17080	26808	3.81	4.8E-02	AF008303.1	NT	Homo sapiens prepro placental TGF-beta gene, complete cds
8777	17707		1.6	4.8E-02	8923880	NT	Homo sapiens CS box-containing WD protein (LOC55884), mRNA
9058	17888		4.4	4.8E-02	M16384.1	NT	Human gamma-B-crystallin (gamma 1-2) and gamma-C-crystallin (gamma 2-1) genes, complete cds
9119	18277		1.28	4.8E-02	Z89116.1	NT	Bacillus subtilis complete genome (section 13 of 21); from 2393281 to 2813730
335	9804	18733	1.4	4.8E-02	D16471.1	NT	Human mRNA, Xq terminal portion
338	9804	18733	3	4.8E-02	D16471.1	NT	Human mRNA, Xq terminal portion
495	9748	18877	7.4	4.8E-02	AF003100.1	NT	Arabidopsis thaliana AP2 domain containing protein RAP2.7 mRNA, partial cds
2238	11433	20657	1.55	4.8E-02	W51883.1	EST_HUMAN	zz49802 s1 Soares, senescent_fibroblasts_NHISF Homo sapiens cDNA clone IMAGE:325811 3' similar to gb:M30808 LUPUS KU AUTOANTIGEN PROTEIN P88 (HUMAN);
3175	12410	21548	2.47	4.8E-02	X17144.1	NT	Tetrahymena rostrata histone H3II and histone H4II intergenic DNA
4874	13888		1.11	4.8E-02	Z54280.1	NT	S. scrofa gene for skeletal muscle myosin receptor
5160	14339	23428	0.63	4.8E-02	U81914.1	NT	Streptococcus constellatus D-alanine:D-alanine ligase gene, partial cds
8647	17630		1.35	4.8E-02	8632803	NT	Streptococcus thermophilus bacteriophage Sfi19, complete genome
6010	15280	24684	3.54	4.7E-02	W01153.1	EST_HUMAN	y29709.r1 Soares melanocyte 2NblHM Homo sapiens cDNA clone IMAGE:291017 5' similar to contains Alu repetitive element
6050	15218	24638	2.13	4.7E-02	M62752.1	NT	Rat statin-related protein (s1) gene, complete CDS
6543	15738	25200	13.84	4.7E-02	X15543.1	NT	B. taurus mRNA for RF-38-DNA-binding protein
6838	16030	25485	12.53	4.7E-02	X15543.1	NT	B. taurus mRNA for RF-38-DNA-binding protein
7338	16555	26043	1.93	4.7E-02	8754565	NT	Mus musculus ligand of numb-protein X (Lnx), mRNA
8080	17225	26760	2.02	4.7E-02	U73621.1	NT	Bos taurus paired box protein (pax-6) gene, partial cds
8090	17225	26761	2.02	4.7E-02	U73621.1	NT	Bos taurus paired box protein (pax-6) gene, partial cds
8580	18360		1.79	4.7E-02	AV948521.1	EST_HUMAN	AV948521 GLC Homo sapiens cDNA clone GLC8KD02 3'
8947	18363		1.48	4.7E-02	P52961	SWISSPROT	HOMEBOX PROTEIN GBX-2 (GASTRULATION AND BRAIN-SPECIFIC HOMEBOX PROTEIN 2)
9189	17985		1.24	4.7E-02	AJ277682.1	NT	Homo sapiens partial TUB gene for tubby (mouse) homolog and LMO1 gene for LIM domain only 1 protein
275	9550	18881	1.16	4.6E-02	BE15383.1	EST_HUMAN	PMO-HT0339-251189-003-g05 HT0339 Homo sapiens cDNA
747	9888	19131	3.98	4.6E-02	AE000445.1	NT	Escherichia coli K-12 MG1655 section 335 of 400 of the complete genome
1299	10514		1.09	4.6E-02	A014255.1	EST_HUMAN	am50d02.s1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1538978 3' similar to TR:P00533
1367	10581	19748	2.77	4.6E-02	AV727059.1	EST_HUMAN	P00533 LIMA, contains element LTR1 repetitive element;
2452	11643	20863	1.64	4.6E-02	AW236023.1	EST_HUMAN	AV727059 HTC Homo sapiens cDNA clone HTCBWC01 5'
							xn24f03.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2694653 3' similar to SW:GRF1_HUMAN
							Q12849 G-RICH SEQUENCE FACTOR-1;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2760	9550	18681	1.53	4.6E-02	BE153583.1	EST_HUMAN	PMO-HT0339-251189-003-g05 HT0339 Homo sapiens cDNA
2869	12207	21343	0.62	4.6E-02	BE153583.1	EST_HUMAN	PMO-HT0339-251189-003-g05 HT0339 Homo sapiens cDNA
3304	12207	21343	0.6	4.6E-02	BE153583.1	EST_HUMAN	PMO-HT0339-251189-003-g05 HT0339 Homo sapiens cDNA
3471	12207	21343	0.67	4.6E-02	BE153583.1	EST_HUMAN	PMO-HT0339-251189-003-g05 HT0339 Homo sapiens cDNA
4103	13310		1.27	4.6E-02	AF220385.1	NT	Mus musculus nucleolar RNA helicase II(Gu (dbx21) gene, complete cds
5765	14984	24383	3.35	4.6E-02	X61824.1	NT	C.reinhardtii atp2 (atpB) mRNA
5765	14984	24384	3.35	4.6E-02	X61824.1	NT	C.reinhardtii atp2 (atpB) mRNA
6870	15885	25325	4.77	4.6E-02	BE154008.1	EST_HUMAN	PMO-HT0339-060400-008-G12 HT0339 Homo sapiens cDNA
7841	17081	26809	4.08	4.6E-02	AA913328.1	EST_HUMAN	Q27H08.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1524737 3'
8928	18358		1.28	4.6E-02	L11892.1	NT	Oryctolagus cuniculus macrophage scavenger receptor type II mRNA, complete cds
9183	17982		4.09	4.6E-02	X57808.1	NT	Human germline immunoglobulin lambda light chain gene
453	9708	18844	2.45	4.5E-02	P22448	SWISSPROT	RETINOIC ACID RECEPTOR BETA (RAR-BETA)
1228	10444	18589	0.95	4.5E-02	AF005730.1	NT	Marburg virus strain M/S Africa/Johannesburg/1975/Ozolin VP35 gene, complete cds
1228	10444	18600	0.95	4.5E-02	AF005730.1	NT	Marburg virus strain M/S Africa/Johannesburg/1975/Ozolin VP35 gene, complete cds
1773	10883	20174	5.37	4.5E-02	P32182	SWISSPROT	HEPATOCYTE NUCLEAR FACTOR 3-BETA (HNF-3B)
2080	11280	20468	1.63	4.5E-02	AE003984.1	NT	Xylella fastidiosa, section 110 of 229 of the complete genome
3703	12823	22042	4.72	4.5E-02	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
5768	14885	24385	1.95	4.5E-02	AJ400877.1	NT	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
6587	15783	25251	2.49	4.5E-02	AF036894.1	NT	Arabidopsis thaliana CCAAT-box binding factor HAP3 homolog gene, complete cds
7054	16231	25708	5.35	4.5E-02	AA325216.1	EST_HUMAN	EST28187 Corbellum II Homo sapiens cDNA 5' end similar to similar to neuro-D4 protein
8578	17592	24000	2.59	4.5E-02	11418013	NT	Homo sapiens ret finger protein-like 3 (RFPL3), mRNA
8989	18250	23708	5.94	4.5E-02	AA191087.1	EST_HUMAN	Zq43f11.1 Stratagene HNT neuron (#937233) Homo sapiens cDNA clone IMAGE:832493 5'
224	9503		4.97	4.4E-02	BE972733.1	EST_HUMAN	601652154F1 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:3835389 5'
1032	10268	19409	0.68	4.4E-02	L19286.1	NT	Drosophila melanogaster extracellular (EXD) mRNA, complete cds
2068	11267		4.78	4.4E-02	P31568	SWISSPROT	HYPOPHYSICAL PROTEIN (ORF 2280)
2453	11644	20884	1.05	4.4E-02	AW1875475.1	EST_HUMAN	QV2-PT0012-010300-070-g02 PT0012 Homo sapiens cDNA
3348	12674	21714	0.93	4.4E-02	X06212.1	NT	Chironomus tentans ecdysone-controlled gene l-18c
3619	12840	21859	1.8	4.4E-02	AF159160.1	NT	Myxococcus xanthus serine/threonine kinase Pkn10 (pkn10) gene, complete cds
4629	13823	22911	1.22	4.4E-02	AF109807.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
4629	13823	22912	1.22	4.4E-02	AF109807.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
4754	13945		2.85	4.4E-02	AJ222689.1	NT	Ovis aries CCAAT-enhancer binding protein epsilon gene

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6702	15897	25358	3.19	4.4E-02	AA736968.1	EST_HUMAN	nwl3h03.s1 NCL_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1239221 3'
7839	16839	26338	5.01	4.4E-02	AF060889.1	NT	Hepatitis E virus strain HEV-US2 polyprotein (ORF1), (ORF3), and capsid protein (ORF2) genes, complete cds
7753	16949	26457	3.27	4.4E-02	AA496739.1	EST_HUMAN	ae33104.1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897631 5'
8280	17403		1.83	4.4E-02	AB040926.1	NT	Homo sapiens mRNA for KIAA1493 protein, partial cds
8477	18373		1.48	4.4E-02	BF241245.1	EST_HUMAN	601878746F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4107418 5'
780	10030	18179	7.71	4.3E-02	AF003249.1	NT	Marone sexatilis myosin heavy chain FM3A (FM3A) mRNA, complete cds
2533	11721	20538	2.39	4.3E-02	AV704878.1	EST_HUMAN	AV704878 ADB Homo sapiens cDNA clone ADBAOH08 6'
3408	12634	21785	8.67	4.3E-02	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3639	12860		1.05	4.3E-02	AF060568.1	NT	Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds
5256	14429	23505	1.34	4.3E-02	D10006.1	NT	yeast RHO3 gene, complete cds
5874	15092	24504	4.79	4.3E-02	P30427	SWISSPROT	PLECTIN
5874	15092	24505	4.79	4.3E-02	P30427	SWISSPROT	PLECTIN
8544	17689		1.41	4.3E-02	AL139077.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 4/8
832	10070	19225	2.2	4.2E-02	AU123327.1	EST_HUMAN	AU123327 NT2RM2 Homo sapiens cDNA clone NT2RM2000020 5'
878	10112		2.66	4.2E-02	AU123327.1	EST_HUMAN	AU123327 NT2RM2 Homo sapiens cDNA clone NT2RM2000020 5'
908	10141	16303	0.71	4.2E-02	AW003845.1	EST_HUMAN	wx34g01.x1 NCL_CGAP_P1H1 Homo sapiens cDNA clone IMAGE:2545584 3' similar to TR:Q63291 Q63291
1685	10907		1.55	4.2E-02	AL445088.1	NT	L1 RETROPOSON, ORF2 MRNA ;contains L1.13 L1 L1 repetitive element ;
1748	10960	20142	1.25	4.2E-02	P23091	SWISSPROT	Thermoplasma acidophilum complete genome; segment 4/5
3845	12868	21984	1.56	4.2E-02	P23091	SWISSPROT	TRANSFORMING PROTEIN MAF
4088	13308	22408	1.01	4.2E-02	BE262805.1	EST_HUMAN	TRANSFORMING PROTEIN MAF
4758	13947	23048	0.87	4.2E-02	BF342865.1	EST_HUMAN	601150833F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3503505 5'
6302	15483	24927	4.38	4.2E-02	AF276752.1	NT	8020717105F1 NCL_CGAP_Brm84 Homo sapiens cDNA clone IMAGE:4152872 5'
6721	15916	26376	5.82	4.2E-02	P05095	SWISSPROT	Legionella pneumophila catalase-peroxidase (katA) gene, complete cds
7855	17045	26582	2.53	4.2E-02	BE815822.1	EST_HUMAN	ALPHA-ACTININ 3, NON MUSCULAR (F-ACTIN CROSS LINKING PROTEIN)
7855	17045	26583	2.53	4.2E-02	BE815822.1	EST_HUMAN	PM3-BN0174-250500-009-410 BN0174 Homo sapiens cDNA
8038	17174	26714	1.97	4.2E-02	AF178458.1	NT	PM3-BN0174-250500-009-410 BN0174 Homo sapiens cDNA
8851	18301		2.53	4.2E-02	A083494.1	EST_HUMAN	PRRS isolate PRRSV36 envelope glycoprotein gene, complete cds
4468	13688		9.32	4.1E-02	AW883484.1	EST_HUMAN	w48g10.x1 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2510850 3'
5152	14331		0.59	4.1E-02	X85880.1	NT	QV1-NN0012-180400-184-06 NN0012 Homo sapiens cDNA
6285	15476	24918	1.84	4.1E-02	7882347	NT	L monocytogenes type 3 partial lap gene (strain 443)
							Homo sapiens KIAA0867 protein (KIAA0867), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6401	15582	25039	2.71	4.1E-02	AF020198.1	NT	Fugu rubripes neural cell adhesion molecule L1 homolog (L1-CAM) gene, complete cds; putative protein 1 (PUT1) gene, partial cds; mitosis-specific chromosome segregation protein SMC1 homolog (SMC1) gene, complete cds; and calcium channel alpha-1 subunit>
6189	18302	23689	23.13	4.1E-02	AJ271809.1	NT	Brassica napus gin gene for plastid glutamine synthetase, exons 1-12
8275	18039	23845	1.3	4.1E-02	AF264822.1	NT	Homo sapiens SMARCA4 isoform (SMARCA4) gene, complete cds, alternatively spliced
3210	12444	21576	3.38	4.0E-02	AB040804.1	NT	Homo sapiens mRNA for KIAA1471 protein, partial cds
3782	13000	22115	0.97	4.0E-02	L11910.1	NT	Human retinoblastoma susceptibility gene exons 1-27, complete cds
5153	14332	23423	0.9	4.0E-02	AB042297.1	NT	Homo sapiens PTS gene for 8-pyruvyltetrahydropterin synthase, complete cds
5385	14614	23727	5.43	4.0E-02	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
6372	15552	25009	5.79	4.0E-02	L23838.1	NT	Strongylocentrotus purpuratus homolog of human bone morphogenetic protein 1 (subimp) mRNA, complete cds
6687	15882	25341	3.68	4.0E-02	P08640	SWISSPROT	GLUCOAMYLASE S1/S2 PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)
8243	17372		1.71	4.0E-02	AJ001018.1	NT	Kluyveromyces fragilis gene for C ₆ ATPase
8481	18114	23808	7.93	4.0E-02	AJ001056.1	NT	Ovis aries mRNA for acetyl-coA carboxylase
1128	10352	19504	4.88	3.9E-02	BF516148.1	EST_HUMAN	UI-H-BW1-arc-h-08-0-U1.s1 NCI CGAP Sub7 Homo sapiens cDNA clone IMAGE:3084134 3'
1352	10587	19731	1.9	3.9E-02	P41047	SWISSPROT	FAS ANTIGEN LIGAND
1831	11136	20330	2.37	3.9E-02	AJ403388.1	NT	M.musculus DNA for desmin-binding fragment DesD7
2685	11846		1.53	3.9E-02	4508882	NT	Homo sapiens succinate dehydrogenase complex, subunit C, integral membrane protein, 15kD (SDHC) mRNA
5077	14257	23340	1.42	3.9E-02	U61380.1	NT	Bacillus megaterium germination protein (gerAA, gerAC, gerAB) genes, complete cds
5077	14257	23341	1.42	3.9E-02	U61380.1	NT	Bacillus megaterium germination protein (gerAA, gerAC, gerAB) genes, complete cds
5117	14297	23365	0.6	3.9E-02	U82882.1	NT	Mus musculus slow skeletal muscle troponin T (Ttn1t) gene, complete cds
5169	14348	23436	1.01	3.9E-02	AW392417.1	EST_HUMAN	RC8-ST0258-171199-021-C09 ST0258 Homo sapiens cDNA
5182	14368	23454	1	3.9E-02	8924019	NT	Homo sapiens hypothetical protein PRO1163 (PRO1163), mRNA
5182	14368	23455	1	3.9E-02	8924019	NT	Homo sapiens hypothetical protein PRO1163 (PRO1163), mRNA
7948	15593	25055	1.69	3.9E-02	P48778	SWISSPROT	ANTIGEN GOR
8317	18258		10.48	3.9E-02	AB042553.1	NT	Felis catus G-CSF gene for granulocyte colony-stimulating factor, complete cds
8386	17857		2.18	3.9E-02	U66061.1	NT	Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV28S1P, TCRBV18S1P, TCRBV15S1, TCRBV11S1A1T, HVB relic, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY5, TRY6, TRY7, TRY8, TCRBD1, TCRBJ1S1, TCRBJ1S2>

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9123	18180		7.38	3.9E-02	AL049868.2	NT	Mus musculus chromosome X contigB; X-linked lymphocyte regulated 5 gene, Zinc finger protein 276, Zinc finger protein 92, mmxq28orf
4898	14084	23177	4.3	3.8E-02	AF000580.1	NT	Dicotyledonum discoidium plasmid Ddp5, complete genome
7248	18468	25957	2.32	3.8E-02	AF143952.2	NT	Homo sapiens PELOTA (PELOTA) gene, complete cds
999	10230	19385	8.13	3.7E-02	P19137	SWISSPROT	LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN)
2203	11400	20925	4.9	3.7E-02	A1984806.1	EST_HUMAN	wf85608.xt NCL_CGAP_Kd11 Homo sapiens cDNA clone IMAGE:2494502 3'
3015	12261	21381	1.02	3.7E-02	P78944	SWISSPROT	EOMESODERMIN
3017	12263	21382	5.68	3.7E-02	BF312963.1	EST_HUMAN	601890233F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125594 5'
8358	17450	26941	4.56	3.7E-02	BF124974.1	EST_HUMAN	601792117F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4024973 5'
9080	18150	23753	12.69	3.7E-02	11418392	NT	Homo sapiens scdute carrier family 22 (organic cation transporter), member 1 (SLC22A1), mRNA
3834	12855	21974	0.78	3.6E-02	X73221.1	NT	H. vulgare Ss1 gene for sucrose synthase
3642	12863	21981	0.84	3.6E-02	AL096808.1	NT	Homo sapiens genomic region containing hypervariable minisatellites chromosome 10[10q26.3] of Homo sapiens
5967	15182	24597	4.28	3.6E-02	AW945516.1	EST_HUMAN	CM2-EN0013-110500-192-b10 EN0013 Homo sapiens cDNA
5967	15182	24598	4.29	3.6E-02	AW945516.1	EST_HUMAN	CM2-EN0013-110500-192-b10 EN0013 Homo sapiens cDNA
6119	15303	24735	1.68	3.6E-02	AF025952.1	NT	Chromatium vinosum sulfur globule protein Cv2 precursor (sgp2) gene, complete cds
6209	15390	24834	2.73	3.6E-02	AA714521.1	EST_HUMAN	hw20605.s1 NCL_CGAP_GC80 Homo sapiens cDNA clone IMAGE:1241024 3' similar to gb:J00314_mae2
6873	16064	25530	3.35	3.6E-02	U20608.1	NT	TUBULIN BETA-1 CHAIN (HUMAN); Dicotyledonum discoidium unknown spore germination-specific protein-like protein, orf1, orf2 and orf3 genes, complete cds
6873	16064	25530	3.35	3.6E-02	U20608.1	NT	Dicotyledonum discoidium unknown spore germination-specific protein-like protein, orf1, orf2 and orf3 genes, complete cds
803	10140	18302	1.14	3.5E-02	U09506.1	NT	Drosophila melanogaster tigrin mRNA, complete cds
1018	10245	18397	1.05	3.5E-02	AF253417.1	NT	Homo sapiens microsomal epoxide hydrolase (EPHX1) gene, complete cds
1546	10760	19833	0.91	3.5E-02	BF678085.1	EST_HUMAN	602085136F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249377 5'
1546	10760	19834	0.91	3.5E-02	BF678085.1	EST_HUMAN	602085136F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249377 5'
4198	13400	22498	1.84	3.5E-02	AE001173.1	NT	Thermobla maritima section 85 of 138 of the complete genome
4306	13507	22603	1.35	3.5E-02	P63780	SWISSPROT	CYSTATHIONINE BETA-L YASE PRECURSOR (CBL) (BETA-CYSTATHIONASE) (CYSTEINE LYASE)
5761	14980	24378	1.69	3.5E-02	J01238.1	NT	Maize actin 1 gene (MAC1), complete cds
6682	15857	25316	3.7	3.5E-02	BE958970.1	EST_HUMAN	601644701R2 NIH_MGC_59 Homo sapiens cDNA clone IMAGE:3929737 3'
8028	17165	26702	1.89	3.5E-02	AW861841.1	EST_HUMAN	PM1-CT0326-261289-002-H03 CT0326 Homo sapiens cDNA
8028	17165	26703	1.89	3.5E-02	AW861841.1	EST_HUMAN	PM1-CT0326-261289-002-H03 CT0326 Homo sapiens cDNA
9054	18193		4.1	3.5E-02	BE276948.1	EST_HUMAN	601178765F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3543633 5'

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Table 4
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
585	9834	18952	1.38	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
585	9834	18953	1.38	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
588	9834	18952	3.54	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
588	9834	18953	3.54	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
1058	10284	18434	4.44	3.4E-02	AW274020.1	EST_HUMAN	x28d07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2814253 3' similar to SW:0211_HUMAN P53801 PUTATIVE SURFACE GLYCOPROTEIN C21ORF1 PRECURSOR:
1214	10432		8.37	3.4E-02	11345459	NT	Homo sapiens hypothetical protein FLJ13220 (FLJ13220), mRNA
2355	11548	20789	1.57	3.4E-02	T57160.1	EST_HUMAN	yc20e06.r1 Stratagene lung (#837210) Homo sapiens cDNA clone IMAGE:81250 5' similar to contains MER29 repetitive element
3409	12835	21768	1.11	3.4E-02	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C008
3757	12978	22081	0.78	3.4E-02	BE839514.1	EST_HUMAN	RC3-FN0155-080700-011-410 FN0155 Homo sapiens cDNA
3887	13113	22231	3.91	3.4E-02	AW794952.1	EST_HUMAN	RC8-UM0015-210200-021-A10 UM0015 Homo sapiens cDNA
4598	13782	22883	3.59	3.4E-02	X59789.1	NT	M.musculus S-antigen gene promoter region
5082	14272		2.41	3.4E-02	Q26457	SWISSPROT	LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTOANTIGEN HOMOLOG)
6108	14288	23373	1.24	3.4E-02	AJ012490.1	NT	Caenorhabditis elegans mRNA for DYS-1 protein, partial
6019	14509	23587	4.27	3.4E-02	AU23493.1	NT	Human lysyl oxidase-like protein gene, exon 3
6548	15744		4.73	3.4E-02	A1869829.1	EST_HUMAN	wf89d04.x1 NCI_CGAP_Bm26 Homo sapiens cDNA clone IMAGE:2433031 3'
							zq04f11.s1 Stratagene muscle 837209 Homo sapiens cDNA clone IMAGE:828749 3' similar to TR:G1017425 G1017425
6751	15948		6.27	3.4E-02	AA194306.1	EST_HUMAN	IPISGKPLPKVTLSDRGVPLKATMRPNTTEAENLTNLKESVTADAGRYEITANSSGTTKAFINIVLDPRG
377	9843		13.74	3.3E-02	AA398735.1	EST_HUMAN	PPT GPWISDITEESVTLKWEPPKYDGGQVNTYLLKRETSTAVWTEVSATVARTMKVMKL...;
1175	10386	19548	15.21	3.3E-02	AB035897.1	NT	z175e08.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728198 3'
1618	10828	20004	1.02	3.3E-02	AF110763.1	NT	Chetulus griseus CYP2A17 mRNA for cytochrome P450 2A17, complete cds
1712	10924		1.2	3.3E-02	AED00700.1	NT	Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds
2053	11284		2.44	3.3E-02	R09112.1	EST_HUMAN	Aquifex aeolicus section 32 of 109 of the complete genome
3337	12668	21704	0.61	3.3E-02	H02389.1	EST_HUMAN	y25c09.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:127888 5'
4158	10828	20004	1.9	3.3E-02	AF110763.1	NT	y35h02.r1 Soares placenta Nb2-IP Homo sapiens cDNA clone IMAGE:160771 5'
4463	13681	22755	2.12	3.3E-02		NT	Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds
4825	14014	23114	0.65	3.3E-02	AW275696.1	EST_HUMAN	Mus musculus tumor rejection antigen gp96 (Trt1), mRNA
5085	14285	23352	1	3.3E-02	AW500191.1	EST_HUMAN	xp40s04.x1 NCI_CGAP_HNT11 Homo sapiens cDNA clone IMAGE:2742789 3'
5843	15080	24468	15.35	3.3E-02	BF245995.1	EST_HUMAN	UI-HF-BNO-atc-g-10-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3076785 5'
5843	15080	24468	15.35	3.3E-02	BF245995.1	EST_HUMAN	601853910F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4073787 5'
7681	16980	26387	4.07	3.3E-02	BF881107.1	EST_HUMAN	601853910F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4073787 5'
							602247171F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4332497 5'

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8583	17683		1.52	3.3E-02	T98545.1	EST_HUMAN	ye49f11.1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:121101 5'
8691	17659		1.26	3.3E-02	AF289885.1	NT	Mus musculus EIF4H gene, partial cds; LIMK1 gene, complete cds; and ELN gene, partial cds
8722	17675		1.73	3.3E-02	MB1890.1	NT	Human interleukin 11 (IL11) gene, complete mRNA
128	8412	18547	2.2	3.2E-02	AJ02005.1	NT	Oryctolagus cuniculus gene encoding ileal sodium-dependent bile acid transporter
1134	10357	18508	26.12	3.2E-02	AF098275.1	NT	Drosophila melanogaster heat shock protein 68 (hsp68) gene, hsp68d allele, complete cds
1134	10357	18509	26.12	3.2E-02	AF098276.1	NT	Drosophila melanogaster heat shock protein 68 (hsp68) gene, hsp68d allele, complete cds
2089	11289		0.9	3.2E-02	P28955	SWISSPROT	LARGE TEGUMENT PROTEIN
3099	12335	21482	13.54	3.2E-02	BE887353.1	EST_HUMAN	601442431F1 NIH_MGC 65 Homo sapiens cDNA clone IMAGE:3848727 5'
3695	12815	22034	1.75	3.2E-02	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
3937	13153	22269	0.86	3.2E-02	Z74103.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL055c
3937	13153	22270	0.86	3.2E-02	Z74103.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL055c
4202	13405		18.44	3.2E-02	X94788.1	NT	H.sapiens RP3 gene (XLRP gene 3)
4778	13967	23069	3.87	3.2E-02	AF114182.1	NT	Sedifraga nidifica maturase (matK) gene, chloroplast gene encoding chloroplast protein, partial cds
4844	14033	23125	4.85	3.2E-02	AF067083.1	NT	Vitreoscilla sp. outer membrane protein homolog gene, complete cds; Trp repressor binding protein gene, partial cds; and unknown genes
5480	14688	24036	1.85	3.2E-02	X68709.1	NT	S.griseocaneum whiG-Siv gene
5480	14688	24037	1.85	3.2E-02	X68709.1	NT	S.griseocaneum whiG-Siv gene
5888	15103	24516	2.33	3.2E-02	M32437.1	NT	Rat/polyomavirus left junction in cell line W88.14
5889	15108						yd33h12.s1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:110087 3' similar to contains
5938	15154	24565	3.79	3.2E-02	T89367.1	EST_HUMAN	Alu repetitive element/contains LTR1 repetitive element;
6560	15758	25219	3.94	3.2E-02	AF173846.1	NT	Sagittaria oedipus tissue kallikrein gene, complete cds
			4.07	3.2E-02	6680565	NT	Mus musculus kinesin family member 3c (Kif3c), mRNA
7082	16269		2.68	3.2E-02	AA719795.1	EST_HUMAN	zg54b12.s1 Soares phaeal_gland_N3-HPG Homo sapiens cDNA clone IMAGE:397151 3' similar to gb108441 CYTOCHROME C OXIDASE POLYPEPTIDE III (HUMAN);
1287	10482		1.86	3.1E-02	4503416	NT	Homo sapiens dual specificity phosphatase 4 (DUSP4) mRNA
1312	10528	18688	2.11	3.1E-02	P18845	SWISSPROT	NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-3 CHAIN PRECURSOR (GF-ALPHA-3)
1957	11084	20265	0.94	3.1E-02	6871584	NT	Mus musculus adaptor-related protein complex AP-3, delta subunit (Ap3d), mRNA
5373	14602		2.56	3.1E-02	AA278478.1	EST_HUMAN	zs81a06.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:703838 5'
1600	10814		1.73	3.0E-02	AF187125.1	NT	Phyoketaines minutus cytochrome oxidase I gene, partial cds; mitochondrial gene for mitochondrial product
3541	12764	21895	1.22	3.0E-02	M94176.1	NT	Saccharomyces cerevisiae stem-loop mutation suppressor SSL2 gene, complete cds
3633	12854	21973	2.78	3.0E-02	AF247644.1	NT	Pseudomonas fluorescens family II aminotransferase gene, complete cds
3726	12845		0.92	3.0E-02	AW820223.1	EST_HUMAN	QV2-ST0288-150200-040-e09 ST0288 Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3824	13140		0.89	3.0E-02	AA384003.1	EST_HUMAN	EST74530 Pituitary gland II Homo sapiens cDNA 5' end
4701	13892		38.75	3.0E-02	A1240487.1	EST_HUMAN	q10g08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1844314 3'
5083	14283	23348	7.54	3.0E-02	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
5083	14283	23349	7.54	3.0E-02	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
5383	14822		3.03	3.0E-02	AB046783.1	NT	Homo sapiens mRNA for KIAA1573 protein, partial cds
5883	15278	24708	3.37	3.0E-02	AJ242808.1	NT	Cyprinus carpio mRNA for inducible nitric oxide synthase (NOS gene)
6044	15212	24831	3.32	3.0E-02	BE888848.1	EST_HUMAN	601512208F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913848 5'
6044	15212	24832	3.32	3.0E-02	BE888848.1	EST_HUMAN	601512208F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913848 5'
6114	15208	24827	1.85	3.0E-02	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
6114	15208	24828	1.85	3.0E-02	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
7203	18380	25881	2.8	3.0E-02	AE001797.1	NT	Thermotoga maritima section 109 of 136 of the complete genome
7784	18879	26492	3.51	3.0E-02	M81357.1	NT	Human coagulation factor VII (F7) gene exon 1 and factor X (F10) gene, exon 1
8187	17319	26862	9.3	3.0E-02	AA483216.1	EST_HUMAN	ne87f04.s1 NCI CGAP_Kd1 Homo sapiens cDNA clone IMAGE:911283
8873	18351	23807	1.99	3.0E-02	R32019.1	EST_HUMAN	yf63d04.s1 Soares placenta NB2HP Homo sapiens cDNA clone IMAGE:134407 3'
8044	17885		7.15	3.0E-02	AW885565.1	EST_HUMAN	QV4-NN0038-270400-187-H05 NN0038 Homo sapiens cDNA
9085	18345		3.1	3.0E-02	AF048887.1	NT	Rattus norvegicus UDP-Gal:glucosylceramide beta-1,4-galactosyltransferase mRNA, complete cds
2949	12187	21320	0.92	2.9E-02	BE565844.1	EST_HUMAN	601338428F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3680695 5'
2949	12187	21321	0.92	2.9E-02	BE565844.1	EST_HUMAN	601338428F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3680695 5'
3903	13119	22237	0.78	2.9E-02	H72805.1	EST_HUMAN	yf07e10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:233130 5'
6782	15000	24403	6.95	2.9E-02	BF032233.1	EST_HUMAN	601452681F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3858598 5'
8184	15386	24808	10.82	2.9E-02	BE271437.1	EST_HUMAN	601140728F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3049830 5'
572	8622		0.7	2.8E-02	AW970153.1	EST_HUMAN	EST382234 MAGE resequences, MAGK Homo sapiens cDNA
3345	12573	21712	1.21	2.8E-02	AF068063.1	NT	Homo sapiens retinal fasciclin (FSCN2) gene, exon 2
3345	12573	21713	1.21	2.8E-02	AF068063.1	NT	Homo sapiens retinal fasciclin (FSCN2) gene, exon 2
6435	14682	23815	11.9	2.8E-02	BE741083.1	EST_HUMAN	601594078F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948087 5'
8977	17846		1.33	2.8E-02	X06322.1	NT	Yeast CN31C chromosome III RAHS DNA (right arm transcription hot-spot)
3410	12838	21767	2.05	2.7E-02	AL161494.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 6
4184	13388	22488	1.81	2.7E-02	N47258.1	EST_HUMAN	yf68h12.r1 Soares multiple sclerosis 2NBHMSHP Homo sapiens cDNA clone IMAGE:280487 5'
4184	13388	22487	1.81	2.7E-02	N47258.1	EST_HUMAN	yf68h12.r1 Soares multiple sclerosis 2NBHMSHP Homo sapiens cDNA clone IMAGE:280487 5'
6112	15208	24825	1.84	2.7E-02	AA933571.1	EST_HUMAN	cd68h03.s1 Soares total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1624681 3'
578	9827	18948	0.81	2.6E-02	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2334	11527	20748	2.34	2.0E-02	AA480021.1	EST_HUMAN	ab02b02.s1 Stragene fetal retina 837202 Homo sapiens cDNA clone IMAGE:839595 3'
2336	11529	20750	2.19	2.0E-02	6754241	NT	Mus musculus histidine rich calcium binding protein (Hic), mRNA
2336	11529	20751	2.19	2.0E-02	6754241	NT	Mus musculus histidine rich calcium binding protein (Hic), mRNA
2898	12104		1.22	2.0E-02	AF109808.1	NT	Mus musculus MHC class III region RD gene, partial cds; Bf, C2, G9A, NG22, G9, HSP70, HSP70, HSC70, end snRNP genes, complete cds; G7A gene, partial cds; and unknown genes
3917	13133		10.04	2.0E-02	AA071307.1	EST_HUMAN	zm73109.s1 Stragene neuroepithelium (8837231) Homo sapiens cDNA clone IMAGE:531305 3'
4278	13481		1.53	2.0E-02	Y07848.1	NT	Homo sapiens EWS, gar22, rrp22 and bam22 genes
4028	14114	23209	3.97	2.0E-02	L12032.1	NT	Chicken dorsalin-1 mRNA, complete cds
5098	14278	23382	1.62	2.0E-02	AE002014.1	NT	Deinococcus radiodurans R1 section 151 of 229 of the complete chromosome 1
5124	14303	23392	1.87	2.0E-02	AW241154.1	EST_HUMAN	xa52b04.x1 NCI_CGAP_Sar4 Homo sapiens cDNA clone IMAGE:2570383 3' similar to SW:Y0689_HUMAN Q15041 HYPOTHETICAL PROTEIN KIAA00689 ;
5278	14449	23522	0.63	2.0E-02	AE000825.1	NT	Methanobacterium thermoautotrophicum from bases 340940 to 352162 (section 31 of 148) of the complete genome
5789	14978		6.88	2.0E-02	AI206030.1	EST_HUMAN	gg27f11.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1762317 3'
5839	15056	24463	2.12	2.0E-02	BE621748.1	EST_HUMAN	601483473T1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3885578 3'
6047	15215	24635	6.57	2.0E-02	6881271	NT	Rattus norvegicus Nerve growth factor receptor, fast (Ngfr), mRNA
7828	17139		2.09	2.0E-02	AA278351.1	EST_HUMAN	zs84c02.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:704162 5'
8067	17231	26770	1.76	2.0E-02	AW500547.1	EST_HUMAN	UI-HF-BN0-ak-e-10-0-ULr1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077488 5'
8585	18338	23804	1.41	2.0E-02	BF343827.1	EST_HUMAN	602015501F1 NCI_CGAP_Bm84 Homo sapiens cDNA clone IMAGE:4160844 5'
838	9789	18912	1.81	2.0E-02	AI783130.1	EST_HUMAN	on28f08.y6 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1557827 5'
538	9789	18913	1.81	2.0E-02	AI783130.1	EST_HUMAN	on28f08.y6 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1557827 5'
818	10057	19210	20.77	2.0E-02	BE974314.1	EST_HUMAN	6016880305R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950965 3'
878	10115	19277	6.14	2.0E-02	BE974314.1	EST_HUMAN	6016880305R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950965 3'
2718	11897		2.78	2.0E-02	U12571.1	NT	Rattus norvegicus rabphilin-3A mRNA, complete cds
2808	12147	21281	3.33	2.0E-02	X99697.1	NT	H. carterae mRNA for fucosanthin chlorophyll a/c binding protein, Fcp1.
2808	12147	21282	3.33	2.0E-02	X99697.1	NT	H. carterae mRNA for fucosanthin chlorophyll a/c binding protein, Fcp1
4022	14469	22337	0.86	2.0E-02	BE701165.1	EST_HUMAN	PM2-NN0128-080700-001-at12 NN0128 Homo sapiens cDNA
4022	14469	22338	0.86	2.0E-02	BE701165.1	EST_HUMAN	PM2-NN0128-080700-001-at12 NN0128 Homo sapiens cDNA
4188	13382	22490	5.88	2.0E-02	AW592114.1	EST_HUMAN	hf38f08.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2834015 3'
5751	14970		4.58	2.0E-02	BE870128.1	EST_HUMAN	7e30c08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284008 3' similar to contains L1.1 L1 repetitive element ;
5758	14975		4.28	2.0E-02	BE748888.1	EST_HUMAN	601579393F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3928054 5'
7387	16801	26089	2.37	2.0E-02	Q10335	SWISSPROT	HYPOTHETICAL 48.7 KD PROTEIN C19G10.05 IN CHROMOSOME I
7387	16801	26090	2.37	2.0E-02	Q10335	SWISSPROT	HYPOTHETICAL 48.7 KD PROTEIN C19G10.05 IN CHROMOSOME I

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Table 4
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7458	16688		4.1	2.5E-02	AF050157.1	NT	Mus musculus major histocompatibility locus class II region: major histocompatibility protein class II alpha chain (IAspha) and major histocompatibility protein class II beta chain (IEbeta) genes, complete cds; butyrophilin-like (NG9), butyrophilin-like
8238	17367		2.11	2.5E-02	AB007548.1	NT	Homo sapiens gene for LEGT2, complete cds
8552	18271		1.92	2.5E-02	11420078	NT	Homo sapiens similar to ALEX3 protein (H. sapiens) (LOC836334), mRNA
8747	18138		2.01	2.5E-02	11433220	NT	Homo sapiens mitogen-activated protein kinase kinase 13 (MAP3K13), mRNA
8842	17751		1.28	2.5E-02	U60189.1	NT	Dichytetium discoideum putative protein kinase Mica (mka) gene, complete cds
8869	17768	23939	1.38	2.5E-02	BE973327.1	EST_HUMAN	901852365R2 NIH_MGC_B2 Homo sapiens cDNA clone IMAGE:3835513 3'
177	9457	18580	0.82	2.4E-02	A1378582.1	EST_HUMAN	lc72c07.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:2070158 3'
1578	10791	18987	1.78	2.4E-02	H65884.1	EST_HUMAN	y76f11.1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:211149 5'
2011	12008	20423	1.44	2.4E-02	P01901	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
2011	12008	20424	1.44	2.4E-02	P01901	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
4382	13364	22659	1.72	2.4E-02	J05110.1	NT	T. thermophila calcium-binding 25 kDa (TCBP 25) protein mRNA, complete cds
4521	13717	22811	1.22	2.4E-02	P01901	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
4521	13717	22812	1.22	2.4E-02	P01901	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
5204	14378		1.01	2.4E-02	AL181595.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 91
6288	14457		0.83	2.4E-02	U18486.1	NT	African swine fever virus, complete genome
6630	15828	25288	17.19	2.4E-02	N69442.1	EST_HUMAN	2a35g11.1.s1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:284598 3' similar to gb K02809 RATSR7K Rat (RNA); contains A3R.b1 A3R repetitive element;
7014	18191	25895	3.55	2.4E-02	AV692854.1	EST_HUMAN	AV692854 GKC Homo sapiens cDNA clone GKDCSC03 5'
7067	18244	25719	4.02	2.4E-02	AA483894.1	EST_HUMAN	rh07b12.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943583 similar to contains Alu repetitive element; contains element PTR5 repetitive element;
8106	17240	26778	2.22	2.4E-02	AF108905.1	NT	Mus musculus major histocompatibility locus class III regions Hec701 gene, partial cds; smRNP, G7A, NG23, Mus homolog, CLCP, NG24, NG25, and NG28 genes, complete cds; and unknown genes
8106	17240	26779	2.22	2.4E-02	AF108905.1	NT	Mus musculus major histocompatibility locus class III regions Hec701 gene, partial cds; smRNP, G7A, NG23, Mus homolog, CLCP, NG24, NG25, and NG28 genes, complete cds; and unknown genes
8341	17438		1.8	2.4E-02	9827909	NT	Bacteriophage bil87, complete genome
8495	17538	24028	2.68	2.4E-02	6753635	NT	Mus musculus DinB homolog 1 (E. coli) (Dinb1), mRNA
8554	17576	23895	1.58	2.4E-02	BE928869.1	EST_HUMAN	MRO-FT0175-310800-202-808 FT0175 Homo sapiens cDNA
8611	17608	23983	1.27	2.4E-02	U78167.1	NT	Rattus norvegicus cAMP-regulated guanine nucleotide exchange factor 1 (cAMP-GEF1) mRNA, complete cds

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8811	17808	24007	1.27	2.4E-02	U78167.1	NT	Rattus norvegicus cAMP-regulated guanine nucleotide exchange factor 1 (cAMP-GEF1) mRNA, complete cds
8783	17720		6.39	2.4E-02	AB008569.1	NT	Caenorhabditis elegans mRNA for iron-sulfur subunit of mitochondrial succinate dehydrogenase, complete cds
8820	17737		1.23	2.4E-02	N42880.1	EST_HUMAN	Y08a08.r1 Soares melanocyte 2NbhM Homo sapiens cDNA clone IMAGE:270810 5'
8828	17740		1.35	2.4E-02	BF878477.1	EST_HUMAN	602153281F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4284173 5'
8282	18378		1.22	2.4E-02	S58844.1	NT	Integrin beta 5 subunit [rat, NRK cells, mRNA Partial, 603 nt]
1838	11046		6.31	2.3E-02	W05340.1	EST_HUMAN	z884g08.r1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:289284 5'
1852	11056		6.86	2.3E-02	U94165.1	NT	4 Homo sapiens mammary tumor-associated protein INT6 (INT6) gene, exon 4
1977	11180	20388	1.04	2.3E-02	AW787955.1	EST_HUMAN	CM2-UM0038-290400-172-b11 UM0038 Homo sapiens cDNA
2319	11512	20733	2.93	2.3E-02	Z74263.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL245c
3682	12883	22004	7.23	2.3E-02	Z20377.1	EST_HUMAN	HSAAACADH P, Human foetal Brain Whole tissue Homo sapiens cDNA
3698	12816		0.64	2.3E-02	L23426.1	NT	Canis beta-galactosidase-binding lectin (LGALS3) mRNA, 3'end
4131	13337	22438	0.87	2.3E-02	L24789.1	NT	Gallus gallus connexin 45.6 (Cx45.6) gene, complete cds
4131	13337	22437	0.87	2.3E-02	L24789.1	NT	Gallus gallus connexin 45.6 (Cx45.6) gene, complete cds
4412	13612	22708	1.19	2.3E-02	AW889107.1	EST_HUMAN	CM4-NN0080-280400-160-b04 NN0080 Homo sapiens cDNA
4443	13843	22735	1.17	2.3E-02	BE835225.1	EST_HUMAN	CM3-MT0118-010900-318-g07 MT0118 Homo sapiens cDNA
4443	13843	22736	1.17	2.3E-02	BE835225.1	EST_HUMAN	CM3-MT0118-010900-318-g07 MT0118 Homo sapiens cDNA
4444	14470	22737	1.01	2.3E-02	AW583683.1	EST_HUMAN	xa25408.xt NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2770671 3'
4444	14470	22738	1.01	2.3E-02	AW583683.1	EST_HUMAN	xa25408.xt NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2770671 3'
4584	13788	22860	2.54	2.3E-02	BF028487.1	EST_HUMAN	601672279F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3855388 5'
4584	13788	22861	2.54	2.3E-02	BF028487.1	EST_HUMAN	601672279F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3855388 5'
5043	14227		1.06	2.3E-02	7882173	NT	Homo sapiens KIAA0547 gene product (KIAA0547), mRNA
5183	14359	23444	0.65	2.3E-02	AF257110.1	NT	Rattus norvegicus guanine nucleotide binding protein gamma subunit 11 mRNA, complete cds
5183	14359	23445	0.65	2.3E-02	AF257110.1	NT	Rattus norvegicus guanine nucleotide binding protein gamma subunit 11 mRNA, complete cds
5183	14369	23456	0.62	2.3E-02	AE000775.1	NT	Aquifex acidicus section 107 of 108 of the complete genome
5383	14612	23725	3.67	2.3E-02	U86303.1	NT	Caulobacter crescentus topoisomerase IV ParE subunit (parE) gene, complete cds, and propionyl-CoA carboxylase beta chain (pccB) homolog gene, partial cds
5842	15158	24570	4.97	2.3E-02	AL161505.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 17
6419	15816	25079	6.05	2.3E-02	U83610.1	NT	Human plectin (PLEC1) gene, exons 3-32, and complete cds
7085	16262	25739	2.2	2.3E-02	AE000199.1	NT	Escherichia coli K-12 MG1655 section 89 of 400 of the complete genome
7085	16262	25740	2.2	2.3E-02	AE000199.1	NT	Escherichia coli K-12 MG1655 section 89 of 400 of the complete genome
7363	16578	26070	2.17	2.3E-02	P08640	SWISSPROT	GLUCOAMYLASE S1/S2 PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8468	18123		5.78	2.3E-02	BE278331.1	EST_HUMAN	601178958F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3546567 5'
8014	17668	23890	2.12	2.3E-02	U39394.1	NT	Streptomyces sp. alpha-1,3/4-fucosidase precursor gene, complete cds
8072	18378		1.87	2.3E-02	U11077.1	NT	Dicystostellum discoideum extracellular signal-regulated protein kinase (ERK1) mRNA, complete cds
745	9886	19129	3.5	2.2E-02	AF018287.1	NT	Columbia lilla nucleoside diphosphate kinase (NDPK) gene, nuclear gene encoding mitochondrial protein, complete cds
1719	10831		1.51	2.2E-02	4557448	NT	Homo sapiens chromodomain helicase DNA binding protein 2 (CHD2) mRNA
1882	11185	20394	1.57	2.2E-02	Z82001.1	NT	S.pneumoniae pcpA gene and open reading frames
2885	12024	21079	1.84	2.2E-02	AF109633.1	NT	Mus musculus ets variant protein ERB1 gene, exons 1 through 4
3413	12839		1.8	2.2E-02	AA577785.1	EST_HUMAN	nm24e04.s1 NCI_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1084782 3'
3825	12848		3.43	2.2E-02	AF083094.1	NT	Infectious bursal disease virus segment B strain IL4 VP1 gene, complete cds
3896	13112	22230	0.63	2.2E-02	Z74283.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL245c
5089	14279	23363	1.85	2.2E-02	Z73587.1	NT	S.cerevisiae chromosome XVI reading frame ORF YPL241c
6183	15365	24805	3.57	2.2E-02	AV689721.1	EST_HUMAN	AV689721 GRB1 Homo sapiens cDNA clone GKBAND03 3'
7758	18654	26462	1.7	2.2E-02	BE797601.1	EST_HUMAN	6011684308F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3838571 5'
8750	17683		2.84	2.2E-02	AA503553.1	EST_HUMAN	ne47h07.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:900541 3' similar to contains Alu repetitive element
426	9878		5.24	2.1E-02	AV761502.1	EST_HUMAN	AV761502 MDS Homo sapiens cDNA clone MDSADG01 5'
455	9708		8.19	2.1E-02	AF028726.1	NT	Dicystostellum discoideum histidine kinase C (dhkC) mRNA, complete cds
1270	10485	19844	8.21	2.1E-02	U72073.1	NT	Bacillus subtilis cotKLM cluster, CotK (cotK), and spore coat protein CotM (cotM) genes, complete cds
1752	10884	20147	0.89	2.1E-02	P02438	SWISSPROT	KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A
1752	10884	20148	0.89	2.1E-02	P02438	SWISSPROT	KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A
1752	10884	20149	0.89	2.1E-02	P02438	SWISSPROT	KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A
2768	10028	19177	3.47	2.1E-02	N28288.1	EST_HUMAN	yx43h07.r1 Soares melanocyte 2NBHM Homo sapiens cDNA clone IMAGE:284541 5'
3500	12783	21912	1.05	2.1E-02	AA461271.1	EST_HUMAN	zx63b09.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:798121 5'
4113	13320	22420	0.84	2.1E-02	Z74283.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL245c
4287	13488	22664	0.77	2.1E-02	BF343655.1	EST_HUMAN	602015308F1 NCI_CGAP_Brm84 Homo sapiens cDNA clone IMAGE:4151161 5'
4437	13637	22730	1.78	2.1E-02	U44914.1	NT	Borrelia burgdorferi plesmid cp32-2, erpC and erpD genes, complete cds; and unknown genes
4449	13848	22744	1.73	2.1E-02	A1768127.1	EST_HUMAN	wg81d11.x1 Soares_NSIF_F8_8W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2371609 3'
4487	13895		0.63	2.1E-02	Y19213.1	NT	Homo sapiens putative psihHbA pseudogene for hair keratin, exons 2 to 7
4881	13895		1.31	2.1E-02	Y19213.1	NT	Homo sapiens putative psihHbA pseudogene for hair keratin, exons 2 to 7
4720	13911	23013	5.72	2.1E-02	Y08501.1	NT	A.thaliana mitochondrial genome, part A
4741	13922	23036	0.63	2.1E-02	AA685737.1	EST_HUMAN	ag55g12.s1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1128918 3'

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Table 4
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4834	14023	23117	0.62	2.1E-02	AB23432.1	EST_HUMAN	wh54a05.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2384528 3'
8731	13885		8.84	2.1E-02	Y18213.1	NT	Homo sapiens putative psih1ba pseudogene for hair keratin, exons 2 to 7
9173	17968	23858	3.85	2.1E-02	AF183913.1	NT	Azospirillum brasilense major outer membrane protein OmaA precursor (omaA) gene, complete cds
8286	18044		2.69	2.1E-02	BF083512.1	EST_HUMAN	CM1-TN0141-140800-407-h08 TN0141 Homo sapiens cDNA
18	9314	18418	0.85	2.0E-02	BF002832.1	EST_HUMAN	7q51c08.x1 NCI_CGAP_P728 Homo sapiens cDNA clone IMAGE:3308988 3' similar to contains MER1.13 MER1 repetitive element;
19	9315	18417	0.16	2.0E-02	AW895565.1	EST_HUMAN	QV4-NN0038-270400-187-h05 NN0038 Homo sapiens cDNA
263	9539	18688	2.89	2.0E-02	6753635	NT	Mus musculus DinB homolog 1 (E. coli) (Dinb1), mRNA
300	9573	18706	2.69	2.0E-02	AA456538.1	EST_HUMAN	aa15b10.r1 Soares_NihMPu_S1 Homo sapiens cDNA clone IMAGE:813307 5'
808	10047	19198	2.09	2.0E-02	6753635	NT	Mus musculus DinB homolog 1 (E. coli) (Dinb1), mRNA
1095	10319	18471	0.86	2.0E-02	AL098805.1	NT	Homo sapiens genomic region containing hypervariable minisatellites chromosome 1(1p36.33) of Homo sapiens
1207	10428	19592	1.71	2.0E-02	8922391	NT	Homo sapiens hypothetical protein FLJ10378 (FLJ10378), mRNA
1207	10428	19593	1.71	2.0E-02	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
1839	11047	20236	1.83	2.0E-02	8922453	NT	Homo sapiens hypothetical protein FLJ10488 (FLJ10488), mRNA
1839	11047	20237	1.83	2.0E-02	8922453	NT	Homo sapiens hypothetical protein FLJ10486 (FLJ10486), mRNA
2761	11830		1.84	2.0E-02	AL161532.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
3044	9314	18418	1.58	2.0E-02	BF002832.1	EST_HUMAN	7q51c08.x1 NCI_CGAP_P728 Homo sapiens cDNA clone IMAGE:3308988 3' similar to contains MER1.13 MER1 repetitive element;
3108	12344		2.29	2.0E-02	7305474	NT	Mus musculus sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 68 (Sema6b), mRNA
3183	12428		1.87	2.0E-02	AF095586.1	NT	Arabidopsis thaliana C2H2 zinc finger protein FZF mRNA, complete cds
3883	13187	22305	1.53	2.0E-02	M18095.1	NT	P. vulgaris hydroxyproline-rich glycoprotein (HRGP) mRNA, 3' end
7031	16208		2.37	2.0E-02	U70408.1	NT	Japanese encephalitis virus envelope protein mRNA, partial cds
7236	16457	25945	2.06	2.0E-02	Z73968.1	NT	Mycobacterium tuberculosis H37Rv complete genome; segment 93/182
7611	17126	26856	3.17	2.0E-02	D88184.1	NT	Equus caballus DNA for 17alpha-hydroxylase/17,20-lyase, complete cds
8281	14502	23587	1.4	2.0E-02	AA456538.1	EST_HUMAN	aa15b10.r1 Soares_NihMPu_S1 Homo sapiens cDNA clone IMAGE:813307 5'
8769	11830		1.55	2.0E-02	AL161532.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
9247	18146		1.53	2.0E-02	BE786595.1	EST_HUMAN	601478819F1 NIH_MGC_98 Homo sapiens cDNA clone IMAGE:3881477 5'
9264	18022		5.01	2.0E-02	T80037.1	EST_HUMAN	yd04c08.r1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:24875 5'
700	8942	19076	2.49	1.9E-02	AA572764.1	EST_HUMAN	nf19a07.s1 NCI_CGAP_P71 Homo sapiens cDNA clone IMAGE:814188 similar to contains L1.1 L1 repetitive element;
2008	11208	20418	2.75	1.9E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103

Table 4

Single Exon Probes Expressed In HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2006	11208	20419	2.75	1.9E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2471	11662	20882	1.22	1.9E-02	AL161550.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 50
2857	12095	21224	8.45	1.9E-02	AA713858.1	EST_HUMAN	hw04f05.s1 NCI CGAP_SS1 Homo sapiens cDNA clone IMAGE:1238337 3'
2805	12143	21279	1.71	1.9E-02	AV648989.1	EST_HUMAN	AV648989 GLC Homo sapiens cDNA clone GLCBLH07 3'
3226	12460		0.63	1.9E-02	AB033811.1	NT	Utricularia lapidacea mitochondrial gene for cytochrome b, complete cds
3589	12610		1.06	1.9E-02	N52250.1	EST_HUMAN	yz28b02.s1 Soares multiple sclerosis 2NblMSP Homo sapiens cDNA clone IMAGE:284331 3'
3683	12904		8.88	1.9E-02	BE738088.1	EST_HUMAN	601672682F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839564 5'
4024	13235	22340	1.34	1.9E-02	AF141840.1	NT	Mycoplasma imitans VihA1 precursor (vihA1) and VihA2 precursor (vihA2) genes, partial cds
4175	13379	22479	1.56	1.9E-02	P09081	SWISSPROT	HOMEOTIC BICOID PROTEIN (PRD-4)
4175	13379	22480	1.56	1.9E-02	P09081	SWISSPROT	HOMEOTIC BICOID PROTEIN (PRD-4)
4538	13733	22831	3.05	1.9E-02	AI452999.1	EST_HUMAN	U48404.x1 Soares NSF_F8_gw_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2144551 3' similar to contains Alu repetitive element
5037	11662	20882	5.49	1.9E-02	AL161550.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 50
8505	18128	23813	3.08	1.9E-02	AF101085.1	NT	Hirudo medicinalis intermediate filament glierin mRNA, complete cds
9203	17988	23882	1.48	1.9E-02	X68271.1	NT	H. sapiens MUC18 gene exon 18
351	9619	18746	1.42	1.9E-02	AW771104.1	EST_HUMAN	hns2c06.x1 NCI CGAP_Co17 Homo sapiens cDNA clone IMAGE:3027274 3' similar to contains element
892	9935	19085	0.65	1.9E-02	BF308122.1	EST_HUMAN	MER29 repetitive element
1168	10389	19541	1.27	1.9E-02	X17684.1	NT	601894328F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139983 5'
2838	11821	21037	1	1.9E-02	AE004544.1	NT	H.francisci mRNA for myelin basic protein (MBP)
3177	12412		0.78	1.9E-02	AI805829.1	EST_HUMAN	Pseudomonas aeruginosa PAO1, section 105 of 529 of the complete genome
3668	13082	22198	1.11	1.9E-02	AW878122.1	EST_HUMAN	ts52a09.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2080288 3'
3696	13082	22198	1.11	1.9E-02	AW878122.1	EST_HUMAN	MR1-OT0011-280300-008-g04 OT0011 Homo sapiens cDNA
4062	13273		1.4	1.9E-02	AA881446.1	EST_HUMAN	MR1-OT0011-280300-008-g04 OT0011 Homo sapiens cDNA
4422	13622	22717	1.36	1.9E-02	AW638363.1	EST_HUMAN	ak24h04.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1406835 3'
4975	14182	23253	1.18	1.9E-02	O60810	SWISSPROT	QV4-DT0021-301289-071-b11 DT0021 Homo sapiens cDNA
6001	16283	24716	4.21	1.9E-02	P14310	SWISSPROT	HYPOTHETICAL PROTEIN DJ845024.2
7974	16409	25894	1.97	1.9E-02	AB002337.2	NT	HYPOTHETICAL 7.8 KD PROTEIN IN FIXW 5 REGION
7974	16409	25895	1.87	1.9E-02	AB002337.2	NT	Homo sapiens mRNA for KIAA0339 protein, partial cds
8136	17289	26814	1.92	1.9E-02	AP000008.1	NT	Homo sapiens mRNA for KIAA0339 protein, partial cds
8145	17277	26821	3.39	1.9E-02	U62749.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1168001-1485000 nt position (877)
9230	18102		1.25	1.9E-02	AF047475.1	NT	Zea mays acidic ribosomal protein P2a-3 (pp2a-3) mRNA, partial cds
918	10151	18311	1.51	1.7E-02	BE384869.1	EST_HUMAN	Drosophila melanogaster projectin (projectin) gene, partial cds
							601310626F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3832160 5'

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1760	10971	20157	2.19	1.7E-02	AW573183.1	EST_HUMAN	h34a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2833740 3' similar to contains L1.L1 L1 repetitive element;
1760	10971	20158	2.19	1.7E-02	AW573183.1	EST_HUMAN	h34a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2833740 3' similar to contains L1.L1 L1 repetitive element;
1837	11045		3.2	1.7E-02	AL163204.2	NT	L1.L1 L1 repetitive element;
2083	11283		12.09	1.7E-02	AB004816.1	NT	Homo sapiens chromosome 21 segment HS21C004
2604	11788		1.15	1.7E-02	7657495	NT	Oryctolagus cuniculus mRNA for mitugumih29, complete cds
2655	12183	21328	1	1.7E-02	AI147815.1	EST_HUMAN	Homo sapiens putative Rab5 GDP/GTP exchange factor homologue (RABEX5), mRNA
3488	12710		4.88	1.7E-02	AW927368.1	EST_HUMAN	qb22a08.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:1898982 3'
3603	12824		0.6	1.7E-02	P04929	SWISSPROT	hnm45a04.x1 NCI_CGAP_RDF1 Homo sapiens cDNA clone IMAGE:3015534 3' similar to contains MER19.b1 MER19 repetitive element;
4151	13357		1.17	1.7E-02	AA689618.1	EST_HUMAN	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
4182	13386		2.03	1.7E-02	R02508.1	EST_HUMAN	ac1904.s1 Stragene ovary (#37217) Homo sapiens cDNA clone IMAGE:858927 3' similar to contains Alu repetitive element; contains element MER24 repetitive element;
4448	13647	22743	0.85	1.7E-02	AI305278.1	EST_HUMAN	ye86f08.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:124647 5'
4725	13918	23017	1.88	1.7E-02	V00841.1	NT	qim08g07.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1881276 3' similar to gb:X52359 ZINC FINGER PROTEIN 30 (HUMAN);
4828	14017		0.58	1.7E-02	AI015078.1	EST_HUMAN	Messenger RNA for anglerfish (Lophius americanus) conotostatin II
5100	14280	23364	0.87	1.7E-02	6981289	NT	ov51e02.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1840858 3'
5721	14639	24335	1.85	1.7E-02	AI768247.1	EST_HUMAN	Rattus norvegicus N-arginine diase convertase 1 (Nrd1), mRNA
5917	15134	24543	1.76	1.7E-02	AI038280.1	EST_HUMAN	wg35f08.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2367113 3' similar to contains Alu repetitive element;
6168	16350	24788	2.17	1.7E-02	8400716	NT	cy65h03.x1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1872681 3'
6394	15574		1.83	1.7E-02	AJ010770.1	NT	Homo sapiens nebulin (NEB), mRNA
6987	18303	23690	2.28	1.7E-02	AW903482.1	EST_HUMAN	Homo sapiens hyperion gene, exons 1-50
9177	17970		1.48	1.7E-02	Q03211	SWISSPROT	GM4-NN1030-040400-130-008 NN1030 Homo sapiens cDNA
517	8708		1.98	1.6E-02	AL021929.1	NT	PISTIL-SPECIFIC EXTENSIN-LIKE PROTEIN PRECURSOR (PELP)
2213	11410	20633	1.09	1.6E-02	Q84178	SWISSPROT	Mycobacterium tuberculosis H37Rv complete genome, segment 13/182
2213	11410	20634	1.09	1.6E-02	Q84178	SWISSPROT	LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
2631	11719	20938	1	1.6E-02	AJ008345.1	NT	LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
2608	11790	21010	0.98	1.6E-02	AA484872.1	EST_HUMAN	Homo sapiens KVLQ11 gene
2654	11837		0.93	1.6E-02	AB014534.1	NT	ne81d08.s1 NCI_CGAP_Ew1 Homo sapiens cDNA clone IMAGE:910687
2681	12218	21353	0.83	1.6E-02	AF112282.1	NT	Homo sapiens mRNA for KIAA0834 protein, partial cds
							Lasaea sp. isolate lBd cytochrome oxidase III gene, partial cds; mitochondrial gene for mitochondrial product

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Table 4
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3499	12723	21859	5.65	1.6E-02	AW850652.1	EST_HUMAN	IL3-CT0219-160200-063-C07 CT0219 Homo sapiens cDNA
3832	13049	22169	1.23	1.6E-02	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
4166	13362		1.49	1.6E-02	AF110520.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG29, KIFC1, Fas-binding protein, BING1, tapasin, RalGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Secm21 gene, partial>
5157	14338		0.68	1.6E-02	N80156.1	EST_HUMAN	z865e07.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:287444 3'
5952	15168	24581	2.2	1.6E-02	AB015281.1	NT	Candida albicans CaGCR3 gene, complete cds
6520	15718		2.8	1.6E-02	X05151.1	NT	Human apoC-II gene for preproapolipoprotein C-II
7087	16284		3.13	1.6E-02	AF079784.1	NT	Drosophila melanogaster enhancer of polycomb (E(Pc)) mRNA, complete cds
7483	18079	26173	2.46	1.6E-02	Z94828.1	NT	G.gallus microsatellite DNA (LEI0260 (=T18IIIIE11))
7785	18881	28471	2.87	1.6E-02	AL161508.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20
7785	18881	28472	2.87	1.6E-02	AL161508.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20
8044	17180	26719	2.23	1.6E-02	A137358.1	EST_HUMAN	qz86e10.x1 Soares_pregnant_uterus_NH/PU Homo sapiens cDNA clone IMAGE:2042442 3'
8478	11410	20633	1.65	1.6E-02	Q64178	SWISSPROT	LIVER CARBOXYLESTERASE 22 PRECURSOR (EQASYN) (ESTERASE-22)
8478	11410	20634	1.65	1.6E-02	Q64178	SWISSPROT	LIVER CARBOXYLESTERASE 22 PRECURSOR (EQASYN) (ESTERASE-22)
8865	17766		1.54	1.6E-02	X92751.1	NT	R.norvegicus gene for choline acetyltransferase, exon 1 (non coding)
759	10000		78.83	1.6E-02	8823734	NT	Homo sapiens transcription factor (HSA130894), mRNA
2110	11309	20522	3.85	1.5E-02	N39521.1	EST_HUMAN	YW27b07.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:243925 3'
2141	11339	20557	1.25	1.5E-02	AL161694.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 80
3705	12825	22044	1.13	1.5E-02	BF082842.1	EST_HUMAN	MR4-TN0115-080800-201-b12 TN0115 Homo sapiens cDNA
4123	13328	22427	0.6	1.5E-02	AA160987.1	EST_HUMAN	zq40g10.r1 Stratagene hNT neuron (#837233) Homo sapiens cDNA clone IMAGE:632228 5'
6217	15388		1.63	1.5E-02	11467282	NT	Cyanophora paradoxa cyanelle, complete genome
6421	15818	25082	5.18	1.5E-02	11417739	NT	Homo sapiens velyl-RNA synthetase 2 (VARS2), mRNA
7727	16925	28435	2.59	1.5E-02	L40609.1	NT	Plasmodium falciparum (strain FCR3) variant-specific surface protein (var-2, var-3) genes, complete cds's
8710	18170		1.65	1.5E-02	AW750834.1	EST_HUMAN	RC4-CN0049-140100-011-g11 CN0049 Homo sapiens cDNA
423	8878		1.48	1.4E-02	AE002230.2	NT	Chlamydomonas reinhardtii AR39, section 58 of 94 of the complete genome
1128	10350	18501	3.57	1.4E-02	7705980	NT	Homo sapiens NESH protein (LOC51228), mRNA
1283	10478		0.8	1.4E-02	U32800.1	NT	Haemophilus influenzae Rd section 115 of 183 of the complete genome
1305	10521		3.25	1.4E-02	U67779.1	NT	Xenopus laevis neurogenin related 1b (X-NGNR-1b) mRNA, complete cds
3179	12414	21548	1.79	1.4E-02	AF160969.2	NT	Bifidobacterium longum Na+/H+ antiporter (nhaB), cytosine deaminase, and alpha-galactosidase (eglL) genes, complete cds; and N-acetylglucosaminylase repressor protein (nagCxyR) gene, partial cds
3378	12804	21739	0.96	1.4E-02	AW074212.1	EST_HUMAN	xb08409.x1 NCJ_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2575783 3'

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3450	12684	21818	6.64	1.4E-02	AL161586.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 82
3459	12684	21819	6.64	1.4E-02	AL161586.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 82
3493	12717	21853	0.59	1.4E-02	4503628	NT	Homo sapiens coagulation factor XII (Hageman factor) (F12), mRNA
3636	12857	21976	7.91	1.4E-02	6986918	NT	Mus musculus histocompatibility 2, complement component factor B (H2-B), mRNA
4486	13684	22774	8.97	1.4E-02	AW982688.1	EST_HUMAN	EST374781 MAGE resequences, MAGG Homo sapiens cDNA
4486	13684	22775	8.97	1.4E-02	AW982688.1	EST_HUMAN	EST374781 MAGE resequences, MAGG Homo sapiens cDNA
4695	13859	22958	0.98	1.4E-02	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
4695	13859	22959	0.98	1.4E-02	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
4893	14081	23174	7.33	1.4E-02	BE733142.1	EST_HUMAN	601567403F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842280 5'
4893	14081	23175	7.33	1.4E-02	BE733142.1	EST_HUMAN	601567403F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842280 5'
5634	15051	24457	4.63	1.4E-02	AA569030.1	EST_HUMAN	nt11c04.s1 NCL_CGAP_B12 Homo sapiens cDNA clone IMAGE:1026990 3' similar to contains Alu repetitive element
5834	15051	24459	4.63	1.4E-02	AA559030.1	EST_HUMAN	nt11c04.s1 NCL_CGAP_B12 Homo sapiens cDNA clone IMAGE:1026990 3' similar to contains Alu repetitive element
6877	16088	25537	2.08	1.4E-02	BE644581.1	EST_HUMAN	601078239F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3464241 5'
8398	17469	26581	4.44	1.4E-02	X60459.1	NT	Human IFNAR gene for interferon alpha/beta receptor
8764	17702		1.95	1.4E-02	AF324685.1	NT	Arabidopsis thaliana F21J9.2 mRNA, complete cds
8958	17869		2.17	1.4E-02	11428988	NT	Homo sapiens sperm associated antigen 7 (SPAG7), mRNA
1825	11129	20323	2.04	1.3E-02	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
3180	12415	21549	2.04	1.3E-02	BF697081.1	EST_HUMAN	602129475F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286203 5'
3180	12415	21550	2.04	1.3E-02	BF697081.1	EST_HUMAN	602129475F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286203 5'
3946	13162		1.42	1.3E-02	AF168288.1	NT	Mus musculus beta-sarcoglycan gene, complete cds
6328	15507	24953	4.62	1.3E-02	A031583.1	EST_HUMAN	ow06g05.x1 Soares_parathyroid_tumor_Nb-IPA Homo sapiens cDNA clone IMAGE:1646072 3' similar to contains Alu repetitive element
6621	15817	25278	2.43	1.3E-02	AF156881.1	NT	Homo sapiens human endogenous retrovirus W gagC3.37 G gag (gag) gene, complete cds
7136	16313	25784	2.67	1.3E-02	M63707.1	NT	Mouse kidney androgen-regulated protein (KAP) gene, complete cds
7564	16768	26259	4.34	1.3E-02	AW268563.1	EST_HUMAN	xv344603.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2815038 3'
7564	16768	26260	4.34	1.3E-02	AW268563.1	EST_HUMAN	xv344603.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2815038 3'
8366	18328		2.68	1.3E-02	X51780.1	NT	Yeast ABP1 gene for actin binding protein
8874	17771		1.98	1.3E-02	9633098	NT	Human herpesvirus 6B, complete genome
9063	18083		12.49	1.3E-02	AF152238.1	NT	Homo sapiens V1b vasopressin receptor (VPR3) gene, complete cds
9268	18364	23008	1.4	1.3E-02	AF009179.1	NT	Oryza sativa replication protein A1 (Os-RPA1) mRNA, complete cds
360	9627	18757	4.87	1.2E-02	AA059299.1	EST_HUMAN	z885g01.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:381840 5' similar to contains element L1 repetitive element

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
459	9712	18847	2.56	1.2E-02	P38898	SWISSPROT	HYPOTHETICAL 17.1 KD PROTEIN IN PUR6 3REGION
748	9887	19130	10.01	1.2E-02	A1183522.1	EST_HUMAN	q488a12.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1734870 3' similar to contains L1.t1 L1
2143	11341	20559	1.46	1.2E-02	AL163213.2	NT	repetitive element;
2406	11598	20819	1.16	1.2E-02	AW172350.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C013
2446	11637	20858	1.3	1.2E-02	AL163218.2	NT	x437e09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2858432 3'
2600	11688	20819	25.94	1.2E-02	AW172350.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C018
3088	12302		6.86	1.2E-02	AA075418.1	EST_HUMAN	x437e09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2858432 3'
3258	12489	21620	2.15	1.2E-02	R62805.1	EST_HUMAN	zm88e03.r1 Strategene ovarian cancer (#637219) Homo sapiens cDNA clone IMAGE:545020 5'
3258	12491	21622	0.84	1.2E-02	A1688894.1	EST_HUMAN	y11b08.s1 Soares_placenta Nb2HP Homo sapiens cDNA clone IMAGE:198903 3'
							zb68a07.x5 Soares_fetal_lung_NHL19W Homo sapiens cDNA clone IMAGE:309532 3' similar to contains element MER22 repetitive element;
							Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
4895	14122	23217	2.88	1.2E-02	U91928.1	NT	Cynops pyrrhogaster GpJbq1 mRNA, partial cds
5087	14247		1.27	1.2E-02	AB018788.1	NT	AV731704 HTF Homo sapiens cDNA clone HTFBHG11 5'
5114	14284	23382	1.49	1.2E-02	AV731704.1	EST_HUMAN	Rana rugosa mRNA for calreticulin, complete cds
5551	14775	24142	1.95	1.2E-02	D78586.1	NT	Mus musculus DNA methyltransferase (Dnmt1) gene, exons 2, 3, 4, and 5
6089	15290	24723	5.53	1.2E-02	AF175412.1	NT	AV732083 HTF Homo sapiens cDNA clone HTFBJC08 5'
6212	15383	24837	8.59	1.2E-02	AV732083.1	EST_HUMAN	CMF-N-ACETYLNEURAMINATE-BETA-GALACTOSAMIDE-ALPHA-2,3-SIALYLTRANSFERASE (BETA-GALACTOSIDE ALPHA-2,3-SIALYLTRANSFERASE) (ALPHA 2,3-ST) (GAL-NAC8S) (GAL-BETA-1,3-GALNAC-ALPHA-2,3-SIALYLTRANSFERASE) (ST3GALA.2) (SIAT4-B)
6463	15680	25132	3.83	1.2E-02	Q11205	SWISSPROT	Norwalk-like virus genogroup 2 gene for capsid protein, complete cds
6977	16155	25826	3.56	1.2E-02	AB031013.1	NT	PERIOD CIRCADIAN PROTEIN 1 (CIRCADIAN PACEMAKER PROTEIN RIGU1) (HPER)
8442	17505	24015	1.26	1.2E-02	Q15534	SWISSPROT	COLLAGEN ALPHA 1(IV) CHAIN PRECURSOR
8877	18187		1.27	1.2E-02	P17139	SWISSPROT	C18119 Human placenta cDNA (TFujimura) Homo sapiens cDNA clone GEN-557G08 5'
9071	17898		4.48	1.2E-02	C18119.1	EST_HUMAN	zm88a11.s1 Strategene neuroepithelium (#637231) Homo sapiens cDNA clone IMAGE:530824 3'
1278	10491	16650	1.91	1.1E-02	AA070384.1	EST_HUMAN	H. sapiens LIPA gene, exon 4
1681	10893	20080	1.32	1.1E-02	X75491.1	NT	H. sapiens LIPA gene, exon 4
1681	10893	20081	1.32	1.1E-02	X75491.1	NT	H. sapiens LIPA gene, exon 4
2005	11208	20417	4.75	1.1E-02	BF345283.1	EST_HUMAN	602018037.F1 NCI_CGAP_Bim67 Homo sapiens cDNA clone IMAGE:4153808 5'
2831	12070		4.23	1.1E-02	N68523.1	EST_HUMAN	za40a05.r1 Soares_fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:285040 5'
							tg95b10.x1 NCI_CGAP_OV23 Homo sapiens cDNA clone IMAGE:2216539 3' similar to SW:XP_F_HUMAN
3496	12720	21857	3.07	1.1E-02	A1653508.1	EST_HUMAN	Q62888 DNA-REPAIR PROTEIN COMPLEMENTING XP-F CELL;
3698	13211		63.05	1.1E-02	BE144637.1	EST_HUMAN	PM3-HT0175-300899-001-408 HT0175 Homo sapiens cDNA

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4085	13284		0.85	1.1E-02	AW813798.1	EST_HUMAN	RC3-ST0197-120200-015-g11 ST0197 Homo sapiens cDNA
4847	14036	23129	2.48	1.1E-02	AL048383.2	EST_HUMAN	DKFZp568E0924_s1 588 (synonym: hule1) Homo sapiens cDNA clone DKFZp568E0924
6331	15512	24958	2.08	1.1E-02	BE149811.1	EST_HUMAN	RC1-HT0256-100300-016-h07 HT0256 Homo sapiens cDNA
6744	18639	25400	7.88	1.1E-02	Q61882	SWISSPROT	NEUROGENIC LOCUS NOTCH 3 PROTEIN
7047	18224	25699	2.79	1.1E-02	AA082578.1	EST_HUMAN	zn24a01.r1 Stratiogene neuroepithelium NT2RAM1 837234 Homo sapiens cDNA clone IMAGE:548328 5'
7107	18284	25785	5.87	1.1E-02	AA314885.1	EST_HUMAN	EST188494 Colon carcinoma (HCC) cell line II Homo sapiens cDNA 5' end
7552	18757	20251	3.86	1.1E-02	11435505	NT	Homo sapiens T-box 5 (TBX5), mRNA
8327	17428		3	1.1E-02	AA688239.1	EST_HUMAN	ab77111.s1 Stratiogene fetal retina 837202 Homo sapiens cDNA clone IMAGE:853005 3' similar to contains
8	8302	18408	8.12	1.0E-02	AW846120.1	EST_HUMAN	Alu repetitive element
2538	11724		0.94	1.0E-02	AA806389.1	EST_HUMAN	MR3-CT0176-111088-003-e10 CT0176 Homo sapiens cDNA
3056	12281	21417	3.03	1.0E-02	BE835558.1	EST_HUMAN	cc22h08.s1 NCI CGAP_G081 Homo sapiens cDNA clone IMAGE:1350495 3'
3228	12463	21595	1.34	1.0E-02	BE868889.1	EST_HUMAN	RCQ-FN0025-250500-021-d02 FN0025 Homo sapiens cDNA
3874	13080	22208	0.8	1.0E-02	AL183302.2	NT	601846867R1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:3933689 3'
4788	13975	23078	4.78	1.0E-02	8753821	NT	Homo sapiens chromosome 21 segment HS21C102
4861	14049	23143	5.39	1.0E-02	R98567.1	EST_HUMAN	Mus musculus corticotropin releasing hormone receptor 2 (Chr2), mRNA
5208	14383		1.84	1.0E-02	BE084970.1	EST_HUMAN	y64h01.r1 Sceres fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:169633 5'
5745	14884	24383	2.8	1.0E-02	AW577113.1	EST_HUMAN	RC1-BT0313-130400-018-e09 BT0313 Homo sapiens cDNA
5745	14884	24384	2.8	1.0E-02	AW577113.1	EST_HUMAN	MR4-BT0358-070100-201-h01 BT0358 Homo sapiens cDNA
6874	16065	25532	7.87	1.0E-02	BF036331.1	EST_HUMAN	MR4-BT0358-070100-201-h01 BT0358 Homo sapiens cDNA
6874	16065	25533	7.87	1.0E-02	BF036331.1	EST_HUMAN	601458570F1 NIH_MGC_86 Homo sapiens cDNA clone IMAGE:3963177 5'
7814	17007		2.34	1.0E-02	AF157559.1	NT	601458570F1 NIH_MGC_86 Homo sapiens cDNA clone IMAGE:3963177 5'
7907	17122	26653	2.08	1.0E-02	AV760016.1	EST_HUMAN	Citridia fasciculata 27 kDa guide RNA-binding protein mRNA, complete cds; mitochondrial gene for
8407	18384		1.45	1.0E-02	Q62203	SWISSPROT	mitochondrial product
8467	18145	23751	4.31	1.0E-02	AW835521.1	EST_HUMAN	AV760016 MDS Homo sapiens cDNA clone MDSBDC10 5'
8497	18202		5.37	1.0E-02	S70330.1	NT	SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SPLICING FACTOR 3A SUBUNIT 2) (SF3A66)
8049	18259		3.4	1.0E-02	X62654.1	NT	RC2-DT0007-120200-018-h02 DT0007 Homo sapiens cDNA
8271	18034	23842	1.34	1.0E-02	AB039887.1	NT	Homo sapiens renal dipeptidase (RDP) gene, complete cds
9280	18105		20.92	1.0E-02	D17522.1	NT	H. sapiens gene for Me491/CD63 antigen
903	10138	18300	1.76	9.0E-03	AI786128.1	EST_HUMAN	H. sapiens WDR4 gene for WD repeat protein, complete cds
1271	10486		1.88	9.0E-03	BE781889.1	EST_HUMAN	Z. mobilis zIE and zIS genes for expression and secretion activator protein, complete cds
							wh42089.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2383433 3' similar to contains element
							MER22 MER22 repetitive element ;
							601470242F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:3873348 5'

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2359	11552	20773	2.28	9.0E-03	AL161559.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 59
2368	11581	20783	1.95	9.0E-03	AF095934.1	NT	Mus musculus MHC class III protein RP1 (Rp1) mRNA, partial cds
2858	12098	21225	0.68	9.0E-03	A1251744.1	EST_HUMAN	q80709.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1854281 3'
2858	12098	21228	0.68	9.0E-03	A1251744.1	EST_HUMAN	q80709.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1854281 3'
3849	12870	21887	1.08	9.0E-03	J05184.1	NT	S.acidocaldarius thermoplasma gene, complete cds
5008	14195	23284	1.11	9.0E-03	BE047949.1	EST_HUMAN	bt44e10.v1 NCI_CGAP_Bms2 Homo sapiens cDNA clone IMAGE:2281488 5'
5948	15164		4.8	9.0E-03	BE745988.1	EST_HUMAN	801673438F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3834752 5'
7558	16763		1.7	9.0E-03	Y18000.1	NT	Homo sapiens NF2 gene
7583	16788	26283	1.77	9.0E-03	BE395380.1	EST_HUMAN	801310881F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3632181 5'
8828	18385		1.56	9.0E-03	BF351141.1	EST_HUMAN	PM1-HT0452-291298-001-008 HT0452 Homo sapiens cDNA
8848	18378		15.49	9.0E-03	BE346385.1	EST_HUMAN	hwt17609.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3183161 3'
9180	17859		14.22	9.0E-03	BF351141.1	EST_HUMAN	PM1-HT0452-291298-001-009 HT0452 Homo sapiens cDNA
9215	17995		1.23	9.0E-03	P16241	SWISSPROT	POU-DOMAIN PROTEIN CF1A (CHORION FACTOR 1A) (CF1-A) (VENTRAL VEINS LACKING PROTEIN) (DRIFTER PROTEIN)
908	9760		5.44	8.0E-03	AA723007.1	EST_HUMAN	zh30e03.s1 Soares_pituitary_gland_N3HPG Homo sapiens cDNA clone IMAGE:413588 3' similar to contains
908	10228	18383	61.85	8.0E-03	AF106856.1	NT	Alu repetitive element
2125	11324	20542	1.11	8.0E-03	AL163283.2	NT	Homo sapiens adenylsuccinate lyase gene, complete cds
2517	11708	20819	1.37	8.0E-03	P10268	SWISSPROT	Homo sapiens chromosome 21 segment HS21C083
3281	12512	21643	1.07	8.0E-03	BE171225.1	EST_HUMAN	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
3334	12563	21701	0.88	8.0E-03	AJ131016.1	NT	RC1-HT0545-120200-011-509 HT0545 Homo sapiens cDNA
3858	12877	21886	1.48	8.0E-03	P32844	SWISSPROT	Homo sapiens SCL gene locus
3858	12877	21997	1.48	8.0E-03	P32844	SWISSPROT	HYPOTHETICAL 127.0 KD PROTEIN IN RAD24-BMH1 INTERGENIC REGION
4244	13447	22538	1.19	8.0E-03	BE940049.1	EST_HUMAN	HYPOTHETICAL 127.0 KD PROTEIN IN RAD24-BMH1 INTERGENIC REGION
4377	13578	22678	6.14	8.0E-03	BF363327.1	EST_HUMAN	QV0-FN0181-140700-304-q10 FN0181 Homo sapiens cDNA
4728	13919	23021	0.65	8.0E-03	P03181	SWISSPROT	CM4-NN0119-300600-223-505 NN0119 Homo sapiens cDNA
4728	13919	23022	0.65	8.0E-03	P03181	SWISSPROT	HYPOTHETICAL BHLF1 PROTEIN
							HYPOTHETICAL BHLF1 PROTEIN
5452	14878	23838	2.83	8.0E-03	AF110520.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG29, KIFC1, Fas-binding protein, BING1, tapasin, RalGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and
5980	15184	24610	4.28	8.0E-03	P55577	SWISSPROT	RPS18 genes, complete cds; Sacm21 gene, partial>
6309	15490		1.8	8.0E-03	AB038287.1	NT	PROBABLY PEPTIDASE Y4NA
6748	15943	25403	4	8.0E-03	AW808692.1	EST_HUMAN	Tursiops truncatus mRNA for p40-phox, complete cds
							MR1-ST0111-111189-011-h08 ST0111 Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7053	16230		8.75	8.0E-03	BE086509.1	EST_HUMAN	QV1-BT0677-040400-131-g03 BT0677 Homo sapiens cDNA
7557	16762		2.97	8.0E-03	Z49852.1	NT	S. cerevisiae chromosome X reading frame ORF YJR152w
7920	17135	26665	1.9	8.0E-03	AA828817.1	EST_HUMAN	cd80a09.s1 NCI CGAP_Ov2 Homo sapiens cDNA clone IMAGE:1374232
7920	17135	26668	1.9	8.0E-03	AA828817.1	EST_HUMAN	cd80a09.s1 NCI CGAP_Ov2 Homo sapiens cDNA clone IMAGE:1374232
8208	17337	26877	5.58	8.0E-03	AF084589.1	NT	Homo sapiens melanoma-associated antigen (MAGE-C1) gene, complete cds
8336	17434		1.97	8.0E-03	M69035.1	NT	Oryctolagus cuniculus eIF-2a kinase mRNA, complete cds
8383	17468		2.41	8.0E-03	AB038161.1	NT	Homo sapiens ABCG1 gene for ABC transporter (ATP-binding cassette, sub-family G (WHITE), member 1), complete cds
701	8943	18077	15.31	7.0E-03	AF097183.1	NT	Cryptosporidium parvum HC-10 gene, complete cds
701	8943	18078	15.31	7.0E-03	AF097183.1	NT	Cryptosporidium parvum HC-10 gene, complete cds
884	10216	18371	9.8	7.0E-03	AF243376.1	NT	Glycine max glutathione S-transferase GST 21 mRNA, partial cds
1124	10348	19489	3.32	7.0E-03	AV731712.1	EST_HUMAN	AV731712 HTF Homo sapiens cDNA clone HTFAZF10 5'
1372	10588		1	7.0E-03	Q81080	SWISSPROT	FORK-HEAD BOX PROTEIN D3 (HNF3/FH TRANSCRIPTION FACTOR GENESIS) (HEPATOCYTE NUCLEAR FACTOR 3 FORK-HEAD HOMOLOG 2) (HNF-2)
1389	10613	19777	3.43	7.0E-03	AA988288.1	EST_HUMAN	ab78809.s1 Stratagene Total retina 937202 Homo sapiens cDNA clone IMAGE:363145 3'
1484	10707	19880	2.64	7.0E-03	AW303589.1	EST_HUMAN	rx21b02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813739 3'
1715	10927	20111	1	7.0E-03	AW950556.1	EST_HUMAN	EST362628 MAGE resequencing, MAGA Homo sapiens cDNA
1715	10927	20112	1	7.0E-03	AW950556.1	EST_HUMAN	EST362626 MAGE resequencing, MAGA Homo sapiens cDNA
2222	12013	20645	1.48	7.0E-03	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
3533	12758	21888	1	7.0E-03	A1160273.1	EST_HUMAN	qf34h02.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1751955 3'
3749	12889	22084	0.87	7.0E-03	AW444463.1	EST_HUMAN	U1-H-B13-ekb-c-10-0-U1.s1 NCI CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733681 3'
3800	13018	22131	0.81	7.0E-03	AF186344.1	NT	Rattus norvegicus neuronal nicotinic acetylcholine receptor subunit (Alpha10) mRNA, complete cds
3895	12889	22084	0.84	7.0E-03	AW444463.1	EST_HUMAN	U1-H-B13-ekb-c-10-0-U1.s1 NCI CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733681 3'
4332	13533		1.12	7.0E-03	U60086.1	NT	Dictyostellium discoideum multidrug resistance transporter/Ser protease (tagC) mRNA, complete cds
4532	13728		1.04	7.0E-03	AW117711.1	EST_HUMAN	xa34f09.x1 NCI CGAP_U11 Homo sapiens cDNA clone IMAGE:2809033 3' similar to TR:Q12987 Q12987
4599	13783		1.38	7.0E-03	AW630888.1	EST_HUMAN	ACIDIC 82 KDA PROTEIN :
5010	14197		2.53	7.0E-03	AL163278.2	NT	h88a05.y1 NCI CGAP_GU1 Homo sapiens cDNA clone IMAGE:2868938 5'
5713	18063		4.89	7.0E-03	AW891059.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C078
5785	18012	24410	1.73	7.0E-03	W68251.1	EST_HUMAN	RC1-CT0286-050-018-c08 CT0286 Homo sapiens cDNA
5808	15113	24524	3.19	7.0E-03	AA327128.1	EST_HUMAN	z833f10.r1 Soares_fetal_heart_NBH19W Homo sapiens cDNA clone IMAGE:342475 5'
6115	15228	24647	1.82	7.0E-03	BE928133.1	EST_HUMAN	EST30874 Cdon1 Homo sapiens cDNA 6' end
							CM2-CT0478-230800-347-b11 CT0478 Homo sapiens cDNA

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Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6268	15480	24923	5.21	7.0E-03	Z35838.1	NT	S. cerevisiae chromosome II reading frame ORF YBL077w
6269	15480	24924	5.21	7.0E-03	Z35838.1	NT	S. cerevisiae chromosome II reading frame ORF YBL077w
6488	15695	25159	4.1	7.0E-03	BE176687.1	EST_HUMAN	RC5-HT0582-160300-011-D02 HT0592 Homo sapiens cDNA
7403	16616	26106	3.29	7.0E-03	AB008882.1	NT	Bos taurus mRNA for NDP52, complete cds
8904	18370		1.5	7.0E-03	H64065.1	EST_HUMAN	yw15h01.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:242833 3' similar to contains Alu repetitive element
8911	17800		2.34	7.0E-03	BE263253.1	EST_HUMAN	601145164F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3160476 5'
9008	17884		1.59	7.0E-03	Y17455.1	NT	Homo sapiens LSFR2 gene, penultimate exon
8147	18387		1.41	7.0E-03	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
8278	18040		1.4	7.0E-03	AW688110.1	EST_HUMAN	RC0-SN0052-110400-021-a04 SN0052 Homo sapiens cDNA
1247	10464	19824	10.61	6.0E-03	AW511148.1	EST_HUMAN	hd22a05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2810224 3' similar to SW:PXRX_HUMAN O75469 ORPHAN NUCLEAR RECEPTOR PXR;
1247	10464	19825	10.61	6.0E-03	AW511148.1	EST_HUMAN	hd22a05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2810224 3' similar to SW:PXRX_HUMAN O75469 ORPHAN NUCLEAR RECEPTOR PXR;
2727	11808	21121	1.11	6.0E-03	AF112374.1	NT	Danio rerio odorant receptor gene cluster
2843	12082	21207	4.79	6.0E-03	AA759135.1	EST_HUMAN	ah78e11.s1 Soares_testis_NHT Homo sapiens cDNA clone 1321772 3'
2843	12082	21208	4.79	6.0E-03	AA759135.1	EST_HUMAN	ah78e11.s1 Soares_testis_NHT Homo sapiens cDNA clone 1321772 3'
3213	12447		2.28	6.0E-03	H75680.1	EST_HUMAN	y77h04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:211351 5'
3275	12508		0.7	6.0E-03	AF190338.1	NT	Notoncus sp. cytochrome c oxidase subunit II gene, partial cds; mitochondrial gene for mitochondrial product
3360	12588	21727	1.3	6.0E-03	U90880.1	NT	Fugu rubripes zinc finger protein, isotocin, fatty acid binding protein, septaplerin reductase and vasotocin genes, complete cds
3360	12588	21728	1.3	6.0E-03	U90880.1	NT	Fugu rubripes zinc finger protein, isotocin, fatty acid binding protein, septaplerin reductase and vasotocin genes, complete cds
3521	12745		1.25	6.0E-03	W37985.1	EST_HUMAN	ze13a11.r1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:322172 5'
3640	12881	21879	2.21	6.0E-03	BF610988.1	EST_HUMAN	UIH-B14-apm-c-08-O-U1.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3087754 3'
3759	12978	22063	1.06	6.0E-03	6754028	NT	Mus musculus glucosamine-6-phosphate deaminase (Gnpl), mRNA
3933	13149		0.99	6.0E-03	BE250108.1	EST_HUMAN	600842804F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2858513 5'
4317	13518		0.95	6.0E-03	N58948.1	EST_HUMAN	y62h10.s1 Soares_multiple_sclerosis_2NbrHMSF Homo sapiens cDNA clone IMAGE:278179 3'
4358	13560		1.94	6.0E-03	AJ018833.1	EST_HUMAN	ov33c11.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1638124 3'
4705	13896	22895	7.35	6.0E-03	AA324242.1	EST_HUMAN	EST27116 Cerebellum II Homo sapiens cDNA 5' and similar to EST containing Alu repeat
5273	14445	23517	0.9	6.0E-03	AF050737.1	NT	Homo sapiens dopamine D2 receptor (DRD2) gene, complete cds
6413	15610	25074	13.87	6.0E-03	AJ033980.1	EST_HUMAN	ow13a04.x1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1848870 3' similar to contains MER10.b1 MER10 repetitive element;

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8453	15650	25118	3.3	6.0E-03	AW788337.1	EST_HUMAN	RCO-UM0051-210300-032-g02 UM0051 Homo sapiens cDNA
8937	16081	25551	10.41	6.0E-03	D10548.1	NT	Subacute sclerosing panencephalitis (SSPE) virus mRNA for fusion protein
7330	16548	26036	2.3	6.0E-03	AW862164.1	EST_HUMAN	EST374237 MAGE resequences, MAGG Homo sapiens cDNA
7388	16602		2.24	6.0E-03	11545814	NT	Homo sapiens hypothetical zinc finger protein FLJ14011 (FLJ14011), mRNA
7423	16633	26127	2.03	6.0E-03	AI420786.1	EST_HUMAN	ts91c12.x1 NCI_CGAP_P28 Homo sapiens cDNA clone IMAGE:2094070 3' similar to TR:O00519 O00519 FATTY ACID AMIDE HYDROLASE.
7423	16633	26128	2.03	6.0E-03	AI420786.1	EST_HUMAN	FATTY ACID AMIDE HYDROLASE.
7655	16760		4.37	6.0E-03	U14558.1	NT	Mus musculus zinc-finger protein mRNA, complete cds
7656	16761	26254	2.84	6.0E-03	BE737895.1	EST_HUMAN	601672748F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839747 5'
8262	17389	26921	1.76	6.0E-03	H70298.1	EST_HUMAN	yr95f01.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:213049 5' similar to SP:6PGD_PIG P14332 6-PHOSPHOGLUCONATE DEHYDROGENASE, DECARBOXYLATING;
8449	17508		1.57	6.0E-03	AF010496.1	NT	Rhodobacter capsulatus strain SB1003, partial genome
8559	18198		1.26	6.0E-03	BF671185.1	EST_HUMAN	602151024F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4292212 5'
8595	18130		6.17	6.0E-03	AE000833.1	NT	Methanobacterium thermoautotrophicum from bases 428192 to 450298 (section 39 of 148) of the complete genome
8689	18194		2.42	6.0E-03	U30790.1	NT	Pneumocystis carinii f. sp. ratti guanine nucleotide binding protein alpha subunit (pog1) gene, complete cds
9022	17873		1.96	6.0E-03	BE788019.1	EST_HUMAN	601482621F1 NIH_MGC_98 Homo sapiens cDNA clone IMAGE:3985388 5'
9045	17899		1.96	6.0E-03	AJ245480.1	NT	Brassica napus sig gene for S-locus glycoprotein, cultivar T2
676	9920	19050	1.9	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORF; aminocycl-tRNA synthase, complete cds; complete ORFA, and grpE- like protein, complete cds
676	9920	19051	1.9	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORF; aminocycl-tRNA synthase, complete cds; complete ORFA, and grpE- like protein, complete cds
678	9920	19050	3.87	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORF; aminocycl-tRNA synthase, complete cds; complete ORFA, and grpE- like protein, complete cds
678	9920	19051	3.87	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORF; aminocycl-tRNA synthase, complete cds; complete ORFA, and grpE- like protein, complete cds
1120	10344	19495	1.83	5.0E-03	AJ010457.1	NT	Arabidopsis thaliana mRNA for DEAD box RNA helicase, RH3
2641	11824	21039	1.97	5.0E-03	AB033006.1	NT	Homo sapiens mRNA for KIAA1180 protein, partial cds
2888	12124	21257	0.79	5.0E-03	BE260057.1	EST_HUMAN	601194798F1 NH_MGC_7 Homo sapiens cDNA clone IMAGE:3538799 5'
3101	12337	21465	4.54	5.0E-03	T87623.1	EST_HUMAN	yc81f09.a1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:22395 3'
3118	12353		2.3	5.0E-03	AL161491.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 3
3131	12366	21498	1.13	5.0E-03	R71794.1	EST_HUMAN	yr89g02.s1 Soares breast 2NbhBst Homo sapiens cDNA clone IMAGE:155888 3'

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Table 4
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3245	12478		0.63	5.0E-03	AJ297357.1	NT	Homo sapiens partial LIMD1 gene for LIM domains containing protein 1 and KIAA0851 gene
3877	12898	22018	4.23	5.0E-03	AF147449.2	NT	Pseudomonas aeruginosa strain PAO1 penicillin-binding protein 1B (ponB) gene, complete cds
3741	12861	22076	0.74	6.0E-03	U38914.1	NT	Citrus sinensis seed storage protein citrin mRNA, complete cds
3948	13164		1.67	5.0E-03	AA298875.1	EST_HUMAN	EST112218 Uterus tumor 1 Homo sapiens cDNA 5' end
4291	13403	22591	0.84	5.0E-03	H78355.1	EST_HUMAN	w78g10.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:240988 5'
4293	12861	22076	0.76	6.0E-03	U38914.1	NT	Citrus sinensis seed storage protein citrin mRNA, complete cds
4609	13803	22893	0.84	5.0E-03	AJ131016.1	NT	Homo sapiens SCL gene locus
4731	13922	23028	1.59	5.0E-03	AF552387.1	EST_HUMAN	cn15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn15c02 random
4834	14141	23235	0.97	5.0E-03	P15285	SWISSPROT	SPERM MITOCHONDRIAL CAPSULE SELENOPROTEIN (MCS)
5570	14785	24168	5.73	5.0E-03	P35500	SWISSPROT	SODIUM CHANNEL PROTEIN PARA (PARALYTIC PROTEIN)
							PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE FAF-Y (UBIQUITIN THIOLESTERASE FAF-Y) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE FAF-Y) (DEUBIQUITINATING ENZYME FAF-Y) (FAT FACETS PROTEIN RELATED, Y-LINKED) (UBIQUITIN-SPECIFIC PROTEASE 9, Y CHROMOSOME)
5894	14904	24297	2.82	5.0E-03	O00507	SWISSPROT	Y (FAT FACETS PROTEIN RELATED, Y-LINKED) (UBIQUITIN-SPECIFIC PROTEASE 9, Y CHROMOSOME)
5891	16147		7.17	5.0E-03	BE300091.1	EST_HUMAN	600944564T1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2880871 3'
6016	14508	23574	6.81	5.0E-03	AB025024.1	NT	Mus musculus AMD1 gene for S-adenosylmethionine decarboxylase, complete cds
6402	15683	25040	7.06	5.0E-03	AB016818.1	NT	Homo sapiens MASL1 mRNA, complete cds
6658	15854		9.12	5.0E-03	M81132.1	NT	Mouse complement receptor (CR2) mRNA, 3' end
7308	16528		7.45	5.0E-03	T18586.1	EST_HUMAN	684F Heart Homo sapiens cDNA clone 684
							xn58g05.x1 Soares_NHCCc_cervical_tumor Homo sapiens cDNA clone IMAGE:2688040 3' similar to contains L1.12 L1 repetitive element;
7513	16718	26207	2.98	5.0E-03	AW170334.1	EST_HUMAN	xn58g05.x1 Soares_NHCCc_cervical_tumor Homo sapiens cDNA clone IMAGE:2688040 3' similar to contains L1.12 L1 repetitive element;
7513	16718	26208	2.98	5.0E-03	AW170334.1	EST_HUMAN	contains L1.12 L1 repetitive element;
7611	16814	26310	2.19	5.0E-03	T48153.1	EST_HUMAN	y609e04.r1 Stratagene placenta (#837225) Homo sapiens cDNA clone IMAGE:70688 5'
7878	17084		3.94	5.0E-03	BE048055.1	EST_HUMAN	tz48c04.y1 NCL_CGAP_Bim52 Homo sapiens cDNA clone IMAGE:2281622 5'
8602	18332		5.41	5.0E-03	AF047874.1	NT	Callus gallus glyceraldehyde-3-phosphate dehydrogenase mRNA, complete cds
8743	17688		10.59	5.0E-03	AF087253.1	NT	Brugia malayi Y chromosome marker
8844	17753		1.75	5.0E-03	L10347.1	NT	Human pro-alpha1 type II collagen (COL2A1) gene exons 1-54, complete cds.
8881	17776						2x75e03.s1 Soares ovary tumor NIHOT Homo sapiens cDNA clone IMAGE:808548 3' similar to SW:DXA2_MOUSE P14885 PROBABLE DIPHENOL OXIDASE A2 COMPONENT ;
8912	18139		5.75	5.0E-03	BF572332.1	EST_HUMAN	60207774F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4252002 5'
9097	17913	23859	2.66	5.0E-03	AW449109.1	EST_HUMAN	UIH-B13-akt-f-08-O-UI.s1 NCL_CGAP_Sub55 Homo sapiens cDNA clone IMAGE:2734215 3'
9118	18211		1.4	5.0E-03	Q02388	SWISSPROT	COLLAGEN ALPHA 1(VII) CHAIN PRECURSOR (LONG-CHAIN COLLAGEN) (LC COLLAGEN)

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Table 4
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
238	9517	18948	3.28	4.0E-03	AW500196.1	EST_HUMAN	U1HF-BNO-alc-h-04-0-UL1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3076831 5'
328	9597	18728	2.1	4.0E-03	R48482.1	EST_HUMAN	y51e04.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:35988 3'
449	9702	18940	0.94	4.0E-03	P54875	SWISSPROT	PHOSPHATIDYLINOSITOL 3-KINASE 3 (P13-KINASE) (PTDINS-3-KINASE) (P13K)
610	9857	18976	2.44	4.0E-03	AA838339.1	EST_HUMAN	on75g12.s1 Soares NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:1582588 3'
887	10122	18288	1.91	4.0E-03	R48482.1	EST_HUMAN	y51e04.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:35988 3'
921	10156		4.09	4.0E-03	AW749101.1	EST_HUMAN	RC3-BT0333-110100-012-01 B10333 Homo sapiens cDNA
1159	10381	19533	24.64	4.0E-03	AA089777.1	EST_HUMAN	z81e08.r1 Stragene colon (#837204) Homo sapiens cDNA clone IMAGE:510988 5'
1177	10398	19551	1.71	4.0E-03	AW794740.1	EST_HUMAN	RC6-UM0014-170400-023-G01 UM0014 Homo sapiens cDNA
1310	10528	19886	0.88	4.0E-03	AA284374.1	EST_HUMAN	zs59a01.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701736 5'
1588	10779		0.95	4.0E-03	AV708305.1	EST_HUMAN	AV708305 ADC Homo sapiens cDNA clone ADCAKB08 5'
1717	10829	20114	2.29	4.0E-03	U33472.1	NT	Rattus norvegicus type 1 astrocyte and olfactory-limbic associated protein AT1-48 mRNA, complete cds
1885	11188	20399	16.08	4.0E-03	AA089777.1	EST_HUMAN	z81e08.r1 Stragene colon (#837204) Homo sapiens cDNA clone IMAGE:510988 5'
2212	11409		1.85	4.0E-03	BE410558.1	EST_HUMAN	601304161F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638510 5'
2243	11438	20862	1.44	4.0E-03	AW794740.1	EST_HUMAN	RC6-UM0014-170400-023-G01 UM0014 Homo sapiens cDNA
							Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase 1 (CAMK1), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
2537	11725	20941	1.4	4.0E-03	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase 1 (CAMK1), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
2637	11726	20942	1.4	4.0E-03	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase 1 (CAMK1), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
2851	11834	21047	1.92	4.0E-03	AJ277365.1	NT	Homo sapiens polyglutamine-containing C14ORF4 gene
2851	11834	21048	1.92	4.0E-03	AJ277365.1	NT	Homo sapiens polyglutamine-containing C14ORF4 gene
2857	11839	21051	1.09	4.0E-03	AL163284.2	NT	Homo sapiens polyglutamine-containing C14ORF4 gene
3191	12426	21560	0.99	4.0E-03	BE154134.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C084
3191	12426	21561	0.99	4.0E-03	BE154134.1	EST_HUMAN	PM1-HT0340-151289-003-H08 HT0340 Homo sapiens cDNA
3504	12728	21864	0.98	4.0E-03	AW189426.1	EST_HUMAN	PM1-HT0340-151289-003-H08 HT0340 Homo sapiens cDNA
3504	12728	21865	0.98	4.0E-03	AW189426.1	EST_HUMAN	x88f04.x1 NCI_CGAP_Cot18 Homo sapiens cDNA clone IMAGE:2685279 3'
3602	12823	21945	0.69	4.0E-03	Q13808	SWISSPROT	x88f04.x1 NCI_CGAP_Cot18 Homo sapiens cDNA clone IMAGE:2685279 3'
3612	12833	21954	0.68	4.0E-03	AV646253.1	EST_HUMAN	OLFACTORY RECEPTOR 51 (OLFACTORY RECEPTOR-LIKE PROTEIN OLF1)
3804	13120	22238	0.77	4.0E-03	AF060868.1	NT	AV646253 GLC Homo sapiens cDNA clone GLCALDO2 3'
3872	13186		1.89	4.0E-03	AJ011712.1	NT	Mus musculus tumor susceptibility protein 101 (tsg101) gene, complete cds
4225	13428	22519	5.3	4.0E-03	AI766727.1	EST_HUMAN	Homo sapiens TNNT1 gene, exons 1-11 (and joined CDS)
5312	14544	23613	1.71	4.0E-03	AF005859.1	NT	w187a08.x1 NCI_CGAP_Kd12 Homo sapiens cDNA clone IMAGE:2400274 3'
							Drosophila melanogaster anon2D7 (anon2D7) mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5395	14824	23737	22.47	4.0E-03	AF169825.1	NT	Rattus norvegicus beta-catenin binding protein mRNA, complete cds
5589	14784	24187	2.5	4.0E-03	P04196	SWISSPROT	(HPRG)
5702	14921		3.78	4.0E-03	U22180.1	NT	Rattus norvegicus opsin gene, complete cds
5791	15008	24412	1.85	4.0E-03	BE548453.1	EST_HUMAN	601078015F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3481954 5'
6163	15348	24783	4.05	4.0E-03	Q02817	SWISSPROT	MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2)
6480	15877	25147	5.72	4.0E-03	AF111944.1	NT	Dicystidium discoidium AX4 development protein DG1122 (DG1122) gene, partial cds
6530	15726	25191	2.26	4.0E-03	7882087	NT	Homo sapiens KIAA0346 gene product (KIAA0346), mRNA
6884	15879	25338	8.28	4.0E-03	AI553883.1	EST_HUMAN	te48b1.1.X1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2080013 3' similar to contains Alu repetitive element
6743	15838	25399	5.44	4.0E-03	AL183278.2	NT	Homo sapiens chromosome 21 segment HS21C078
7859	16888	26395	6.92	4.0E-03	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C008
8242	17371	26907	2.1	4.0E-03	AE002102.1	NT	Ureaplasma urealyticum section 3 of 59 of the complete genome
8569	18347		3.68	4.0E-03	BE815173.1	EST_HUMAN	PM4-BN0138-180600-002-b08 BN0138 Homo sapiens cDNA
8592	17801		1.6	4.0E-03	BE298290.1	EST_HUMAN	601118184F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028095 5'
8878	17848		2.3	4.0E-03	AW504273.1	EST_HUMAN	UI-HF-BN0-8lp-g-04-0-J1.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3080822 5'
8923	17807		3.28	4.0E-03	BF224125.1	EST_HUMAN	7q74c09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3' similar to contains Alu repetitive element; contains element MER31 repetitive element;
8965	18253		1.91	4.0E-03	AW614598.1	EST_HUMAN	h102c07.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2853832 3' similar to contains element
8978	17845		1.75	4.0E-03	AW819141.1	EST_HUMAN	LTR5 repetitive element;
378	9842	18777	2.68	3.0E-03	AF011920.1	NT	RC3-ST0281-240400-016-f03 ST0281 Homo sapiens cDNA
899	10124	19287	7.37	3.0E-03	AF011920.1	NT	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1
1638	10850	20028	3.13	3.0E-03	AA488110.1	EST_HUMAN	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1
2223	11419		1.08	3.0E-03	AF055088.1	NT	no73c05.a1 NCI_CGAP_P12 Homo sapiens cDNA clone IMAGE:782984 similar to contains Alu repetitive element;
2257	11452		7.21	3.0E-03	Z32521.1	NT	Homo sapiens MHC class 1 region
2850	12188		0.77	3.0E-03	Y08008.1	NT	S.cereale (cv. Halo) mRNA for triosephosphate isomerase
3048	12284	21411	3.88	3.0E-03	BE379286.1	EST_HUMAN	Arabidopsis thaliana rpm1t gene
3114	12349	21477	2.88	3.0E-03	AW802887.1	EST_HUMAN	601237882F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3605833 5'
3395	12822	21753	3.37	3.0E-03	U34606.1	NT	IL2-UM0076-240300-058-D03 UM0076 Homo sapiens cDNA
3405	12831		7.98	3.0E-03	Y12500.1	NT	Mus musculus alpha-1(XVIII) collagen (COL18A1) gene, exon 1 and 2
3955	13170	22285	7.39	3.0E-03	AV782392.1	EST_HUMAN	C.elegans samdc gene
3955	13170	22286	7.39	3.0E-03	AV782392.1	EST_HUMAN	AV782392 MDS Homo sapiens cDNA clone MDSBSG01 5'
4014	13226	22327	1.73	3.0E-03	AI792278.1	EST_HUMAN	AV782392 MDS Homo sapiens cDNA clone MDSBSG01 5'
							ah04f09.y5 Gessler Williams tumor Homo sapiens cDNA clone IMAGE:1155689 5'

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Table 4
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4132	13338		1.01	3.0E-03	Z32521.1	NT	S. cereale (cv. Halo) mRNA for triosephosphate isomerase
4389	13560	22692	2.97	3.0E-03	AJ011432.1	NT	Rattus norvegicus gdnf gene
4465	13653		0.71	3.0E-03	BE348739.1	EST_HUMAN	h88g08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3161834 3'
4518	13714	22808	3.35	3.0E-03	AI536141.1	EST_HUMAN	aaB.P10.H3 conorm Homo sapiens cDNA 3'
4850	14039	23132	2.54	3.0E-03	AI732754.1	EST_HUMAN	ab18a08.x5 Strategene lung (#837210) Homo sapiens cDNA clone IMAGE:841142 3' similar to contains Alu repetitive element
4870	14058	23152	8.15	3.0E-03	BE787845.1	EST_HUMAN	601482716F1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:3885483 5'
5148	14327		0.68	3.0E-03	BF204380.1	EST_HUMAN	601868437F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4106860 5'
5307	14538	23543	3.87	3.0E-03	8922408	NT	Homo sapiens hypothetical protein FLJ10539 (FLJ10539), mRNA
5902	15119	24530	9.51	3.0E-03	AA458701.1	EST_HUMAN	eat13f10.r1 Scores_NhiMIPu_S1 Homo sapiens cDNA clone IMAGE:813183 5'
6300	15481	24925	3.2	3.0E-03	AB021738.1	NT	Oryza sativa gene for bZIP protein, complete cds
6763	15958		10.15	3.0E-03	AW813774.1	EST_HUMAN	hh80f10.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2869131 3' similar to contains L1.1 L1 repetitive element
6782	15977	25435	3.28	3.0E-03	AL161589.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 85
6783	15986	25449	9.71	3.0E-03	AI018731.1	EST_HUMAN	0403d12.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1636247 3' similar to gb:X57138_ma1 HISTONE H2B.2 (HUMAN);
6984	16172		3.95	3.0E-03	P08872	SWISSPROT	CIRCUMSPOROITE PROTEIN PRECURSOR (CS)
7121	16298	25780	6.83	3.0E-03	AL103303.2	NT	Homo sapiens chromosome 21 segment HS21C103
7425	16835		2.75	3.0E-03	5803028	NT	Homo sapiens ATP/GTP-binding protein (HEAB), mRNA
7738	15481	24925	1.72	3.0E-03	AB021738.1	NT	Oryza sativa gene for bZIP protein, complete cds
7918	17133	26883	2.14	3.0E-03	AF008222.1	NT	Pneumocystis carinii kedin-like serine endoprotease mRNA, partial cds
7983	16418	26905	2.09	3.0E-03	AF288285.1	NT	Homo sapiens gclgln-like protein (GLP) gene, complete cds
8015	17154	26888	3.08	3.0E-03	AF094481.1	NT	Homo sapiens trinucleotide repeat DNA binding protein p20-CGGBP (CGGBP) gene, complete cds
8015	17154	26880	3.06	3.0E-03	AF094481.1	NT	Homo sapiens trinucleotide repeat DNA binding protein p20-CGGBP (CGGBP) gene, complete cds
8088	17223	26758	1.74	3.0E-03	P11389	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE; ENDONUCLEASE]
8249	17377		1.63	3.0E-03	AW284812.1	EST_HUMAN	UIH-B12-ah1-4-08-0-UJ.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2726842 3'
8330	18163		3.61	3.0E-03	AI525058.1	EST_HUMAN	promina-5.E07.1 bVlumar Homo sapiens cDNA 5'
8367	17454	26582	1.75	3.0E-03	AA983154.1	EST_HUMAN	alpha7b10.s1 Scores_total_fetus_Nb24F8_9w Homo sapiens cDNA clone IMAGE:1822778 3' similar to contains L1.13 MER28 repetitive element
8424	18288		1.79	3.0E-03	AB009888.1	NT	Homo sapiens gene for CMP-N-acetylneuraminic acid hydroxylase, partial cds
8615	17612	23988	1.7	3.0E-03	AJ298282.1	NT	Rattus norvegicus mRNA for connexin36 (cx36 gene)
521	9772	18886	0.88	2.0E-03	Q04652	SWISSPROT	RING CANAL PROTEIN (KELCH PROTEIN)
521	9772	18887	0.88	2.0E-03	Q04652	SWISSPROT	RING CANAL PROTEIN (KELCH PROTEIN)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
795	11978		11.98	2.0E-03	T70874.1	EST_HUMAN	y415h03.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:108341 5'
1371	10585	19752	2.08	2.0E-03	M20783.1	NT	Human alpha-2-plasmin inhibitor gene, exons 8 and 7
1374	10588	19754	1.38	2.0E-03	AA661805.1	EST_HUMAN	nu86f01.s1 NCI_CGAP_Alv1 Homo sapiens cDNA clone IMAGE:1217593
1382	10598	19782	13.81	2.0E-03	AF284446.1	NT	Homo sapiens tumor-related protein DRC2 (DRC2) gene, complete cds
1481	10694	19869	0.86	2.0E-03	P48509	SWISSPROT	PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN)
1505	10718	19889	1.65	2.0E-03	4557836	NT	Homo sapiens procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome type VI) (PLOD) mRNA
1505	10718	19890	1.65	2.0E-03	4557836	NT	Homo sapiens procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome type VI) (PLOD) mRNA
1571	10784		6.81	2.0E-03	P28400	SWISSPROT	COLLAGEN ALPHA 5(IV) CHAIN PRECURSOR
1741	10663	20138	1.09	2.0E-03	AA450138.1	EST_HUMAN	zc42a10.r1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone IMAGE:789114 5'
1864	11168	20373	1.15	2.0E-03	AF302891.1	NT	Mus musculus myelin expression factor-3-like protein gene, partial cds
2214	11411	20635	0.81	2.0E-03	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
2643	11731		5.05	2.0E-03	AW137782.1	EST_HUMAN	UI-H-B11-adf-g-10-Q-UJ.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2717010 3'
3394	12821	21762	4.7	2.0E-03	AA450138.1	EST_HUMAN	zc42a10.r1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone IMAGE:789114 5'
3401	12827	21758	0.79	2.0E-03	BF568955.1	EST_HUMAN	602183960.T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300070 3'
3647	12868	21985	5.81	2.0E-03	X87344.1	NT	H. sapiens DNA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes
4091	13288	22308	2.3	2.0E-03	P03374	SWISSPROT	ENV POLYPROTEIN [CONTAINS: COAT PROTEIN GP52; COAT PROTEIN GP38]
4204	13407		9.81	2.0E-03	U68491.1	NT	Rattus norvegicus 5-hydroxytryptamine7 receptor gene, partial cds
4405	13605		0.94	2.0E-03	L35079.1	NT	Porcine rotavirus major outer capsid protein (VP7) mRNA, complete cds
4419	13619		1.04	2.0E-03	AW287380.1	EST_HUMAN	UI-H-BW0-air-g-03-Q-UJ.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:2730413 3'
4543	13738	22838	2.05	2.0E-03	L42512.1	NT	Drosophila melanogaster shortlight class 2 (shs) mRNA, complete cds
4543	13739	22837	2.05	2.0E-03	L42512.1	NT	Drosophila melanogaster shortlight class 2 (shs) mRNA, complete cds
4721	13912		1.94	2.0E-03	R87773.1	EST_HUMAN	yo45e02.s1 Soares adult brain N2b4HB55Y Homo sapiens cDNA clone IMAGE:180890 3'
4751	13942	23044	1.3	2.0E-03	AA908466.1	EST_HUMAN	cl14f05.s1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1623457 3'
5044	14228	23310	0.8	2.0E-03	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
5071	14251	23334	0.71	2.0E-03	P45969	SWISSPROT	HYPOTHETICAL 37.4 KD PROTEIN T08A5.9 IN CHROMOSOME III
6245	14418		1.1	2.0E-03	BE019692.1	EST_HUMAN	b628h05.x1 NIH_MGC_5 Homo sapiens cDNA clone IMAGE:2884249 3'
5503	18057	24091	1.91	2.0E-03	AB014593.1	NT	Homo sapiens mRNA for KIAA0683 protein, partial cds
5541	14765	24131	2.05	2.0E-03	U63711.1	NT	Xenopus laevis xellin mRNA, complete cds
5712	14931	24326	3.67	2.0E-03	P23477	SWISSPROT	ATP-DEPENDENT NUCLEASE SUBUNIT B

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5712	14931	24328	3.67	2.0E-03	P23477	SWISSPROT	ATP-DEPENDENT NUCLEASE SUBUNIT B
5809	15028	24428	2.05	2.0E-03	Q95203	SWISSPROT	CARBONIC ANHYDRASE-RELATED PROTEIN 2 PRECURSOR (CARP 2) (CA-RP II) (CA-XI)
5809	15028	24427	2.05	2.0E-03	Q95203	SWISSPROT	CARBONIC ANHYDRASE-RELATED PROTEIN 2 PRECURSOR (CARP 2) (CA-RP II) (CA-XI)
5811	15028	24429	7.05	2.0E-03	BF308187.1	EST_HUMAN	601887434F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4121408 5'
5826	15043	24447	2.07	2.0E-03	Q8UKP4	SWISSPROT	ADAM-TS 7 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 7) (ADAMTS-7) (ADAM-TS7)
5833	15050	24456	1.68	2.0E-03	X94451.1	NT	L. esculentum mRNA for lysyl-tRNA synthetase (LysRS)
6088	14515	23573	1.76	2.0E-03	AB038502.1	NT	Caenorhabditis elegans mRNA for galectin LEC-11, complete cds
6117	16230	24649	2.9	2.0E-03	BE067688.1	EST_HUMAN	CM4-BT0388-061289-034-d01 BT0388 Homo sapiens cDNA
6481	15678	25148	5.15	2.0E-03	AW592004.1	EST_HUMAN	h07b08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2934035 3' similar to TR:Q80978
6534	15730	25193	7.65	2.0E-03	N20287.1	EST_HUMAN	yx42g06.s1 Soares melanocyte 2N1bHM Homo sapiens cDNA clone IMAGE:264442 3' similar to contains L1.b2 L1 repetitive element;
6534	15730	25194	7.65	2.0E-03	N20287.1	EST_HUMAN	yx42g06.s1 Soares melanocyte 2N1bHM Homo sapiens cDNA clone IMAGE:264442 3' similar to contains L1.b2 L1 repetitive element;
6941	16085	25553	3.18	2.0E-03	P24821	SWISSPROT	TENASCIN PRECURSOR (TN) (HEXABRACHION) (CYTOTACTIN) (NEURONECTIN) (GMEIN) (JI) (MIOTENDINOUS ANTIGEN) (GLIOMA-ASSOCIATED-EXTRACELLULAR MATRIX ANTIGEN) (GP 160- 225) (TENASCIN-C) (TN-C)
7088	16265		6.2	2.0E-03	AA261378.1	EST_HUMAN	zs10a06.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:684754 3'
7685	16780		3.24	2.0E-03	M98524.1	NT	Human dystrophin gene
8022	15522	24970	2.31	2.0E-03	P07354	SWISSPROT	PROTEOGLYCAN LINK PROTEIN PRECURSOR (CARTILAGE LINK PROTEIN) (LP)
8078	17211		2.26	2.0E-03	BF330009.1	EST_HUMAN	RC3-BT0333-310800-115-g04 BT0333 Homo sapiens cDNA
8083	17218	26753	15.54	2.0E-03	Z11740.1	NT	H. sapiens variable number tandem repeat (VNTR) locus DNA
8313	17417		2.5	2.0E-03	A1825745.1	EST_HUMAN	ly65h03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2283989 3' similar to SW:VATG_MANSE
8328	17430	26937	2.71	2.0E-03	AF167618.2	NT	Q25532 VACUOLAR ATP SYNTHASE SUBUNIT G;
8353	17448	26940	1.28	2.0E-03	A084325.1	EST_HUMAN	oy43g06.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1688634 3' similar to TR:P97535 P97535 PS-PLA1 PRECURSOR.;
8378	14500		4.25	2.0E-03	AJ245187.1	NT	Camelus dromedarius crfp19 gene for immunoglobulin heavy chain variable region
8597	18326		2.72	2.0E-03	AV697866.1	EST_HUMAN	AV697868 GKC Homo sapiens cDNA clone GKCXG005 5'
8685	17663	23947	1.54	2.0E-03	Y00508.1	NT	H. sapiens M1 gene for muscarinic acetylcholine receptor
8813	17733		1.56	2.0E-03	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
8870	18181		1.24	2.0E-03	A1375037.1	EST_HUMAN	ta6802.x1 Soares_tad1_fetus_Nb2Hf8_9w Homo sapiens cDNA clone IMAGE:2049051 3' similar to contains Alu repetitive element;

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8995	17856		1.34	2.0E-03	AF129758.1	NT	Homo sapiens MSH55 gene, partial cds; and CLIC1, DDAH, G6b, G6c, G5b, G6d, G6e, G6f, BAT5, G5b, CSK2B, BAT4, G4, Apo M, BAT3, BAT2, AIF-1, 1C7, LST-1, LTB, TNF, and LTA genes, complete cds
9172	18131		2.37	2.0E-03	AV687988.1	EST_HUMAN	AV687988 GKC Homo sapiens cDNA clone GKCGX005 5'
445	8699	18835	1.13	1.0E-03	H98471.1	EST_HUMAN	y98c03.1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:232334 5'
839	10076	19235	2.02	1.0E-03	A1720263.1	EST_HUMAN	as70b08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825
839	10076	19236	2.02	1.0E-03	A1720263.1	EST_HUMAN	Q13825 AU-BINDING PROTEINENYOYL-COA HYDRATASE. ;
1103	10327	19477	2.73	1.0E-03	A1865788.1	EST_HUMAN	as70b08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825
1123	10347	19498	1.49	1.0E-03	A1954572.1	EST_HUMAN	Q13825 AU-BINDING PROTEINENYOYL-COA HYDRATASE. ;
1174	10393	19547	3.1	1.0E-03	A1692616.1	EST_HUMAN	wk88a08.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2422258 3'
1997	11200	20411	4.08	1.0E-03	P47808	SWISSPROT	wk83e10.x1 NCI_CGAP_Mel15 Homo sapiens cDNA clone IMAGE:2551242 3'
2122	11321	20539	7.75	1.0E-03	AJ131018.1	NT	wk88a01.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2339440 3' similar to contains Alu repetitive element;
2837	12175	21308	1.43	1.0E-03	AB033117.1	NT	HIGH MOLECULAR WEIGHT FORM OF MYOSIN I (HMWMI)
3154	12389	21521	1.49	1.0E-03	P18915	SWISSPROT	Homo sapiens SGL gene locus
3154	12389	21522	1.49	1.0E-03	P18915	SWISSPROT	Homo sapiens mRNA for KIAA1291 protein, partial cds
3271	12504	21635	0.84	1.0E-03	P08547	SWISSPROT	Homo sapiens SGL gene locus
3848	12887		1.34	1.0E-03	AB044400.1	NT	Homo sapiens mRNA for KIAA1291 protein, partial cds
3808	13124	22242	0.63	1.0E-03	Z49849.1	NT	CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED)
4427	13627	22721	3.45	1.0E-03	BE839162.1	EST_HUMAN	CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED)
4471	13669	22760	5.28	1.0E-03	BE246536.1	EST_HUMAN	CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED)
4840	14028	23121	2.09	1.0E-03	A1073485.1	EST_HUMAN	CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED)
4840	14028	23122	2.09	1.0E-03	A1073485.1	EST_HUMAN	CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED)
4841	14030		4.02	1.0E-03	BE154087.1	EST_HUMAN	CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED)
5107	14287	23372	7.78	1.0E-03	D49409	SWISSPROT	CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED)
5336	14567	23641	1.91	1.0E-03	AA230951.1	EST_HUMAN	CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED)
5398	14625	23738	3.07	1.0E-03	AJ008345.1	NT	CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED)
5422	14849	23783	1.99	1.0E-03	K03332.1	NT	CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED)
5422	14849	23784	1.99	1.0E-03	K03332.1	NT	CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED)

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Table 4
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5479	14708	24060	1.85	1.0E-03	Q02388	SWISSPROT	COLLAGEN ALPHA (VII) CHAIN PRECURSOR (LONG-CHAIN COLLAGEN) (LC COLLAGEN)
5687	14889		2.54	1.0E-03	X07699.1	NT	Mouse nucleolin gene
5692	14912	24308	3.07	1.0E-03	BE963939.2	EST_HUMAN	601657519R1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875693 3'
5760	14989		9.14	1.0E-03	11526176	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
6141	15325	24780	2.83	1.0E-03	D16826.1	NT	Human gene for fourth somatostatin receptor subtype
6352	15332						Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMK1), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
6379	15559	24984	1.65	1.0E-03	U52111.2	NT	Human TRPM-2 protein gene, exons 1,2 and 3
6442	15639	25108	3.58	1.0E-03	M63378.1	NT	Homo sapiens partial stearin-1 gene
6541	15737	25188	8.04	1.0E-03	AJ251973.1	NT	Homo sapiens exocytosis-like protein 1 (EXTL1) gene, exons 2 through 11, and complete cds
6813	16008	26470	2.89	1.0E-03	AF153980.1	NT	Human class III alcohol dehydrogenase (ADH5) cII subunit mRNA, complete cds
6813	16008	25471	3	1.0E-03	M30471.1	NT	Human class III alcohol dehydrogenase (ADH5) cII subunit mRNA, complete cds
6986	16144	25613	2.52	1.0E-03	AF011400.1	NT	Thermotoga neopolitana alpha-1,6-galactosidase (agaA) gene, complete cds
6986	16144	25614	2.52	1.0E-03	AF011400.1	NT	Thermotoga neopolitana alpha-1,6-galactosidase (agaA) gene, complete cds
7258	16478	25689	1.89	1.0E-03	AW962383.1	EST_HUMAN	RC1-CT0279-181099-011-409 CT0279 Homo sapiens cDNA
7258	16478	25670	1.89	1.0E-03	AW362383.1	EST_HUMAN	RC1-CT0279-181099-011-409 CT0279 Homo sapiens cDNA
7336	16552	26041	3.07	1.0E-03	BE170859.1	EST_HUMAN	QV3-HT0543-220300-130-403 HT0543 Homo sapiens cDNA
7400	16813		3.38	1.0E-03	AI583847.1	EST_HUMAN	R73612.x1 NCI_CGAP_HSC3 Homo sapiens cDNA clone IMAGE:2248446 3' similar to TR:Q28185 Q28185 PVA1 GENE.;
7468	16876	26159	1.64	1.0E-03	AW237482.1	EST_HUMAN	Xm72d12.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2688751 3'
7717	16916		4.02	1.0E-03	AV768949.1	EST_HUMAN	AV759949 MDS Homo sapiens cDNA clone MDSDDF11 5'
8307	17413	26835	5.13	1.0E-03	BE694488.1	EST_HUMAN	601433087F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918524 6'
8778	17708	23958	1.55	1.0E-03	9507208	NT	Rattus norvegicus transformation related protein 63 (Trp63), mRNA
8903	18308		3.08	1.0E-03	AI347355.1	EST_HUMAN	tc05h11.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:2065013 3' similar to contains Alu repetitive element
8921	18330	23802	4.03	1.0E-03	BE780572.1	EST_HUMAN	601468878F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3872035 5'
8225	14389	23482	1.31	9.0E-04	L11910.1	NT	Human retinoblastoma susceptibility gene exons 1-27, complete cds
5527	14751		1.66	9.0E-04	P06727	SWISSPROT	APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV)
4161	13365		5.66	8.0E-04	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
4776	13685	23068	2.33	8.0E-04	U28185.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
7705	16804		2.81	8.0E-04	AA777084.1	EST_HUMAN	z24c10.s1 Soares_fetal_NbHH19W Homo sapiens cDNA clone IMAGE:377874 3'
7843	17035		2.58	8.0E-04	AI571089.1	EST_HUMAN	br55a08.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2176310 3'
1795	11004	20189	1.5	7.0E-04	L41825.1	NT	Homo sapiens CYP17 gene, 5' end

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2363	11558	20778	0.99	7.0E-04	U28185.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
2874	11858	21071	1.13	7.0E-04	AL183210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3248	12481	21613	1.3	7.0E-04	4885170	NT	Homo sapiens chromosome X open reading frame 8 (CXORF8) mRNA
5880	15087		2.17	7.0E-04	AI768331.1	EST_HUMAN	wg38092.x1 Soares NSF_F8_GW_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2387209 3'
8100	17234		3.32	7.0E-04	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
8120	17234	28785	2.18	7.0E-04	Z40561.1	EST_HUMAN	HSC28A072 normalized infant brain cDNA Homo sapiens cDNA clone c-28a07 3'
8847	17755		3.88	7.0E-04	BE077941.1	EST_HUMAN	CM1-BT0814-110300-142-b12 BT0814 Homo sapiens cDNA
8098	17912		3.4	7.0E-04	R17338.1	EST_HUMAN	Y913c08.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:32298 5'
8125	17838		3.87	7.0E-04	6005855	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
2856	11838		1.75	6.0E-04	BF341380.1	EST_HUMAN	602013339F1 NCI CGAP_Bim84 Homo sapiens cDNA clone IMAGE:4149287 5'
3938	13152	22288	1.76	6.0E-04	AI862525.1	EST_HUMAN	WJ15a11.x1 NCI CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2402878 3'
4085	13275	22375	1.44	6.0E-04	K01315.1	NT	Homo sapiens epsilon-1 pseudogene (IGHEP1) gene, 5' flanking region
4085	13275	22376	1.44	6.0E-04	K01315.1	NT	Homo sapiens epsilon-1 pseudogene (IGHEP1) gene, 5' flanking region
4188	13370	22489	3.95	6.0E-04	U45983.1	NT	Homo sapiens COR8 chemokine receptor (CMKBR8) gene, complete cds
7088	18243		5.71	8.0E-04	AL048507.2	EST_HUMAN	DKFZp588M2024_r1 588 (synonym: hute1) Homo sapiens cDNA clone DKFZp588M2024
7101	18278	25758	2.89	6.0E-04	BE005850.1	EST_HUMAN	RC2-BN0120-250400-012-h11 BN0120 Homo sapiens cDNA
8019	17158	28694	2.73	6.0E-04	AJ220042.1	NT	Homo sapiens 859 kb contig between AML1 and CBR1 on chromosome 21q22, segment 2/3
8101	17235	26771	3.28	6.0E-04	AW013847.1	EST_HUMAN	UI-H-B10-sab-e-09-0-UJ.s1 NCI CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708825 3'
8152	17284		2.49	6.0E-04	Q01768	SWISSPROT	NUCLEOSIDE DIPHOSPHATE KINASE B (NDK B) (NDP KINASE B) (NIM23-M2) (P18)
8488	18208		2.39	6.0E-04	AW380519.1	EST_HUMAN	RC1-HT0289-261189-012-d08 HT0289 Homo sapiens cDNA
867	8903	18028	7.85	6.0E-04	O10341	SWISSPROT	HYPOTHETICAL 29.3 KD PROTEIN (ORF82)
1483	10708		1.5	5.0E-04	AW851844.1	EST_HUMAN	QV0-CT0225-021099-030-a07 CT0225 Homo sapiens cDNA
3391	12818	21749	1.57	5.0E-04	AA548831.1	EST_HUMAN	nk27611.s1 NCI CGAP_Co11 Homo sapiens cDNA clone IMAGE:1014784 3' similar to contains Alu repetitive element
5428	14858	23794	2.85	5.0E-04	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
5947	15183	24577	4.71	5.0E-04	AA156080.1	EST_HUMAN	z033b08.r1 StrataGene cdon (#937204) Homo sapiens cDNA clone IMAGE:588883 5'
8248	15427	24887	12.78	5.0E-04	M23604.1	NT	Gorilla gorilla involucrin gene medium allele, complete cds
8444	15641	25107	6.01	5.0E-04	AI188382.1	EST_HUMAN	qd13f08.x1 Soares_placenta_8t6weeks_2N6HP8b6W Homo sapiens cDNA clone IMAGE:1723818 3' similar to gb:X51802_cds1 VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPTOR 1 (HUMAN)/contains Alu repetitive element
8988	16148	25817	5.82	5.0E-04	AW270938.1	EST_HUMAN	xs08a02.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2788858 3'
7649	16764		4.31	5.0E-04	AL048507.2	EST_HUMAN	DKFZp588M2024_r1 588 (synonym: hute1) Homo sapiens cDNA clone DKFZp588M2024

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8203	14658	23784	12.77	5.0E-04	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
8428	18140		2.42	5.0E-04	AA568513.1	EST_HUMAN	h15102.s1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:913875
878	9823	19054	1.37	4.0E-04	U32748.1	NT	Haemophilus influenzae Rd section 63 of 163 of the complete genome
857	10083	19255	1.36	4.0E-04	A1720263.1	EST_HUMAN	es70b08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334038 3' similar to TR:Q13825
857	10083	19256	1.38	4.0E-04	A1720263.1	EST_HUMAN	es70b08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334038 3' similar to TR:Q13825
1481	10874	19847	2.46	4.0E-04	AW753358.1	EST_HUMAN	Q13825 AU-BINDING PROTEIN/ENOYL-COA HYDRATASE.;
2052	11253	20487	1.21	4.0E-04	AL183278.2	NT	RC3-CT0254-130100-023-401 CT0254 Homo sapiens cDNA
2103	11303		0.9	4.0E-04	AL046704.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C078
2580	11778	20895	2.53	4.0E-04	O86815	SWISSPROT	DKFZp434D059_r1 434 (synonym: hbs3) Homo sapiens cDNA clone DKFZp434D059 5'
3128	12363	21483	1.41	4.0E-04	AF281074.1	NT	SERICIN-2 (SILK GUM PROTEIN 2)
3335	12584	21702	0.81	4.0E-04	AV686824.1	EST_HUMAN	Homo sapiens neurophilin 2 (NRP2) gene, complete cds, alternatively spliced
4314	13515	22808	3.3	4.0E-04	AA576331.1	EST_HUMAN	AV686824 GKC Homo sapiens cDNA clone GKCFFH07 5'
4314	13515	22809	3.3	4.0E-04	AA576331.1	EST_HUMAN	nh10a10.s1 NCI_CGAP_Cot1 Homo sapiens cDNA clone IMAGE:951930 3' similar to gb:M21121 T-CELL
4334	13730	22827	2.26	4.0E-04	AA086324.1	EST_HUMAN	SPECIFIC RANTES PROTEIN PRECURSOR (HUMAN);
5119	14286	23388	2.98	4.0E-04	BE580680.1	EST_HUMAN	zn61c08.s1 Stratagene muscle 837208 Homo sapiens cDNA clone IMAGE:562870 3'
5180	14388		0.88	4.0E-04	BE178880.1	EST_HUMAN	801345895F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3678910 5'
6037	15832	25283	2.88	4.0E-04	N25507.1	EST_HUMAN	PM4-HT0608-030400-001-h11 HT0608 Homo sapiens cDNA
8814	18112		1.78	4.0E-04	AF254822.1	NT	yc30a12.r1 Soares melanocyte 2Nblm Homo sapiens cDNA clone IMAGE:264142 5'
8874	18085		1.81	4.0E-04	Q06880	SWISSPROT	Homo sapiens SMARCA4 isoform (SMARCA4) gene, complete cds, alternatively spliced
159	9441	18574	3.52	3.0E-04	AL119428.1	EST_HUMAN	FORMIN (LIMB DEFORMITY PROTEIN)
200	9480	18613	2.15	3.0E-04	P49259	SWISSPROT	DKFZp761J221_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761J221 5'
880	10125	19288	2.39	3.0E-04	U83991.1	NT	180 KD SECRETORY PHOSPHOLIPASE A2 RECEPTOR PRECURSOR (PLA2-R)
1807	11018	20209	1.27	3.0E-04	AI282100.1	EST_HUMAN	Human short chain acyl CoA dehydrogenase gene, exons 1 and 2
1821	11028		1.12	3.0E-04	AI368674.1	EST_HUMAN	q228403.y1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2028187 5'
3270	12511	21641	3.59	3.0E-04	P25147	SWISSPROT	h23a02.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2118082 3'
3941	13157	22274	3.38	3.0E-04	P49448	SWISSPROT	INTERNALIN B PRECURSOR
4033	13243		1.73	3.0E-04	AJ271735.1	NT	GLUTAMATE DEHYDROGENASE 2 PRECURSOR (GDH)
4089	13279		1.92	3.0E-04	BE140809.1	EST_HUMAN	Homo sapiens Xq pseudautosomal region: segment 1/2
4831	14020		5.35	3.0E-04	BE153778.1	EST_HUMAN	RCO-HT0014-310589-028 HT0014 Homo sapiens cDNA
							PMO-HT0339-180200-007-g12 HT0339 Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4803	14081	23184	0.85	3.0E-04	AW837723.1	EST_HUMAN	QV3-DT0045-221288-048-d09 DT0045 Homo sapiens cDNA
5288	14480	23528	1.22	3.0E-04	L78833.1	NT	Human BRCA1, Rho7 and vcl genes, complete cds, and lpf35 gene, partial cds
5732	14951		5.43	3.0E-04	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081
6008	15256	24880	1.93	3.0E-04	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
6548	15742	25203	6.87	3.0E-04	P22807	SWISSPROT	FIBROBLAST GROWTH FACTOR RECEPTOR 3 PRECURSOR (FGFR-3)
7202	16379	25860	7.45	3.0E-04	AA781201.1	EST_HUMAN	aj24g05.s1 Soares testis NHT Homo sapiens cDNA clone 1391288 3' similar to gb:M36072 80S RIBOSOMAL PROTEIN L7A (HUMAN);
8380	18348	23808	2.85	3.0E-04	AA228301.1	EST_HUMAN	nc38604.r1 NCL CGAP_P2 Homo sapiens cDNA clone IMAGE:1010430 similar to contains L1.L2 L1 repetitive element;
8770	18188	23758	2.87	3.0E-04	AB018292.1	NT	Homo sapiens mRNA for KIAA0749 protein, partial cds
9191	17079		2.55	3.0E-04	AL134483.1	EST_HUMAN	DKFZp547L185_r1 547 (synonym: hfbt1) Homo sapiens cDNA clone DKFZp547L185 5'
179	9459	18591	1.76	2.0E-04	AF217798.1	NT	Homo sapiens SCG10 like-protein, helicase-like protein NHL, M88, and ADP-ribosylation factor related protein 1 (AFRFRP1) genes, complete cds
485	9737	18870	3.32	2.0E-04	AU146707.1	EST_HUMAN	AU146707 HEMBB1 Homo sapiens cDNA clone HEMBB1001263 3'
917	10182	18312	10.84	2.0E-04	M88524.1	NT	Human dystrophin gene
917	10182	18313	10.84	2.0E-04	M88524.1	NT	Human dystrophin gene
1187	10408		4.9	2.0E-04	AI286021.1	EST_HUMAN	qh88e11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1855052 3' similar to contains MER3.b2 MER3 repetitive element;
1184	10414		2.28	2.0E-04	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
1800	11008		1.44	2.0E-04	AF224268.1	NT	Mus musculus 5' flanking region of Pitk3 gene
2160	11348		1.37	2.0E-04	AA478980.1	EST_HUMAN	zu39b05.s1 Soares ovary tumor NBHOT Homo sapiens cDNA clone IMAGE:740337 3' similar to contains Alu repetitive element;
2539	11727	20944	2.71	2.0E-04	U68081.1	NT	Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV28S1P, TCRBV18S1P, TCRBV16S1, TCRBV11S1A1T, HVB nalic, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY5, TRY6, TRY7, TRY8, TCRBD1, TCRBJ1S1, TCRBJ1S2,>
2844	12182	21315	1.02	2.0E-04	AI124529.1	EST_HUMAN	am58c09.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1539760 3'
3308	12538	21872	0.74	2.0E-04	5174736	NT	Homo sapiens tubulin, beta, 4 (TUBB4) mRNA
3414	12840	21768	2.01	2.0E-04	BE092317.1	EST_HUMAN	QV2-BT0638-070500-194-507 BT0638 Homo sapiens cDNA
3880	13106	22224	0.7	2.0E-04	AW978441.1	EST_HUMAN	EST380550 MAGe reductase, MAGP Homo sapiens cDNA
4125	13331		8.15	2.0E-04	U01028.1	NT	Phaseolus vulgaris nitrate reductase (PVNR2) gene, complete cds
4672	13868	22987	1.32	2.0E-04	H88285.1	EST_HUMAN	y001011.1 Soares pineal gland_N3HPG Homo sapiens cDNA clone IMAGE:232558 5'
4872	13866	22968	1.32	2.0E-04	H88285.1	EST_HUMAN	y001011.1 Soares pineal gland_N3HPG Homo sapiens cDNA clone IMAGE:232558 5'
4807	13996		1.61	2.0E-04	U09228.1	NT	Gallus gallus proteasome 28 kDa subunit homolog mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5090	14270	23354	1.31	2.0E-04	AB037897.1	NT	Danio rerio hegagrono gene, exons 1 to 6, partial cds
5470	14898	24049	1.85	2.0E-04	AI890892.1	EST_HUMAN	ig03b11.x1 NCI_CGAP_U13 Homo sapiens cDNA clone IMAGE:2207709 3'
6178	16360		2.39	2.0E-04	AU121712.1	EST_HUMAN	AU121712 MAMMA1 Homo sapiens cDNA clone MAMMA1000788 5'
6343	15524		13.77	2.0E-04	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
7428	16638	26131	6.33	2.0E-04	AV730373.1	EST_HUMAN	AV730373 HTF Homo sapiens cDNA clone HTFAA01 5'
7853	17043	26560	6.26	2.0E-04	AI440282.1	EST_HUMAN	ig01111.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2140269 3' similar to contains Alu repetitive element
7864	17143	26678	3.15	2.0E-04	AW136740.1	EST_HUMAN	UI-H-B10-aa-b-e-09-0-J1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2717190 3'
8287	17394	26824	7.68	2.0E-04	AA320338.1	EST_HUMAN	EST22678 Adipose tissue, white II Homo sapiens cDNA 5' end similar to EST containing Alu repeat
776	10015	19163	1.88	1.0E-04	H89846.1	EST_HUMAN	yz26c09.s1 Soares melanocytes 2NBM Homo sapiens cDNA clone IMAGE:262864 3' similar to contains L1.1 L1 repetitive element
1082	10307	19458	2.39	1.0E-04	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
1122	10346	19496	3.89	1.0E-04	AW013847.1	EST_HUMAN	UI-H-B10-aa-b-e-09-0-J1.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708825 3'
1122	10348	19497	3.89	1.0E-04	AW013847.1	EST_HUMAN	UI-H-B10-aa-b-e-09-0-J1.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708825 3'
1340	10554		3.92	1.0E-04	U62918.1	NT	Anguilla anguilla dopamine D1A1 receptor (d1A1) gene, complete cds
1605	10819	19894	3.55	1.0E-04	AF148805.1	NT	Kaposi's sarcoma-associated herpesvirus ORF 68 gene, partial cds; and ORF 69, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GPCR, putative phosphoribosylformylglycinamide synthase, and LAMP (LAMP) genes, complete cds
1605	10819	19895	3.55	1.0E-04	AF148805.1	NT	Kaposi's sarcoma-associated herpesvirus ORF 68 gene, partial cds; and ORF 69, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GPCR, putative phosphoribosylformylglycinamide synthase, and LAMP (LAMP) genes, complete cds
1829	11037	20233	1.75	1.0E-04	AB048342.1	NT	Equus caballus DNA, chromosome 24q14, microsatellite TKY36
2648	11831	21044	0.91	1.0E-04	BE218833.1	EST_HUMAN	hw45c08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176368 3'
2648	11831	21045	0.91	1.0E-04	BE218833.1	EST_HUMAN	hw45c08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176368 3'
3252	12485	21617	0.95	1.0E-04	Q82203	SWISSPROT	SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SPLICING FACTOR 3A SUBUNIT 2) (SF3A66)
3716	12638	22054	0.82	1.0E-04	AI440282.1	EST_HUMAN	ig01111.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2140269 3' similar to contains Alu repetitive element
4037	13247	22360	2.01	1.0E-04	M14042.1	NT	Mouse alpha 1 type-IV collagen mRNA
4058	13269	22371	1.18	1.0E-04	AV847727.1	EST_HUMAN	AV847727 GLC Homo sapiens cDNA clone GLCBB04 3'
4460	13658	22752	1.09	1.0E-04	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
6169	16342	24779	9.99	1.0E-04	AI251980.1	EST_HUMAN	qv57d10.x1 NCI_CGAP_Ov62 Homo sapiens cDNA clone IMAGE:1985683 3'
6322	16342	24779	12.88	1.0E-04	AI251980.1	EST_HUMAN	qv57d10.x1 NCI_CGAP_Ov62 Homo sapiens cDNA clone IMAGE:1985683 3'
6863	16053	25521	3.89	1.0E-04	AI806220.1	EST_HUMAN	wf26c08.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2358742 3'

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Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7128	16305		5.3	1.0E-04	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
7881	17069		2.28	1.0E-04	M28587.1	NT	Mouse alpha leukocyte interferon gene, complete cds
8159	17291	26832	1.93	1.0E-04	AB032988.1	NT	Homo sapiens mRNA for KIAA1142 protein, partial cds
8189	17321	26864	1.97	1.0E-04	AW269061.1	EST_HUMAN	xx49g12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2816518 3'
8214	17345	26894	1.65	1.0E-04	Q03696	SWISSPROT	NEURONAL-GLIAL CELL ADHESION MOLECULE PRECURSOR (NG-CAM)
8214	17345	26885	1.65	1.0E-04	Q03696	SWISSPROT	NEURONAL-GLIAL CELL ADHESION MOLECULE PRECURSOR (NG-CAM)
8549	18158		1.5	1.0E-04	BE676398.1	EST_HUMAN	7f28a10.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3286058 3' similar to contains L1.13 L1 repetitive element;
705	6847	19083	2.78	9.0E-05	AA718933.1	EST_HUMAN	sh45c11.1.s1 Soares_testis_NHT Homo sapiens cDNA clone 1282488 3'
6805	18062		2.8	9.0E-05	D85808.1	NT	Homo sapiens gene for cholesterylkin type-A receptor, complete cds
7697	18898	26405	2.85	9.0E-05	AW073078.1	EST_HUMAN	xx3-4g05.x1 NCI_CGAP_Br18 Homo sapiens cDNA clone IMAGE:2568728 3' similar to contains L1.12 L1 repetitive element;
7794	18987	26501	1.84	9.0E-05	AI287878.1	EST_HUMAN	qv23f08.x1 NCI_CGAP_Lym8 Homo sapiens cDNA clone IMAGE:1882435 3' similar to contains element
8139	14862	24247	4.58	9.0E-05	Q60716	SWISSPROT	MIR repetitive element; PROLYL 4-HYDROXYLASE ALPHA-2 SUBUNIT PRECURSOR
8604	18218		3.76	9.0E-05	AF128756.1	NT	Homo sapiens MSH55 gene, partial cds; and CLIC1, DDAH, G6b, G6c; G5b, G6d, G6e, G6f, BAT5, G5b, CSK2B, BAT4, G4, Apo M, BAT3, BAT2, AIF-1, 1C7, LST-1, LTB, TNF, and LTA genes, complete cds
831	10089	19224	1.8	8.0E-05	AJ251848.1	NT	Pisum sativum mRNA for beta-1,3 glucanase (gns2 gene)
874	10110		7.89	8.0E-05	AJ251848.1	NT	Pisum sativum mRNA for beta-1,3 glucanase (gns2 gene)
4477	13675	22784	0.69	8.0E-05	AW044605.1	EST_HUMAN	wy79a04.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2654638 3'
7710	18809	26419	2.96	8.0E-05	M89197.1	NT	Human haptoglobin and haptoglobin-related protein (HP and HPR) genes, complete cds
8228	18201		2.43	8.0E-05	AA279333.1	EST_HUMAN	z88h01.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:704593 3' similar to contains Alu repetitive element; contains element MSR1 repetitive element;
352	9620	18747	7.26	7.0E-05	AW847445.1	EST_HUMAN	RC3-CT0208-220899-011-E04 CT0208 Homo sapiens cDNA
352	9620	18748	7.26	7.0E-05	AW847445.1	EST_HUMAN	RC3-CT0208-220899-011-E04 CT0208 Homo sapiens cDNA
674	9824	18943	1.33	7.0E-05	L48075.1	EST_HUMAN	HUM072014F Human foetus cDNA Homo sapiens cDNA clone EST HFD072014
574	9824	18944	1.33	7.0E-05	L48075.1	EST_HUMAN	HUM072014F Human foetus cDNA Homo sapiens cDNA clone EST HFD072014
1002	10288	19439	1.12	7.0E-05	Q22949	SWISSPROT	PROBABLE GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE, MITOCHONDRIAL PRECURSOR (GPAT)
2678	11860	21074	4.06	7.0E-05	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
3122	12367	21486	5.35	7.0E-05	AB009080.1	NT	Dichostellium discoidium gene for TRFA, complete cds
3678	12800		0.97	7.0E-05	AI432413.1	EST_HUMAN	tg73c08.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:2114418 3'
4368	13588	22664	1.5	7.0E-05	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001

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Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4440	13640	22731	0.61	7.0E-05	U00980.1	NT	Caenorhabditis elegans Skip1p homolog mRNA, complete cds
4947	14134	23228	0.85	7.0E-05	9845300	NT	Rat cytomegalovirus Mgastricht, complete genome
6636	16080	26550	6.65	7.0E-06	T07085.1	EST_HUMAN	EST04984 Fetal brain, Stratagene (cat#836208) Homo sapiens cDNA clone HFBED80
7720	16819		6.81	7.0E-05	10835048	NT	Homo sapiens aeroglycan, epsilon (SGCE), mRNA
1898	11189	20409	1.41	6.0E-05	4885170	NT	Homo sapiens chromosome X open reading frame 8 (CXORF8) mRNA
1898	11189	20410	1.41	6.0E-05	4885170	NT	Homo sapiens chromosome X open reading frame 8 (CXORF8) mRNA
2549	11737	20855	1.06	6.0E-05	A1653241.1	EST_HUMAN	wb54H08.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2309631 3' similar to gb.J03250 DNA
2768	9829	19059	2.78	6.0E-05	AF053830.1	NT	TOPOISOMERASE I (HUMAN);
5822	14845	24225	3.42	6.0E-05	Q12860	SWISSPROT	Homo sapiens monocyte/neutrophil elastase inhibitor gene, complete cds
5822	14845	24226	3.42	6.0E-05	Q12860	SWISSPROT	CONTACTIN PRECURSOR (GLYCOPROTEIN GP135)
6814	15810	25286	3.79	6.0E-05	AW866829.1	EST_HUMAN	CONTACTIN PRECURSOR (GLYCOPROTEIN GP135)
7334	16550	26040	4.35	6.0E-05	R75639.1	EST_HUMAN	PM4-NN0050-310300-001-f10 NN0050 Homo sapiens cDNA
8050	17186	26725	4.17	6.0E-05	AA044015.1	EST_HUMAN	y160408.s1 Soares placenta Nib2HP Homo sapiens cDNA clone IMAGE:143535 3' similar to contains Alu repetitive element; contains LTR7 repetitive element;
8922	18169	23782	8.66	6.0E-05	AW890110.1	EST_HUMAN	z159802.1 Soares_pregnant_uterus_NHPU Homo sapiens cDNA clone IMAGE:487035 5'
1407	10620	19784	59.84	5.0E-05	AW382088.1	EST_HUMAN	MF0-NT0038-250400-001-f09 NT0038 Homo sapiens cDNA
1831	11039		1.35	5.0E-05	8823891	NT	QV4-ST0234-241106-040-h11 ST0234 Homo sapiens cDNA
3957	13172	22287	3.89	6.0E-05	AJ251894.1	NT	Homo sapiens 22kDa peroxisomal membrane protein-like (LOC55895), mRNA
5453	14679	23839	11.84	5.0E-05	X58855.1	NT	Homo sapiens partial SLC22A3 gene for extraneuronal monoamine transporter (EMT), exon 1
5651	14874	24261	3.01	5.0E-05	AV633544.1	EST_HUMAN	Human MLC1emb gene for embryonic myosin alkaline light chain, 3'UTR
8601	17776		3.79	5.0E-05	P49193	SWISSPROT	AV633544 GLC Homo sapiens cDNA clone GLCMA06 3'
8878	17776		4.48	5.0E-05	P49183	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
2759	9511		3.93	4.0E-05	U12821.1	NT	RETINAL-BINDING PROTEIN (RALBP)
4479	13677	22768	0.73	4.0E-05	P49193	SWISSPROT	Human renin (REN) gene, 5' flanking region
4479	13677	22767	0.73	4.0E-05	P49183	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
4862	14080		0.95	4.0E-05	AF164488.1	NT	RETINAL-BINDING PROTEIN (RALBP)
5042	14226	23309	0.66	4.0E-05	AF212313.1	NT	Cryptosporidium parvum isolate Zaire 15 kDa glycoprotein gp15 gene, partial cds
6823	16116		5.98	4.0E-05	AF202635.1	NT	Drosophila melanogaster senseless protein (sens) gene, complete cds
7352	16588	28058	5.03	4.0E-05	AW627048.1	EST_HUMAN	Homo sapiens PP1200 mRNA, complete cds
8471	17524	24025	1.47	4.0E-05	AL163262.2	NT	h136c07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2874380 3' similar to contains element MIR repetitive element;
8560	17581		1.54	4.0E-05	AW117580.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C052
8258	18024		1.29	4.0E-05	AA417756.1	EST_HUMAN	xd63c08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2605182 3'

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Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
687	9830	19081	0.64	3.0E-05	AI248081.1	EST_HUMAN	qh84c10.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849458 3' similar to contains Alu repetitive element; contains element KER repetitive element;
1068	10292	19443	0.87	3.0E-05	AW273851.1	EST_HUMAN	xy24g03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2814100 3'
1139	10382	19511	2.89	3.0E-05	BF037898.1	EST_HUMAN	601461483.F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3885142 5'
1139	10382	19512	2.89	3.0E-05	BF037898.1	EST_HUMAN	601461483.F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3885142 5'
3261	12484		0.87	3.0E-05	AI288819.1	EST_HUMAN	q191g11.x1 Soares_NhlMPu_S1 Homo sapiens cDNA clone IMAGE:1878748 3' similar to TR:O08632
4378	13578	22878	5.19	3.0E-05	BE168211.1	EST_HUMAN	O08632 GLYCINE TYROSINE-RICH HAIR PROTEIN.;
4378	13578	22877	5.19	3.0E-05	BE168211.1	EST_HUMAN	PM1-HT0521-120200-001-e10 HT0521 Homo sapiens cDNA
4482	13680	22763	0.9	3.0E-05	AA368879.1	EST_HUMAN	PM1-HT0521-120200-001-e10 HT0521 Homo sapiens cDNA
4482	13680	22764	0.8	3.0E-05	AA368879.1	EST_HUMAN	EST79898 Placenta 1 Homo sapiens cDNA similar to similar to p53-associated protein
4589	13783		0.89	3.0E-05	AL163302.2	NT	EST79898 Placenta 1 Homo sapiens cDNA similar to similar to p53-associated protein
4621	13815	22905	0.83	3.0E-05	AF148773.1	NT	Homo sapiens chromosome 21 segment H921G102
4855	9830	19081	0.83	3.0E-05	AI248081.1	EST_HUMAN	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
5471	14697	24050	1.83	3.0E-05	11072102	NT	qh84c10.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849458 3' similar to contains Alu repetitive element; contains element KER repetitive element;
6881	16169		4.49	3.0E-05	AI768331.1	EST_HUMAN	Mus musculus myosin light chain 2, precursor lymphocyte-specific (MyLC2a), mRNA
8484	17532		1.87	3.0E-05	L77570.1	NT	wg36f09.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2387209 3'
2292	11487	20707	2.08	2.0E-05	AI286021.1	EST_HUMAN	Homo sapiens DIGeorge syndrome critical region, centromeric end
2545	11733	20950	4.57	2.0E-05	M13782.1	NT	qh88e11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1855052 3' similar to contains MER3.b2 MER3 repetitive element;
2873	11855		6.59	2.0E-05	AA160582.1	EST_HUMAN	Human adenosine deaminase (ADA) gene, complete cds
3102	12338	21496	1.76	2.0E-05	BE060036.1	EST_HUMAN	zq46a12.r1 Stratagene hNT neuron (#837233) Homo sapiens cDNA clone IMAGE:632734 5' similar to contains Alu repetitive element; contains element L1 repetitive element;
3322	12551	21695	0.86	2.0E-05	AF184614.1	NT	RC3-BT0319-120200-014-H08 BT0319 Homo sapiens cDNA
3348	12578	21717	0.93	2.0E-05	X89211.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
3489	12894		0.89	2.0E-05	X95465.1	NT	H. sapiens DNA for endogenous retroviral like element
3785	13013		1.31	2.0E-05	AL038107.1	EST_HUMAN	S. cerevisiae 12.8 Kbp fragment of the left arm of chromosome XV
4802	14080	23183	0.77	2.0E-05	AJ131016.1	NT	DKFZ568084_r1 588 (synonym: hfrd2) Homo sapiens cDNA clone DKFZp5881084 5'
5287	14440	23513	32.31	2.0E-05	AA084052.1	EST_HUMAN	Homo sapiens SCL gene locus
5555	14778	24147	1.75	2.0E-05	AJ011712.1	NT	zn16b10.s1 Stratagene neuroepithelium NT2RAM1 937234 Homo sapiens cDNA clone IMAGE:547579 3' similar to contains L1.11 L1 repetitive element;
5944	15180	24573	2.4	2.0E-05	AA714330.1	EST_HUMAN	Homo sapiens TNNT1 gene, exons 1-11 (and joined CDS)
6042	15210	24630	1.9	2.0E-05	Y08926.1	NT	rw06d12.s1 NCI CGAP_SS1 Homo sapiens cDNA clone IMAGE:1238519 3'
							P. falciparum mRNA for AARP1 protein, partial

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6052	15220		9.31	2.0E-05	AI991025.1	EST_HUMAN	wu35h07.x1 Soares_Dieckgraefe_cdon_NHCD Homo sapiens cDNA clone IMAGE:2522077 3'
6142	15328	24761	2.28	2.0E-05	AF224282.1	NT	Heterodontus francisci HoxA10 (HoxA10), HoxA9 (HoxA9), HoxA7 (HoxA7), HoxA6 (HoxA6), HoxA5 (HoxA5), HoxA4 (HoxA4), HoxA3 (HoxA3), HoxA2 (HoxA2), and HoxA1 (HoxA1) genes, complete cds
6142	15328	24762	2.28	2.0E-05	AF224282.1	NT	Heterodontus francisci HoxA10 (HoxA10), HoxA9 (HoxA9), HoxA7 (HoxA7), HoxA6 (HoxA6), HoxA5 (HoxA5), HoxA4 (HoxA4), HoxA3 (HoxA3), HoxA2 (HoxA2), and HoxA1 (HoxA1) genes, complete cds
7223	18400	25885	5.08	2.0E-05	N41751.1	EST_HUMAN	yw81a08.r1 Soares_placenta_8to8weeks_2NbHP8b9W Homo sapiens cDNA clone IMAGE:258570 5'
7223	18400	25888	5.08	2.0E-05	N41751.1	EST_HUMAN	yw81a08.r1 Soares_placenta_8to8weeks_2NbHP8b9W Homo sapiens cDNA clone IMAGE:258570 5'
7238	15220		2.39	2.0E-05	AI991025.1	EST_HUMAN	wu35h07.x1 Soares_Dieckgraefe_cdon_NHCD Homo sapiens cDNA clone IMAGE:2522077 3'
7888	18423	25910	3.15	2.0E-05	BE17580.1	EST_HUMAN	RCS-HT0582-280300-012-E12 HT0582 Homo sapiens cDNA
8610	18125		5.28	2.0E-05	BE348228.1	EST_HUMAN	hw21a03.x1 NCI_CGAP_Ki67 Homo sapiens cDNA clone IMAGE:3183532 3' similar to TR:Q12832
8723	18298		6.07	2.0E-05	AW074804.1	EST_HUMAN	Q12832 GLYCOPHORIN HEP2; x888a03.x1 NCI_CGAP_Co17 Homo sapiens cDNA clone IMAGE:2573832 3' similar to contains L1.b3 L1 repetitive element
8773	18110		1.62	2.0E-05	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
8936	17816	23928	1.39	2.0E-05	AU131513.1	EST_HUMAN	AU131513 NT2RP3 Homo sapiens cDNA clone NT2RP3002707 5'
2855	12023	21050	1.24	1.0E-05	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C032
3629	12850	21869	1.97	1.0E-05	AF088273.1	NT	Drosophila melanogaster strain Larito 120 Suppressor of Hairless (Su(H)) gene, partial cds
3801	13019		1.02	1.0E-05	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
3944	13160	22278	11.49	1.0E-05	P81274	SWISSPROT	MOSAIC PROTEIN LGN
4282	13485	22556	1.66	1.0E-05	AA431119.1	EST_HUMAN	zw68g04.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:781494 5'
4887	14055	23149	1.7	1.0E-05	AW419134.1	EST_HUMAN	xy48g11.x1 NCI_CGAP_Lu34.1 Homo sapiens cDNA clone IMAGE:2850548 3'
4988	14173	23283	0.87	1.0E-05	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
6116	15228	24848	2.8	1.0E-05	AA641848.1	EST_HUMAN	ns18g02.at1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1184114 3' similar to contains L1.t1 L1 L1 repetitive element
6118	15302	24734	12.58	1.0E-05	4505844	NT	Homo sapiens phospholipase A2, group X (PLA2G10) mRNA, and translated products
6750	15945		3.79	1.0E-05	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
6789	15984	25444	2.49	1.0E-05	AA452578.1	EST_HUMAN	z35h12.at1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:788519 3' similar to gb:L02832 PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (HUMAN);

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Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6861	16040	26504	15.7	1.0E-05	AA236110.1	EST_HUMAN	zs05e11.1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:684332 5' similar to contains Alu repetitive element/contains element TAR1 repetitive element;
7493	16700	26185	2.48	1.0E-05	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
7493	16700	26186	2.48	1.0E-05	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
2632	11815	21034	5.6	9.0E-06	AI583811.1	EST_HUMAN	h73606.x1 NCI_CGAP_HSC3 Homo sapiens cDNA clone IMAGE:2240386 3'
3061	12297	21421	5.75	9.0E-06	AI218883.1	EST_HUMAN	qg11b08.x1 Soares_placenta_8tc0wec0s_2Nbt-IP8t09W Homo sapiens cDNA clone IMAGE:1759181 3'
3598	12809		3.68	9.0E-06	M81755.1	NT	Human alanine:glyoxylate aminotransferase (AGXT) gene, exons 1 and 2
5617	14840	24218	2.46	9.0E-06	L23416.1	NT	Homo sapiens differentiation antigen CD20 gene, exons 5, 6
6408	15587	25048	11.37	9.0E-06	AI034370.1	EST_HUMAN	cc20g01.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1656912 3' similar to contains Alu repetitive element
6833	16027	25483	4.11	9.0E-06	U36114.1	NT	Human apolipoprotein E (APOE) gene, hepatic control region HCR-2
7612	16717	26206	3.57	9.0E-06	Q10394	SWISSPROT	PUTATIVE SERINE/THREONINE-PROTEIN KINASE C22E12.14C
2495	12017	20802	2.21	8.0E-06	AW362539.1	EST_HUMAN	RC3-CT0283-201189-011-h11 CT0283 Homo sapiens cDNA
988	10217		2.15	7.0E-06	AA688729.1	EST_HUMAN	ab90f10.s1 Stratagene lung (#837210) Homo sapiens cDNA clone IMAGE:854251 3' similar to contains MER20.11 MER20 repetitive element;
1440	10654	19828	2.53	7.0E-06	7682177	NT	Homo sapiens KIAA0555 gene product (KIAA0555), mRNA
2825	12064		5.04	7.0E-06	AI368262.1	EST_HUMAN	qw16g09.x1 NCI_CGAP_U03 Homo sapiens cDNA clone IMAGE:1991298 3' similar to contains Alu repetitive element
3538	12761		0.76	7.0E-06	AA365542.1	EST_HUMAN	EST89205 Thyroid Homo sapiens cDNA 6' and similar to EST containing L1 repeat
5533	14767		5.93	7.0E-06	AW883141.1	EST_HUMAN	QV2-OT0082-250400-173-h01 OT0082 Homo sapiens cDNA
8333	16321	23597	2.35	7.0E-06	BF215972.1	EST_HUMAN	501881522F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4063972 5'
2888	12108	21235	1.48	6.0E-06	BE069189.1	EST_HUMAN	QV3-BT0378-010300-106-d11 BT0378 Homo sapiens cDNA
4764	12130	21265	2.05	6.0E-06	Q01456	SWISSPROT	OVARIAN ABUNDANT MESSAGE PROTEIN (OAM PROTEIN)
4771	13980	23061	2.03	6.0E-06	AI040099.1	EST_HUMAN	cc08e02.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1655738 3' similar to contains MER8.12 MER8 repetitive element;
7025	16202		2.82	6.0E-06	AW801912.1	EST_HUMAN	IL5-UJ0070-110400-063-g02 UM0070 Homo sapiens cDNA
8220	17986	23867	2.28	6.0E-06	11418157	NT	Homo sapiens calcium channel, voltage-dependent, alpha 11 subunit (CACNA11), mRNA
5684	14914	24308	4.05	5.0E-06	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C046

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5805	15022	24423	1.88	5.0E-08	U07561.1	NT	Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds
7113	18280	25771	10.33	5.0E-08	AA313820.1	EST_HUMAN	EST185498 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' and
9104	17826	23876	3.8	5.0E-08	AI065045.1	EST_HUMAN	HA0877 Human fetal liver cDNA library Homo sapiens cDNA
663	9899	19024	8.88	4.0E-08	R16287.1	EST_HUMAN	ye48c03.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:53254 5' similar to contains Alu repetitive element; contains L1 repetitive element:
856	10092	19254	11.86	4.0E-08	AW103354.1	EST_HUMAN	xc88g12.x1 NCI CGAP Esc2 Homo sapiens cDNA clone IMAGE:2589574 3' similar to contains Alu repetitive element; contains element MER21 repetitive element:
1342	10558	19721	4.4	4.0E-08	AI334928.1	EST_HUMAN	ts33c09.x1 NCI CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2056188 3'
1342	10558	19722	4.4	4.0E-08	AI334928.1	EST_HUMAN	ts33c09.x1 NCI CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2056188 3'
1469	10682	19856	5.73	4.0E-08	BF365612.1	EST_HUMAN	QV2-NT0046-200800-250-H07 NT0048 Homo sapiens cDNA
2230	11426	20852	1.39	4.0E-08	AW015401.1	EST_HUMAN	UH-HB10-sat-1-05-0-J1.s1 NCI CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2710425 3'
3028	12284	21392	1	4.0E-08	AF108349.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
3872	13088	22204	1.34	4.0E-08	AW848285.1	EST_HUMAN	IL3-CT0214-150200-074-B03 CT0214 Homo sapiens cDNA
4821	14010	23108	1.81	4.0E-08	AI886839.1	EST_HUMAN	w84c10.x1 NCI CGAP_Bim28 Homo sapiens cDNA clone IMAGE:2432562 3' similar to contains element MER22 repetitive element:
8718	15911	25369	2.81	4.0E-08	AF009880.1	NT	Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region
7885	16420	25907	4.04	4.0E-08	AB007855.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0486
2129	11328	20546	1.11	3.0E-08	AA700582.1	EST_HUMAN	z34b08.s1 Soares fetal liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:432863 3' similar to contains L1.11 L1 repetitive element:
2129	11328	20547	1.11	3.0E-08	AA700582.1	EST_HUMAN	z34b08.s1 Soares fetal liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:432863 3' similar to contains L1.11 L1 repetitive element:
2232	11427		2.13	3.0E-08	AF202635.1	NT	Homo sapiens PP1200 mRNA, complete cds
2872	12110	21238	1.04	3.0E-08	AA888218.1	EST_HUMAN	ak48g11.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1408262 3' similar to contains LTR1.13 LTR1 repetitive element:
3232	12488		2.55	3.0E-08	AI857779.1	EST_HUMAN	w22a05.x1 NCI CGAP_UH1 Homo sapiens cDNA clone IMAGE:2426616 3' similar to TR:O80734 O80734 LINE-1 LIKE PROTEIN; contains L1.12 L1 repetitive element:
3768	12884	22098	1.35	3.0E-08	BE047094.1	EST_HUMAN	hg84d12.x1 NCI CGAP_HN13 Homo sapiens cDNA clone IMAGE:3124151 3'
3768	12884	22100	1.35	3.0E-08	BE047094.1	EST_HUMAN	hg84d12.x1 NCI CGAP_HN13 Homo sapiens cDNA clone IMAGE:3124151 3'
4560	13754	22852	3.87	3.0E-08	X54818.1	NT	Homo sapiens gene for alpha-1-microglobulin-bikunin, exons 1-5 (encoding alpha-1-microglobulin, N- terminus.)
6177	15359		2.52	3.0E-08	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
8781	17710		7.4	3.0E-08	AW385262.1	EST_HUMAN	RC0-LT0001-261189-011-A03 LT0001 Homo sapiens cDNA
207	9487		2.17	2.0E-08	P54366	SWISSPROT	HOMEBOX PROTEIN GOOSECOID

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Table 4
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1549	10763		4.53	2.0E-08	P21414	SWISSPROT	POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; ENDONUCLEASE] wa04a03.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2287068 3' similar to contains MER30.b1
2344	11537	20761	2	2.0E-08	A1672138.1	EST_HUMAN	MER30 repetitive element;
2429	11620	20841	1.48	2.0E-08	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
2632	11720	20837	1.7	2.0E-08	P06719	SWISSPROT	KNOB-ASSOCIATED HISTIDINE-RICH PROTEIN PRECURSOR (KAHRP)
3492	12716	21852	1.07	2.0E-08	AV657555.1	EST_HUMAN	AV657555 GLC Homo sapiens cDNA clone GLCFDB05 3'
3744	12884	22079	1.19	2.0E-08	AA173518.1	EST_HUMAN	zp02a05.t1 Stratiogene ovarian cancer (#637210) Homo sapiens cDNA clone IMAGE:595232 5'
3752	12971	22066	0.62	2.0E-08	AW450215.1	EST_HUMAN	UJ-H-B13-ely-g-05-0-U1.s.1 NCL CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2738176 3'
3758	12977	22092	1.66	2.0E-08	AB030896.1	NT	Mus musculus gene for odorant receptor A16, complete cds
5845	15082	24470	5.38	2.0E-08	A1819424.1	EST_HUMAN	wj90b04.x1 NCL CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2410083 3'
8683	18322	23598	1.83	2.0E-08	P23249	SWISSPROT	PROTEIN MOV-10
8687	17747		2.74	2.0E-08	BE328232.1	EST_HUMAN	hs8202.x1 NCL CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3144689 3' similar to contains L1.12 L1 repetitive element;
35	9331	18438	2.01	1.0E-08	O78082	SWISSPROT	ORGANIC CATION/CARNITINE TRANSPORTER 2 (SOLUTE CARRIER FAMILY 22, MEMBER 5) (HIGH-AFFINITY SODIUM-DEPENDENT CARNITINE CO-TRANSPORTER)
983	9809	19038	1.28	1.0E-08	AF094394.1	NT	Mus musculus D6MIM5E protein (D6MIM5e) mRNA, complete cds
1452	10665	18638	1.48	1.0E-08	P09125	SWISSPROT	MEROZOITE SURFACE PROTEIN CMZ-8
1510	10724	18696	1.14	1.0E-08	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
1552	10766	18639	0.95	1.0E-08	AA034141.1	EST_HUMAN	z06a12.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:428982 3' similar to contains Alu repetitive element
1552	10766	18940	0.95	1.0E-08	AA034141.1	EST_HUMAN	z06a12.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:428982 3' similar to contains Alu repetitive element;
1563	10777		1.12	1.0E-08	P27825	SWISSPROT	DNA-DIRECTED RNA POLYMERASE III LARGEST SUBUNIT
1963	11187	20371	10.85	1.0E-08	AF184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
1963	11187	20372	10.85	1.0E-08	AF184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
4363	13585	22660	13.16	1.0E-08	U07561.1	NT	Human ABL gene, exon 1b and Intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds
5268	14439	23512	2.15	1.0E-08	U07561.1	NT	Human ABL gene, exon 1b and Intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds
5268	14459		0.61	1.0E-08	U61297.1	NT	Human progesterone receptor (PGR) gene, far 5' flanking region
5320	14552	23622	5.34	1.0E-08	BF333015.1	EST_HUMAN	MR1-BT0800-030700-002-c08 BT0800 Homo sapiens cDNA
6028	15236	24659	5.56	1.0E-08	P02671	SWISSPROT	FIBRINOGEN ALPHA/ALPHA-E CHAIN PRECURSOR
6365	16103	25634	2.58	1.0E-08	U82688.1	NT	Homo sapiens shox gene, alternatively spliced products, complete cds
6365	16103	25635	2.58	1.0E-08	U82688.1	NT	Homo sapiens shox gene, alternatively spliced products, complete cds

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Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7011	16169		4.28	1.0E-06	AA449257.1	EST_HUMAN	z04d111.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:785483 3' similar to
8158	17280		5.02	1.0E-06	AW890941.1	EST_HUMAN	gb:D28129 RIBONUCLEASE PANCREATIC PRECURSOR (HUMAN);
8721	17874	23949	3.45	1.0E-06	L78810.1	NT	RC4-NT0054-120500-012-503 NT0054 Homo sapiens cDNA
8824	11167	20371	1.88	1.0E-06	AF184614.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
8824	11167	20372	1.88	1.0E-06	AF184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
365	9632	18764	2.24	9.0E-07	AF003529.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
365	9632	18765	2.24	9.0E-07	AF003529.1	NT	Homo sapiens glycocalyx 3 (GPC3) gene, partial cds and flanking repeat regions
5223	14397		1.4	9.0E-07	AW971932.1	EST_HUMAN	Homo sapiens glycocalyx 3 (GPC3) gene, partial cds and flanking repeat regions
7789	16982	26505	2.85	9.0E-07	AL163281.2	NT	EST384021 IMAGE resequences, MAGL Homo sapiens cDNA
4781	13970	23072	4.52	8.0E-07	AI288596.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C081
4781	13970	23073	4.52	8.0E-07	AI288596.1	EST_HUMAN	q182g07.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1878876 3'
5308	14832		8.53	8.0E-07	P21414	SWISSPROT	q182g07.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1878876 3'
6465	15682		14.61	8.0E-07	AF135416.1	NT	POL POLYPROTEIN (CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; ENDONUCLEASE)
8142	17274		8.94	8.0E-07	T07770.1	EST_HUMAN	Homo sapiens UDP-glucuronosyltransferase gene, complete cds
8316	17420		5.59	8.0E-07	AL163280.2	NT	EST05660 Fetal brain, Striatum (cat838206) Homo sapiens cDNA clone HFBEN89
1877	11084	20274	2.64	6.0E-07	AW655558.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C080
						EST_HUMAN	CM3-CT0277-221089-024-e11 CT0277 Homo sapiens cDNA
2455	11648	20887	2.48	6.0E-07	AF019413.1	NT	Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SK12W), RD, complement factor B (Bf), and complement component C2 (C2) genes;>
3949	13165		2.04	6.0E-07	P41479	SWISSPROT	(Bf), and complement component C2 (C2) genes;>
6576	18267		2.08	6.0E-07	AW803222.1	EST_HUMAN	HYPOHETICAL 24.1 KD PROTEIN IN LEF-4-P33 INTERGENIC REGION
331	9601		1.48	5.0E-07	AI831883.1	EST_HUMAN	CM4-NN1028-250300-121-H12 NN1028 Homo sapiens cDNA
1094	10290		2.65	5.0E-07	AA380630.1	EST_HUMAN	wh84f10.x1 NCI CGAP_Kd11 Homo sapiens cDNA clone IMAGE:2385547 3'
2887	12233		0.8	5.0E-07	AI831883.1	EST_HUMAN	EST83615 Supr cells Homo sapiens cDNA 5' end
4647	13841	22831	1.29	5.0E-07	AF149774.1	NT	wh84f10.x1 NCI CGAP_Kd11 Homo sapiens cDNA clone IMAGE:2385547 3'
						EST_HUMAN	Homo sapiens NOD1 protein (NOD1) gene, exons 4 through 14 and complete cds
8290	16411	24852	19.2	5.0E-07	AW070885.1	EST_HUMAN	xs31a02.x1 NCI CGAP_Br16 Homo sapiens cDNA clone IMAGE:2588362 3' similar to gb:X16341
7163	16360	25639	5.84	5.0E-07	AI808597.1	EST_HUMAN	CYTCHROME C OXIDASE POLYPEPTIDE VIA-LIVER (HUMAN);
8048	17184	26723	4.83	5.0E-07	P11087	SWISSPROT	CM4-BT178-220498-014 BT178 Homo sapiens cDNA
8110	17244		2.42	5.0E-07	AJ271735.1	NT	COLLAGEN ALPHA 1(I) CHAIN PRECURSOR
8013	18167		2.19	5.0E-07	AW862637.1	EST_HUMAN	Homo sapiens Xq pseudautosomal region; segment 1/2
3978	13180	22289	1.79	4.0E-07	AW009802.1	EST_HUMAN	QV0-CT0383-210400-204-b12 CT0383 Homo sapiens cDNA
8788	16981	26441	3.15	4.0E-07	AW419134.1	EST_HUMAN	ws84h05.x1 NCI CGAP_Co3 Homo sapiens cDNA clone IMAGE:2504687 3'
						EST_HUMAN	xy48g11.x1 NCI CGAP_Lu34.1 Homo sapiens cDNA clone IMAGE:2856548 3'

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Table 4
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7511	16716	26204	4.28	4.0E-07	AI765528.1	EST_HUMAN	w181b08.x1 NCI_CGAP_K412 Homo sapiens cDNA clone IMAGE:2398703 3'
7511	16716	26205	4.28	4.0E-07	AI765528.1	EST_HUMAN	w181b08.x1 NCI_CGAP_K412 Homo sapiens cDNA clone IMAGE:2398703 3'
7774	16969		2.08	4.0E-07	BE001828.1	EST_HUMAN	PM1-BN0083-030300-003-e12 BN0083 Homo sapiens cDNA
447	9701	18837	4.33	3.0E-07	U19719.1	NT	Human microfibril-associated glycoprotein (MIFAP2) gene, putative promoter region and alternatively spliced untranslated exons
590	9838	18957	2.19	3.0E-07	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
1381	10595	19781	2.2	3.0E-07	M89149.1	NT	Human polymorphic microsatellite DNA
1603	10817		3.12	3.0E-07	M84857.1	NT	Human IgK subgroup 1 germline gene, exons 1 and 2, V-region 018 allele
2013	11215		3.54	3.0E-07	AA526763.1	EST_HUMAN	n156b08.s1 NCI_CGAP_Ov2 Homo sapiens cDNA clone IMAGE:980825 similar to contains Alu repetitive element; contains L1, L3 L1 repetitive element;
2262	11447	20688	1.24	3.0E-07	M89149.1	NT	Human polymorphic microsatellite DNA
2432	11623	20845	11.76	3.0E-07	BE005077.1	EST_HUMAN	MRO-BN0115-020300-001-f11 BN0115 Homo sapiens cDNA
2432	11623	20846	11.76	3.0E-07	BE005077.1	EST_HUMAN	MRO-BN0115-020300-001-f11 BN0115 Homo sapiens cDNA
3000	12236	21369	1.23	3.0E-07	T84704.1	EST_HUMAN	yd50f12.r1 Soares fetal liver spleen 1NFS Homo sapiens cDNA clone IMAGE:111695 5'
3123	12358	21487	1.82	3.0E-07	P38739	SWISSPROT	HYPOTHETICAL 63.8 KD PROTEIN IN GUT1-RIM1 INTERGENIC REGION PRECURSOR
4738	13829	23033	8.7	3.0E-07	AV650201.1	EST_HUMAN	AV650201 GLC Homo sapiens cDNA clone GLCCDD01 3'
4774	13963	23065	0.78	3.0E-07	AI797238.1	EST_HUMAN	we86b12.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2347087 3'
5096	14276	23359	1.39	3.0E-07	T57850.1	EST_HUMAN	yc14h09.s1 Stragene lung (#837210) Homo sapiens cDNA clone IMAGE:80705 3' similar to similar to
5096	14278	23360	1.39	3.0E-07	T57850.1	EST_HUMAN	gb-M62882 ARACHIDONATE 12-LIPOXYGENASE (HUMAN)
5241	14415	23495	1.00	3.0E-07	BE072335.1	EST_HUMAN	yc14h09.s1 Stragene lung (#837210) Homo sapiens cDNA clone IMAGE:80705 3' similar to similar to
5620	14746	24113	11.02	3.0E-07	O88907	SWISSPROT	QV3-BT0537-221298-048-a07 BT0537 Homo sapiens cDNA
5965	15180		4.7	3.0E-07	AA815175.1	EST_HUMAN	PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4)
6283	15474	24916	3.2	3.0E-07	AW787188.1	EST_HUMAN	(PEPTIDYLARGININE DEIMINASE TYPE ALPHA)
8268	18028		4.28	3.0E-07	AJ132352.1	NT	cc04c10.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1336890 3'
30	8326	18430	2.76	2.0E-07	AF262888.1	NT	QV1-UJM0036-200300-115-g02 UM0036 Homo sapiens cDNA
157	9439	18572	7.69	2.0E-07	L77569.1	NT	Rattus norvegicus mRNA for 45 kDa secretory protein, partial
157	9439	18573	7.69	2.0E-07	L77569.1	NT	Homo sapiens TRF2-interacting telomeric RAP1 protein (RAP1) mRNA, complete cds
188	9465	18598	76.92	2.0E-07	U38849.1	NT	Homo sapiens DiGeorge syndrome critical region, telomeric end
756	9897	19142	2.28	2.0E-07	AF003530.1	NT	Homo sapiens DiGeorge syndrome critical region, telomeric end
756	9897	19143	2.28	2.0E-07	AF003530.1	NT	Fugu rubripes beta-cytoplasmic(vesicular) actin gene, complete cds
							Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
							Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
788	10008		1.13	2.0E-07	P11389	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
951	10184	18340	3.38	2.0E-07	AA223280.1	EST_HUMAN	z08b07.s1 Stratiene NT2 neuronal precursor 937230 Homo sapiens cDNA clone IMAGE:650889 3' similar to gb:L31860 GLYCOPHORIN A PRECURSOR (HUMAN); contains Alu repetitive element
952	10185	18341	12.92	2.0E-07	T63042.1	EST_HUMAN	yc15g04.s1 Stratiene lung (#837210) Homo sapiens cDNA clone IMAGE:80780 3' similar to contains L1 repetitive element ;
1171	10392	18544	1.22	2.0E-07	Q26768	SWISSPROT	I/6 AUTOANTIGEN
1580	10793	18870	1.82	2.0E-07	Q08701	SWISSPROT	HYPOTHETICAL 72.5 KD PROTEIN C2F7.10 N CHROMOSOME 1
3597	12818		0.8	2.0E-07	BF131397.1	EST_HUMAN	601818916F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4044891 5'
3688	12889	22010	22.49	2.0E-07	AF126348.1	NT	Homo sapiens caveolin 1 (CAV1) gene, exon 3 and partial cds
5292	14463	23531	9.22	2.0E-07	P23289	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN 13
5957	15173	24588	1.77	2.0E-07	AL208715.1	EST_HUMAN	qg58405.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1839177 3'
7005	16183		2.32	2.0E-07	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
7167	16334	25817	8.58	2.0E-07	AW892507.1	EST_HUMAN	CM4-NN0003-280300-124-608 NN0003 Homo sapiens cDNA
8289	17917		1.89	2.0E-07	BE163717.1	EST_HUMAN	PMO-HT0339-280100-006-H07 HT0339 Homo sapiens cDNA
8357	18168		1.95	2.0E-07	AI732492.1	EST_HUMAN	zn85h11.x6 Stratiene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:565028 3' similar to contains THR.b2 THR repetitive element ;
1110	10334		1.83	1.0E-07	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
1840	11144	20342	0.85	1.0E-07	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
1840	11144	20343	0.85	1.0E-07	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
2416	11607	20829	0.91	1.0E-07	7548818	NT	Homo sapiens RAB, member of RAS oncogene family-like 2A (RABL2A), transcript variant 2, mRNA
2778	10723	18896	1.75	1.0E-07	P08256	SWISSPROT	GLYCOPROTEIN GPV
3725	10334		1.43	1.0E-07	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
4280	13483	22580	3.17	1.0E-07	AV718882.1	EST_HUMAN	AV718882 GLC Homo sapiens cDNA clone GLCFNF04 5'
4280	13483	22581	3.17	1.0E-07	AV718882.1	EST_HUMAN	AV718882 GLC Homo sapiens cDNA clone GLCFNF04 5'
6024	15232	24652	4.81	1.0E-07	BE047871.1	EST_HUMAN	tz43d08.y1 NCI CGAP_Bim52 Homo sapiens cDNA clone IMAGE:2281339 5'
6024	15232	24653	4.81	1.0E-07	BE047871.1	EST_HUMAN	tz43d08.y1 NCI CGAP_Bim52 Homo sapiens cDNA clone IMAGE:2281339 5'
6287	15468	24910	8.24	1.0E-07	N55081.1	EST_HUMAN	yy43c07.s1 Soares fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:245484 3'
6755	15950	25407	4.48	1.0E-07	AA893576.1	EST_HUMAN	z51e10.s1 Soares_fetal_liver_spleen_1N1LS_S1 Homo sapiens cDNA clone IMAGE:434346 3'
7051	16228	25704	4.17	1.0E-07	BF874524.1	EST_HUMAN	602137714F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4274426 5'
7204	16381		2.32	1.0E-07	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8841	18143	23750	3.08	1.0E-07	BE048770.1	EST_HUMAN	h53c11.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3132212 3' similar to TR:O95722 O95722 DJ1163J1.1
8784	17713		1.56	1.0E-07	X84487.1	NT	H.sapiens ALAD gene for porphobilinogen synthase
8858	17831		1.35	1.0E-07	X51755.1	NT	Human lambda-Igmunoglobulin constant region complex (germline)
7036	18213	25680	2.8	9.0E-08	AV734819.1	EST_HUMAN	AV734819 cda Homo sapiens cDNA clone cdABFB08 5'
7737	18934	28442	3.18	9.0E-08	AI891052.1	EST_HUMAN	wn30a07.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2446832 3' similar to contains OFR.12
8171	17303	28848	4.6	9.0E-08	AL163301.2	NT	OFR repetitive element;
8591	17600		3.94	9.0E-08	AJ251973.1	NT	Homo sapiens chromosome 21 segment HS21C101
613	11972		3.63	8.0E-08	AI911352.1	EST_HUMAN	Homo sapiens partial sterarfn-1 gene
1057	10283		0.66	8.0E-08	BE785489.1	EST_HUMAN	wd16b05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2328273 3'
3519	12743		1.84	8.0E-08	BE785489.1	EST_HUMAN	601590133F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943976 5'
							601590133F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943976 5'
6885	15880	25351	4.48	8.0E-08	AI752387.1	EST_HUMAN	cn15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn15c02 random
6895	15890	25352	4.48	8.0E-08	AI752387.1	EST_HUMAN	cn15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn15c02 random
6872	16150	25621	4.01	8.0E-08	AW970683.1	EST_HUMAN	EST382776 MAGC resequences, MAGK Homo sapiens cDNA
7797	16880		2.74	8.0E-08	AF253417.1	NT	Homo sapiens microsomal epoxide hydrolase (EPHX1) gene, complete cds
80	8373	18503	2.48	7.0E-08	Q02357	SWISSPROT	ANKYRIN 1 (ERYTHROCYTE ANKYRIN)
1389	10583	19750	36.64	7.0E-08	X04809.1	NT	Rat mRNA for ribosomal protein L31
3551	12774	21802	1.31	7.0E-08	PI5305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
3551	12774	21803	1.31	7.0E-08	PI5305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
7391	18905		7.83	7.0E-08	AI535743.1	EST_HUMAN	cong3.P11.A5 conorm Homo sapiens cDNA 3'
8176	17307	28850	6.73	7.0E-08	U24070.1	NT	Rattus norvegicus Munc13-1 mRNA, complete cds
8076	12774	21802	3.5	7.0E-08	PI5305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
8076	12774	21803	3.5	7.0E-08	PI5305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
8149	17851		1.31	7.0E-08	AJ131016.1	NT	Homo sapiens SCL gene locus
827	10085	19217	2.5	6.0E-08	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
827	10085	19218	2.5	6.0E-08	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
2331	11524	20747	1.88	8.0E-08	BE144388.1	EST_HUMAN	MRO-HT0168-191189-004-g08 HT0168 Homo sapiens cDNA
3028	12282	21390	0.83	6.0E-08	7862473	NT	Homo sapiens KIAA1074 protein (KIAA1074), mRNA
4234	13437	22630	1.15	6.0E-08	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
7853	17092	28822	2.48	8.0E-08	PI1389	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE; ENDONUCLEASE]

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8084	17189		1.82	6.0E-08	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
84	9377	18507	2.87	5.0E-08	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2202	11398	20624	2.64	5.0E-08	AA483851.1	EST_HUMAN	nr03b09.at NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943183 similar to contains Alu repetitive element
8318	17421		3.74	5.0E-08	P06881	SWISSPROT	COMPLEMENT C2 PRECURSOR (C3/C5 CONVERTASE)
8515	17549	23986	1.29	5.0E-08	AW851878.1	EST_HUMAN	QV6-CT0225-131089-034-a12 CT0225 Homo sapiens cDNA
1731	10943	20125	0.92	4.0E-08	P25723	SWISSPROT	DORSAL-VENTRAL PATTERNING TOLLOID PROTEIN PRECURSOR
1731	10943	20128	0.92	4.0E-08	P25723	SWISSPROT	DORSAL-VENTRAL PATTERNING TOLLOID PROTEIN PRECURSOR
3891	13107	22225	0.72	4.0E-08	U82688.1	NT	Homo sapiens shox gene, alternatively spliced products, complete cds
7185	18382	25842	2.55	4.0E-08	A1050027.1	EST_HUMAN	an22d10.x1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1689411 3' similar to contains Alu repetitive element; contains element MER22 repetitive element ;
7477	16885		1.77	4.0E-08	AJ238617.1	NT	Homo sapiens mRNA for UGA suppressor tRNA-associated antigenic protein (tRNA48 gene)
7856	16858	26358	4.35	4.0E-08	BF682493.1	EST_HUMAN	602248024F1 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:4333300 5'
7856	16858	26357	4.35	4.0E-08	BF682493.1	EST_HUMAN	602248024F1 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:4333300 5'
8323	18300		2.4	4.0E-08	W78169.1	EST_HUMAN	z65g03.r1 Soares_fetal_heart_Nb2H18W Homo sapiens cDNA clone IMAGE:345556 5' similar to contains L1.11 L1 repetitive element ;
9002	17881		2.01	4.0E-08	A1343353.1	EST_HUMAN	b65a11.x1 NCI_CGAP_Cot16 Homo sapiens cDNA clone IMAGE:2062076 3' similar to contains MER18.03
5496	14722	24080	2.88	3.0E-08	BE018348.1	EST_HUMAN	bb79a10.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3048570 5' similar to TR:Q8Z188 Q8Z158
6075	14521	23584	3.72	3.0E-08	AI782737.1	EST_HUMAN	qs78f11.y5 NCI_CGAP_P228 Homo sapiens cDNA clone IMAGE:1944045 5'
6397	15578		3.43	3.0E-08	AI438352.1	EST_HUMAN	tr63h08.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2126273 3' similar to TR:Q13537 Q13537 MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE. ;
8288	17402		13.41	3.0E-08	R18420.1	EST_HUMAN	yp02f04.r1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:30848 5' similar to contains Alu repetitive element
211	9491		12.34	2.0E-08	AW302886.1	EST_HUMAN	xb77f06.x1 NCI_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2787139 3'
233	9512		6.42	2.0E-08	AA425598.1	EST_HUMAN	zw48f07.r1 Soares_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:779317 5' similar to contains Alu repetitive element; contains element MER15 repetitive element ;
503	8755	18883	3.37	2.0E-08	AF188348.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
688	9812	18040	10.21	2.0E-08	AW888438.1	EST_HUMAN	MFR0-OT0080-240200-001-g08 OT0080 Homo sapiens cDNA
688	9812	18041	10.21	2.0E-08	AW888438.1	EST_HUMAN	MFR0-OT0080-240200-001-g08 OT0080 Homo sapiens cDNA
887	10229		35.03	2.0E-08	BE280477.1	EST_HUMAN	601155321F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138883 5'
1350	10565	19730	85.22	2.0E-08	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047

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Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1714	10828		1.55	2.0E-08	BE734871.1	EST_HUMAN	601570463F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3845198 5'
1822	11030		4.08	2.0E-08	AW270271.1	EST_HUMAN	XP43111.X1 NCI_CGAP_HN11 Homo sapiens cDNA clone IMAGE:2743149 3'
2508	11687		1.91	2.0E-08	K00216.1	NT	Sheep His-4RNA-GUG
3174	12409	21544	6.99	2.0E-08	O42280	SWISSPROT	WNT-14 PROTEIN PRECURSOR
3174	12409	21545	6.99	2.0E-08	O42280	SWISSPROT	WNT-14 PROTEIN PRECURSOR
3842	13059		1.59	2.0E-08	AW813620.1	EST_HUMAN	RC3-ST0197-161088-012-503 ST0197 Homo sapiens cDNA
4399	13600		1.47	2.0E-08	AA459040.1	EST_HUMAN	aa28c07.t1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:814380 5' similar to contains L1.12 L1 repetitive element;
4977	14164		2.92	2.0E-08	AW572881.1	EST_HUMAN	hs17h08.x2 NCI_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2818327 3' similar to contains Alu repetitive element
1745	10957	20140	1.06	1.0E-08	AF126348.1	NT	Homo sapiens cavinolin 1 (CAV1) gene, exon 3 and partial cds
2018	11218		2.7	1.0E-08	BE141859.1	EST_HUMAN	PM2-HT0130-150899-001-112 HT0130 Homo sapiens cDNA
3155	12390	21523	1.07	1.0E-08	BE248944.1	EST_HUMAN	TCBAP1D5232 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP5232
3155	12390	21524	1.07	1.0E-08	BE248944.1	EST_HUMAN	TCBAP1D5232 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP5232
5490	14718	24073	4.44	1.0E-08	AJ010770.1	NT	Homo sapiens hyperon gene, exons 1-50
6839	16834	26298	2.76	1.0E-08	AJ016304.1	EST_HUMAN	cd35a05.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1618738 3'
7882	17052	26573	4.24	1.0E-08	AF044083.1	NT	Homo sapiens major histocompatibility locus class III region
8715	17671		2.18	1.0E-08	X51755.1	NT	Human lambs-1-immunoglobulin constant region complex (germline)
4228	13431	22524	2.66	9.0E-09	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
4228	13431	22525	2.66	9.0E-09	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
6193	16375	24815	7.03	8.0E-09	A1183500.1	EST_HUMAN	qd42a07.x1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:1732164 3' similar to contains MSR1.t1 MSR1 repetitive element;
6484	15861	23133	3.54	8.0E-09	AW800159.1	EST_HUMAN	CMO-NN1004-100300-273-c08 NN1004 Homo sapiens cDNA
6761	15856		3.3	8.0E-09	AA938892.1	EST_HUMAN	op74a08.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1582575 3'
3595	12808		2.2	7.0E-08	D88842.1	NT	Homo sapiens DNA for 3-ketacyl-CoA thiolase beta-subunit of mitochondrial trifunctional protein, exon 2, 3
7295	16484		3.06	7.0E-08	T87830.1	EST_HUMAN	ye58a12.s1 Soares_fetal_liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121918 3'
5000	14187	23277	6.35	8.0E-09	BE169421.1	EST_HUMAN	PM1-HT0527-180200-001-h05 HT0527 Homo sapiens cDNA
5398	14615	23728	6.99	8.0E-09	AW195784.1	EST_HUMAN	zn85h08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2701311 3'
6823	16017	25482	2.71	6.0E-09	4503710	NT	Homo sapiens fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism) (FGFR3) mRNA
7161	16338		4.91	8.0E-09	AF200823.2	NT	Homo sapiens testis-specific kinase substrate (TSKS) gene, complete cds

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1419	10832	19800	3.26	5.0E-09	BE149284.1	EST_HUMAN	RC2-HT0252-120200-014-110 HT0252 Homo sapiens cDNA
1820	11028	20223	1.02	5.0E-09	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
5830	15047	24451	1.78	5.0E-09	AA359454.1	EST_HUMAN	EST68748 Fetal lung II Homo sapiens cDNA 5' end
7108	16285	25768	2.57	5.0E-09	AW798867.1	EST_HUMAN	PM2-UM0053-240300-005-c09 UM0053 Homo sapiens cDNA
9028	18224		1.24	5.0E-09	BE963272.2	EST_HUMAN	601656707R1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3865897 3'
627	9778		1.76	4.0E-09	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
972	10204		2.43	4.0E-09	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
1465	10878	19851	1.81	4.0E-09	8558718	NT	Homo sapiens hypothetical protein (AF038168), mRNA
2363	11686	20804	37.61	4.0E-09	AA350878.1	EST_HUMAN	EST58385 Infant brain Homo sapiens cDNA 5' end similar to similar to heat shock protein, 80 kDa
7641	16841	26338	3.63	4.0E-09	AI886401.1	EST_HUMAN	wm94f10.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2443627 3'
2320	11513	20734	4.11	3.0E-09	BE222239.1	EST_HUMAN	hu08609.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3168120 3' similar to contains MER18.13
2519	11707	20922	0.91	3.0E-09	BE222239.1	EST_HUMAN	hu08609.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3168120 3' similar to contains MER18.13
3302	12633	21685	3.20	3.0E-09	BE222239.1	EST_HUMAN	hu08609.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3168120 3' similar to contains MER18.13
3355	12683		0.68	3.0E-09	AA44272.1	EST_HUMAN	MER18 repetitive element;
4074	13284		0.69	3.0E-09	X16874.1	NT	z54404.1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:757422 5'
4416	13618	22714	10.9	3.0E-09	AF176325.1	NT	H. sapiens PADPRP-I gene for NAD(+) ADP-ribosyltransferase
4513	13709	22802	1.53	3.0E-09	Q9Y3R5	SWISSPROT	Homo sapiens eukaryotic initiation factor 4A1 (EIF4A1) gene, partial cds
7151	16328	23611	2.31	3.0E-09	AL163247.2	NT	258.1 KDA PROTEIN C21ORF5 (KIAA0933)
7501	16795	26287	3.99	3.0E-09	BF108943.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C047
7591	16765	26288	3.89	3.0E-09	BF108943.1	EST_HUMAN	7172c08.x1 Scores_NSF_FB_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3527030 3'
822	10060		0.78	2.0E-09	X16874.1	NT	7172c08.x1 Scores_NSF_FB_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3527030 3'
1265	10480	19841	5.78	2.0E-09	AL163284.2	NT	H. sapiens PADPRP-I gene for NAD(+) ADP-ribosyltransferase
1834	10948		11.64	2.0E-09	AL118573.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C084
2295	11490	20710	4.74	2.0E-09	Q9Y3R5	SWISSPROT	DKFZp761B1710_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761B1710 5'
3911	13127	22244	3.74	2.0E-09	O60241	SWISSPROT	258.1 KDA PROTEIN C21ORF5 (KIAA0933)
6274	15454	24895	7.44	2.0E-09	AA461430.1	EST_HUMAN	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 2 PRECURSOR
8263	17390		1.79	2.0E-09	AF111168.2	NT	z68308.1 Scores_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:786187 5' similar to contains Alu repetitive element
8884	10060		14.48	2.0E-09	X16874.1	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
8839	18369		1.35	2.0E-09	AA226070.1	EST_HUMAN	H. sapiens PADPRP-I gene for NAD(+) ADP-ribosyltransferase
							nc11c02.r1 NCI_CGAP_P11 Homo sapiens cDNA clone IMAGE:1007810 similar to contains Alu repetitive element

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Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1002	10233		2.24	1.0E-09	W78152.1	EST_HUMAN	z378403.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:348853 3' similar to
1117	10341	19491	5.1	1.0E-09	5031824	NT	gb.L02832 PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (HUMAN);
1117	10341	19492	5.1	1.0E-09	5031824	NT	Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA
2842	12081	21208	1.57	1.0E-09	U80017.1	NT	Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA
2878	12114	21242	12.67	1.0E-09	M28689.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (nrip) and survival motor neuron protein (smn) genes, complete cds
2878	12114	21243	12.67	1.0E-09	M28689.1	NT	Homo sapiens nuclear phosphoprotein B23 (NPM1) mRNA, complete cds
3003	12239	21389	0.72	1.0E-09	BE535440.1	EST_HUMAN	Homo sapiens nuclear phosphoprotein B23 (NPM1) mRNA, complete cds
4811	14000		6.59	1.0E-09	AA718297.1	EST_HUMAN	601058502F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3445177 5'
5258	14431	23508	0.68	1.0E-09	U80017.1	NT	z335003.s1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:414028 3' similar to contains
5733	14952	24350	3.38	1.0E-09	P26894	SWISSPROT	Alu repetitive element; contains element MER22 repetitive element;
7171	16348		2.4	1.0E-09	AL163283.2	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (nrip) and survival motor neuron protein (smn) genes, complete cds
8255	17382		1.72	1.0E-09	AL163283.2	NT	CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS)
8650	17633		2.2	1.0E-09	P08547	SWISSPROT	Homo sapiens chromosome 21 segment HS21C083
8788	18310	23691	2.32	1.0E-09	11418127	NT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
1318	10332	18804	2.22	9.0E-10	AW887740.1	EST_HUMAN	Homo sapiens GTP binding protein 1 (GTPBP1), mRNA
2787	12027	21154	7.73	9.0E-10	A1870071.1	EST_HUMAN	MRO-SN0040-050500-002-c07 SN0040 Homo sapiens cDNA
6012	15262	24688	5.41	9.0E-10	A1452882.1	EST_HUMAN	wa78h03.x1 Soares_Dickgraefe_cdon_NHCD Homo sapiens cDNA clone IMAGE:2347263 3' similar to
149	9431	18555	12.37	8.0E-10	U63630.2	NT	SW:RL29_HUMAN P47814 60S RIBOSOMAL PROTEIN L29 ;contains element PTR5 repetitive element ;
3316	12548	21679	0.68	8.0E-10	BE080748.1	EST_HUMAN	146b09.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2144537 3' similar to
4183	13387	22485	4.81	8.0E-10	AA376832.1	EST_HUMAN	TR:O00372 O00372 PUTATIVE P150. ;
7060	16237		3	8.0E-10	U36308.2	NT	Homo sapiens MCM4 (MCM4) and DNA-PKcs (PRKDC) genes, partial cds
708	9950	18088	23.91	7.0E-10	7708225	NT	QV1-BT0631-150200-071-01 BT0631 Homo sapiens cDNA
708	9950	18089	23.91	7.0E-10	7708225	NT	EST89564 Small Intestine I Homo sapiens cDNA 5' end
1589	10813	19900	3.1	7.0E-10	Q13342	SWISSPROT	Homo sapiens lens major intrinsic protein (MIP) gene, complete cds
1889	11182		1.2	7.0E-10	P08548	SWISSPROT	Homo sapiens TPA inducible protein (LOC51586), mRNA
2525	11713		13.32	7.0E-10	P08547	SWISSPROT	Homo sapiens TPA inducible protein (LOC51586), mRNA
3053	12289	21414	2.97	7.0E-10	X00856.1	NT	LYSP100 PROTEIN (LYMPHOID-RESTRICTED HOMOLOG OF SP100)
							LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
							LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
							H.sapiens DHFR gene, exon 3

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5747	14988	24365	3.58	7.0E-10	AA345220.1	EST_HUMAN	EST51247 Gall bladder II Homo sapiens cDNA 5' end
823	10158	18315	3.28	8.0E-10	AJ400877.1	NT	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf18 gene and C11orf17 gene
2837	11820	21038	1.54	8.0E-10	AI424405.1	EST_HUMAN	U02607.x1 NCI_CGAP_P728 Homo sapiens cDNA clone IMAGE:2095021 3'
4750	13941		2.61	8.0E-10	AW853719.1	EST_HUMAN	RC3-CT0254-031088-012-g12 CT0254 Homo sapiens cDNA
8354	17447		1.84	8.0E-10	AW971923.1	EST_HUMAN	EST384012 MAGE resequences, MAGL Homo sapiens cDNA
769	10008		5.57	5.0E-10	AL046804.1	EST_HUMAN	DKFZp434N219.1 434 (synonym: hbs3) Homo sapiens cDNA clone DKFZp434N219 5'
6012	14189	23288	1.35	5.0E-10	AF181897.1	NT	Homo sapiens WRN (WRN) gene, complete cds
8219	15400		1.71	5.0E-10	BF105159.1	EST_HUMAN	601822184F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4042413 5'
111	9399		1.83	4.0E-10	AI221083.1	EST_HUMAN	qg09f08.x1 Soares_placenta_8to9weeks_2NbhP8b6W Homo sapiens cDNA clone IMAGE:1759049 3'
588	8836	18955	1.89	4.0E-10	AA515280.1	EST_HUMAN	similar to contains LTR8.b2 LTR8 repetitive element;
1985	11189	20374	1.75	4.0E-10	AW594709.1	EST_HUMAN	m64601.s1 NCI_CGAP_C03 Homo sapiens cDNA clone IMAGE:924648 3'
2638	11726	20943	4.74	4.0E-10	AL163303.2	NT	hg58g03.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2849844 3' similar to contains Alu repetitive element;
6155	15339	24778	14.13	4.0E-10	AF224688.1	NT	Homo sapiens chromosome 21 segment HS21C103
925	10158	18317	1.78	3.0E-10	N36113.1	EST_HUMAN	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
1359	10574		4.68	3.0E-10	AY005150.1	NT	W32708.s1 Soares_melanocyte 2NbhHM Homo sapiens cDNA clone IMAGE:272863 3' similar to contains L1.11 L1 repetitive element;
5755	14974	24373	1.92	3.0E-10	P20350	SWISSPROT	Homo sapiens extracellular glycoprotein lactoferrin precursor, gene, complete cds
5813	15030	24431	3.41	3.0E-10	BE302970.1	EST_HUMAN	RHOMBOLD PROTEIN (VEINLET PROTEIN)
6784	16979	25438	2.33	3.0E-10	AW850731.1	EST_HUMAN	ba76d08.y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2806319 5'
6784	15979	25439	2.33	3.0E-10	AW850731.1	EST_HUMAN	IL3-CT0219-160200-064-B06 CT0219 Homo sapiens cDNA
7224	18401		2.23	3.0E-10	AA768284.1	EST_HUMAN	IL3-CT0219-160200-064-B06 CT0219 Homo sapiens cDNA
9041	17883	23896	2.19	3.0E-10	BE178517.1	EST_HUMAN	n238g03.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1288808 3'
37	9333	18438	1.24	2.0E-10	P48688	SWISSPROT	IL3-HT0818-110500-136-E07 HT0818 Homo sapiens cDNA
37	9333	18439	1.24	2.0E-10	P48688	SWISSPROT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)
1882	11068		3.01	2.0E-10	U80017.1	NT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)
2843	12181		0.75	2.0E-10	BF875047.1	EST_HUMAN	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (nail) and survival motor neuron protein (smn) genes, complete cds
5574	14788		2.78	2.0E-10	Q28640	SWISSPROT	602138840F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4279377 5' (HPRG)

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Table 4
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5772	14990	24390	2.13	2.0E-10	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
5247	15428	24868	5.7	2.0E-10	BE781082.1	EST_HUMAN	601588208F1 NIH_MGC 7 Homo sapiens cDNA clone IMAGE:3940824 5'
1498	10711		13.64	1.0E-10	AW897767.1	EST_HUMAN	MRO-SN0038-280300-001-01 SN0038 Homo sapiens cDNA
1588	10789	19975	2.68	1.0E-10	AV652123.1	EST_HUMAN	AV652123 GLC Homo sapiens cDNA clone GLCXA11 3'
2544	11732		1.68	1.0E-10	AW652001.1	EST_HUMAN	QVQ-CT0226-101189-058-e08 CT0226 Homo sapiens cDNA
3473	12697	21833	0.87	1.0E-10	AW632912.1	EST_HUMAN	QV2-TT0003-101189-013-g10 TT0003 Homo sapiens cDNA
3516	12739		0.68	1.0E-10	AL041685.1	EST_HUMAN	DKFZp434N1317_r1 434 (synonym: hnc3) Homo sapiens cDNA clone DKFZp434N1317 5'
3829	12739		0.68	1.0E-10	AL041685.1	EST_HUMAN	DKFZp434N1317_r1 434 (synonym: hnc3) Homo sapiens cDNA clone DKFZp434N1317 5'
3991	13205		7	1.0E-10	AF213894.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
4109	13318	22414	6.01	1.0E-10	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase 1 (CAMK1), creatine transporter (CRT), CDM protein (CDM), adrenoleukodystrophy protein >
4109	13318	22415	6.01	1.0E-10	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase 1 (CAMK1), creatine transporter (CRT), CDM protein (CDM), adrenoleukodystrophy protein >
4116	13323	22424	1.91	1.0E-10	AB031069.1	NT	Homo sapiens PCCX1 mRNA for protein containing CXXC domain 1, complete cds
4152	13358		2.45	1.0E-10	M30628.1	NT	Human pregnancy-specific glycoprotein beta-1 (SP1) mRNA, last exon
6191	14367		0.99	1.0E-10	A1797745.1	EST_HUMAN	we8204.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2347615 3' similar to contains MER31.11 MER31 repetitive element;
7134	16311		8.18	1.0E-10	AA081868.1	EST_HUMAN	zn23g08.r1 Stratagene neuroepithelium NT2RAM1 937234 Homo sapiens cDNA clone IMAGE:548314 5'
7488	16895	26179	3.77	1.0E-10	AI038280.1	EST_HUMAN	cy65h03.x1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1672661 3'
8267	14504		1.53	1.0E-10	X87344.1	NT	H. sapiens DNA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes
268	9541	18671	1.07	9.0E-11	BE145600.1	EST_HUMAN	IL2-HT0203-281089-016-c08 HT0203 Homo sapiens cDNA
2074	11274	20489	5.61	9.0E-11	AL134395.1	EST_HUMAN	DKFZp547D225_r1 547 (synonym: hfrb1) Homo sapiens cDNA clone DKFZp547D225 5'
2074	11274	20490	5.61	9.0E-11	AL134395.1	EST_HUMAN	DKFZp547D225_r1 547 (synonym: hfrb1) Homo sapiens cDNA clone DKFZp547D225 5'
3361	12589	21729	2.52	9.0E-11	AL134395.1	EST_HUMAN	DKFZp547D225_r1 547 (synonym: hfrb1) Homo sapiens cDNA clone DKFZp547D225 5'
3361	12589	21730	2.52	9.0E-11	AL134395.1	EST_HUMAN	DKFZp547D225_r1 547 (synonym: hfrb1) Homo sapiens cDNA clone DKFZp547D225 5'
4503	13700	22794	0.94	9.0E-11	AA776986.1	EST_HUMAN	ae18f01.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:970287 3'
5477	14704		4.92	9.0E-11	BE079780.1	EST_HUMAN	RC8-BT0827-140200-011-E06 BT0827 Homo sapiens cDNA

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Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8080	17658	23981	3.31	9.0E-11	C16635.1	EST_HUMAN	C16635 Clontech human aorta polyA+ mRNA (#6572) Homo sapiens cDNA clone GEN-508B08 6'
3080	12316		9.13	8.0E-11	H19971.1	EST_HUMAN	Y15311.1 s1 Soares adult brain N2b5HB55Y Homo sapiens cDNA clone IMAGE:172173 3' similar to contains L1 repetitive element;
3940	13156	22273	0.61	8.0E-11	A1478617.1	EST_HUMAN	bm54c09.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2161836 3'
4020	13232	22335	5.63	8.0E-11	N23712.1	EST_HUMAN	yw46c06.s1 Wellmann Olfactory Epithelium Homo sapiens cDNA clone IMAGE:255288 3'
1449	10862	19837	1.67	7.0E-11	AA330842.1	EST_HUMAN	EST34392 Embryo, 6 week 1 Homo sapiens cDNA 5' end
5825	15821	26281	3.07	7.0E-11	AF163884.1	NT	Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced
8835	17745		1.38	7.0E-11	AV701656.1	EST_HUMAN	AV701656 ADB Homo sapiens cDNA clone ADBAB009 5'
418	9671	18812	6.1	8.0E-11	M55270.1	NT	Human matrix Gla protein (MGP) gene, complete cds
418	9671	18813	6.1	8.0E-11	M55270.1	NT	Human matrix Gla protein (MGP) gene, complete cds
6373	15553	25010	3.18	8.0E-11	P08547	SWISSPROT	LNE-1 REVERSE TRANSCRIPTASE HOMOLOG
6584	15780	25240	9.08	8.0E-11	AV727859.1	EST_HUMAN	AV727859 HTC Homo sapiens cDNA clone HTCASC06 5'
11	6307	18409	1.38	5.0E-11	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
3342	9307	18409	1.91	5.0E-11	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
4213	13416	22512	1.55	5.0E-11	P48034	SWISSPROT	ALDEHYDE OXIDASE
5883	15100	24511	1.94	5.0E-11	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
6303	15484	24828	13.54	5.0E-11	11416789	NT	Homo sapiens protocadherin beta 3 (PCDH3), mRNA
1405	10018		1.28	4.0E-11	AA438042.1	EST_HUMAN	zu01b12.1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:730559 5'
2743	11822	21138	7.91	4.0E-11	BE885000.1	EST_HUMAN	601507531F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3908295 5'
2824	12162	21297	1.04	4.0E-11	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
4620	13814	22804	1.18	4.0E-11	D44666.1	EST_HUMAN	HUMSUPY068 Human brain cDNA Homo sapiens cDNA clone 069
5860	15078	24491	3.34	4.0E-11	P20065	SWISSPROT	PRE-MRNA SPLICING FACTOR RNA HELICASE PRP2
6244	15425		3.86	4.0E-11	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
8906	17797	23928	1.42	4.0E-11	11545732	NT	Homo sapiens SH3-domain binding protein 1 (SH3BP1), mRNA
1463	10896	19871	14.62	3.0E-11	6878077	NT	Mus musculus expressed in non-metastatic cells 2, protein (NM23B) (Nme2), mRNA
4261	13464		1.48	3.0E-11	AA308248.1	EST_HUMAN	EST180120 Liver, hepatocellular carcinoma Homo sapiens cDNA 5' end
987	10200	19355	1.59	2.0E-11	AI150502.1	EST_HUMAN	qf36c04.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1752102 3' similar to contains MER10.13
1183	10413	19568	5.2	2.0E-11	R24807.1	EST_HUMAN	MER10 repetitive element;
1193	10413	19568	5.2	2.0E-11	R24807.1	EST_HUMAN	y943e12.1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:35144 5'
						EST_HUMAN	y943e12.1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:35144 5'
1592	10805	19880	10.06	2.0E-11	L17432.1	NT	Gallus gallus rho-globin, beta-H globin, beta-A globin, epsilon-globin, and erythrocyte receptor-like protein
						NT	COR3 beta (COR3beta) genes, complete cds

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1592	10805	18981	10.08	2.0E-11	L17432.1	NT	Gallus gallus rho-globin, beta-H globin, epsilon-globin, and olfactory receptor-like protein
1594	10808	18984	0.95	2.0E-11	A1126371.1	EST_HUMAN	COR3beta (COR3beta) genes, complete cds
2720	11899	21115	0.93	2.0E-11	AF087913.1	NT	qc51c10.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:171338 3' similar to gb:L02832 PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (HUMAN); contains L1.H1 L1 repetitive element:
3160	12395	21531	4.04	2.0E-11	P10283	SWISSPROT	Human endogenous retrovirus HERV-P-T47D
3298	12529	21660	1.62	2.0E-11	A1478617.1	EST_HUMAN	RETROVIRUS-RELATED GAG POLYPROTEIN (VERSION 1)
3339	12568	21706	0.66	2.0E-11	Q10473	SWISSPROT	fm54c09.x1 NCI_CGAP_K411 Homo sapiens cDNA clone IMAGE:2161938 3'
4438	13838		0.85	2.0E-11	BE06537.1	EST_HUMAN	POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE (PROTEIN-UDP ACETYL GALACTOSAMINYLTRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N- ACETYL GALACTOSAMINYLTRANSFERASE) (GALNAC-T1)
4808	13800		0.85	2.0E-11	AL163227.2	NT	ACETYL GALACTOSAMINYLTRANSFERASE (GALNAC-T1)
4955	14142		1.38	2.0E-11	BE062558.1	EST_HUMAN	RC3-BT0316-170200-014-e05 BT0316 Homo sapiens cDNA
5028	14214	23298	3.62	2.0E-11	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C027
5792	15009	24413	1.68	2.0E-11	AA581028.1	EST_HUMAN	QV2-BT0258-281099-014-a01 BT0258 Homo sapiens cDNA
6834	16028		2.21	2.0E-11	AF026308.1	NT	Homo sapiens chromosome 21 segment HS21C079
7184	16341	25820	8.37	2.0E-11	Q13606	SWISSPROT	nc83x05.r1 NCI_CGAP_GGI Homo sapiens cDNA clone IMAGE:787433 5' similar to SW:PR16_YEAST
7674	16873	26377	2.64	2.0E-11	AA035369.1	EST_HUMAN	P16938 PRE-MRNA SPLICING FACTOR RNA HELICASE PRP18. ;
7674	16873	26378	2.64	2.0E-11	AA035369.1	EST_HUMAN	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families
7702	16901	26409	2.16	2.0E-11	AA281958.1	EST_HUMAN	OLFACTORY RECEPTOR 5H1 (OLFACTORY RECEPTOR-LIKE PROTEIN OLF1)
8456	17513		2.3	2.0E-11	AW842143.1	EST_HUMAN	zk27g02.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:471704 3'
8485	17533	24027	1.65	2.0E-11	BF377859.1	EST_HUMAN	zk27g02.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:471784 3'
8765	17703		1.99	2.0E-11	D25217.2	NT	zs18x04.r1 NCI_CGAP_GC81 Homo sapiens cDNA clone IMAGE:685519 5'
8922	17808		1.83	2.0E-11	P08547	SWISSPROT	RCO-CN0027-210100-011-c01 CN0027 Homo sapiens cDNA
8248	18018		2.34	2.0E-11	11417968	NT	CN2-TN0140-070900-372-g01 TN0140 Homo sapiens cDNA
682	9925	19058	1.28	1.0E-11	AJ131016.1	NT	Homo sapiens mRNA for KIAA0027 protein, partial cds
783	10033	19182	1.21	1.0E-11	AL163209.2	NT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
1225	10443	19598	2.73	1.0E-11	AL163279.2	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
1490	10703		1.81	1.0E-11	AF119914.1	NT	Homo sapiens SCL gene locus
2098	11298	20508	2.85	1.0E-11	AF000573.1	NT	Homo sapiens chromosome 21 segment HS21C009
3472	12696	21832	1.08	1.0E-11	BE004315.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C079
							Homo sapiens PRO3078 mRNA, complete cds
							Homo sapiens homogenisate 1,2-dioxygenase gene, complete cds
							CMO-BN0105-170300-292-412 BN0105 Homo sapiens cDNA

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Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4944	14131	23228	0.91	1.0E-11	AI186625.1	EST_HUMAN	cc65H08.s1 Soares_NIHMPu_S1 Homo sapiens cDNA clone IMAGE:1681243 3'
5354	14584	23660	13.76	1.0E-11	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
6648	16943	26304	7.4	1.0E-11	RI13174.1	EST_HUMAN	y73d08.r1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:28106 5'
7835	17027	26544	1.73	1.0E-11	BF680078.1	EST_HUMAN	602154807F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4295977 5'
8001	18088		1.62	1.0E-11	Z20377.1	EST_HUMAN	HSAACACADHP.Human [foetal Brain Whole tissue Homo sapiens cDNA
2804	12142	21278	1.11	9.0E-12	P20742	SWISSPROT	PREGNANCY ZONE PROTEIN PRECURSOR
8540	17665		4.76	8.0E-12	AJ271738.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
4684	13658	22657	1.62	7.0E-12	Q05904	SWISSPROT	34 KD SPICULE MATRIX PROTEIN PRECURSOR (LSM34)
7889	17105	26635	12.51	7.0E-12	AA704735.1	EST_HUMAN	z123g01.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:451152 3'
3522	12748		0.73	8.0E-12	AV730554.1	EST_HUMAN	AV730554 HTF Homo sapiens cDNA clone HTFAWF08 5'
4341	13543	22634	9.71	6.0E-12	AA732516.1	EST_HUMAN	n28f11.s1 NCI_CGAP_GC81 Homo sapiens cDNA clone IMAGE:1302573 3' similar to contains Alu repetitive element
9603	16060		2.9	6.0E-12	AA847868.1	EST_HUMAN	cd10g11.s1 NCI_CGAP_GC81 Homo sapiens cDNA clone IMAGE:1367588 similar to contains MER29.12
1050	10276	19428	3.76	5.0E-12	TO6573.1	EST_HUMAN	MER28 repetitive element;
3708	12828	22048	6.27	5.0E-12	AJ271738.1	NT	EST04462 Fetal brain, Stralagene (cat#838208) Homo sapiens cDNA clone HFBDV33
5688	14890	24281	5.11	5.0E-12	AL163278.2	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
5688	14890	24281	5.11	5.0E-12	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
5871	15069	24502	10.34	5.0E-12	AW1974760.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C078
6810	16005	26468	3.01	5.0E-12	AJ271735.1	NT	EST388950 IMAGE resequences, MAGN Homo sapiens cDNA
7160	16337		6.25	5.0E-12	AL163303.2	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
248	9525	18655	5.28	4.0E-12	AA700326.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C103
248	9525	18655	6.58	4.0E-12	AA700326.1	EST_HUMAN	z174g11.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:460676 3'
4822	13816	22808	0.88	4.0E-12	AI689884.1	EST_HUMAN	z174g11.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:460676 3'
6540	16736		2.37	4.0E-12	AF109907.1	NT	z174g11.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:460676 3'
7648	16848	26348	4.08	4.0E-12	AJ228043.1	NT	z174g11.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:460676 3'
8808	17730		1.89	4.0E-12	U78027.1	NT	z174g11.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:460676 3'
622	9867	18968	4.22	3.0E-12	AW341683.1	EST_HUMAN	z174g11.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:460676 3'
622	9867	18969	4.22	3.0E-12	AW341683.1	EST_HUMAN	z174g11.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:460676 3'

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Table 4
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7248	18488	25858	3.45	3.0E-12	U37672.1	NT	Human prostate specific antigen gene, 5' flanking region
7248	18488	25860	3.45	3.0E-12	U37672.1	NT	Human prostate specific antigen gene, 5' flanking region
1629	10842	20019	1.81	2.0E-12	AW802131.1	EST_HUMAN	IL5-JM0071-120400-065-a05 UM0071 Homo sapiens cDNA
3443	12888	21803	0.75	2.0E-12	6754489	NT	Mus musculus keratin-associated protein 6.2 (Krtap6-2), mRNA
4082	13300	22399	1.19	2.0E-12	J01894.1	NT	Rat U3A small nuclear RNA
4082	13300	22400	1.19	2.0E-12	J01894.1	NT	Rat U3A small nuclear RNA
4413	13613		2.27	2.0E-12	BE063509.1	EST_HUMAN	CMO-BT0281-031189-087-a03 BT0281 Homo sapiens cDNA
4919	14107	23201	0.59	2.0E-12	O70308	SWISSPROT	TBX15 PROTEIN (T-BOX PROTEIN 15)
4919	14107	23202	0.59	2.0E-12	O70308	SWISSPROT	TBX15 PROTEIN (T-BOX PROTEIN 15)
5881	15079		1.87	2.0E-12	AW971857.1	EST_HUMAN	EST383948 MAGE resequences, MAGL Homo sapiens cDNA
6164	15338	24775	3.16	2.0E-12	T08169.1	EST_HUMAN	EST060000 Infant Brain, Benito Soares Homo sapiens cDNA clone HIBBA13 5' end
6862	15542	24987	2.07	2.0E-12	11422228	NT	Homo sapiens Ac-like transposable element (ALTE), mRNA
7089	16246		17.59	2.0E-12	BE165980.1	EST_HUMAN	MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA
8440	17603		2.41	2.0E-12	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
8654	17634		1.49	2.0E-12	11418248	NT	Homo sapiens sulfotransferase-related protein (SULTX3), mRNA
121	9407	18540	3.27	1.0E-12	AW627674.1	EST_HUMAN	h180a09.x1 NCL_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2970040 3' similar to contains MER18.11
1856	11160		1.62	1.0E-12	AI871726.1	EST_HUMAN	repetitive element ; wms1107.x1 NCL_CGAP_U12 Homo sapiens cDNA clone IMAGE:2439463 3' similar to contains L1.B3 L1
3035	12271	21398	1.76	1.0E-12	AF000591.1	NT	Homo sapiens testis-specific Testis Transcript Y 2 (TTY2) mRNA, partial cds
3035	12271	21399	1.76	1.0E-12	AF000591.1	NT	Homo sapiens testis-specific Testis Transcript Y 2 (TTY2) mRNA, partial cds
3855	13071	22185	41.19	1.0E-12	AU132248.1	EST_HUMAN	AU132248 NT2RP3 Homo sapiens cDNA clone NT2RP3004070 5'
3855	13071	22186	41.19	1.0E-12	AU132248.1	EST_HUMAN	AU132248 NT2RP3 Homo sapiens cDNA clone NT2RP3004070 5'
5839	14883		1.92	1.0E-12	U82828.1	NT	Homo sapiens ataxia telangiectasia (ATM) gene, complete cds
5881	14801		1.82	1.0E-12	Q87237	SWISSPROT	HYPOPHOSPHATASE 1 (HPP1) protein, complete cds
6127	15311	24745	1.76	1.0E-12	AF186864.1	NT	Homo sapiens putative BPES syndrome breakpoint region protein gene, complete cds
6139	15323	24757	9.56	1.0E-12	AI248533.1	EST_HUMAN	qh68a04.x1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1848614 3' similar to gb:M19503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN); contains MER10.11 MER10 repetitive element ;
6139	15323	24758	9.56	1.0E-12	AI248533.1	EST_HUMAN	qh68a04.x1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1848614 3' similar to gb:M19503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN); contains MER10.11 MER10 repetitive element ;
8048	17441	26839	4.2	1.0E-12	AW882184.1	EST_HUMAN	EST374237 MAGE resequences, MAGG Homo sapiens cDNA
8729	18288		1.63	1.0E-12	AL163288.2	NT	Homo sapiens chromosome 21 segment HS21C088

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Table 4

Single Exon Probes Expressed In HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3922	13138	22257	0.83	9.0E-13	AB026900.1	NT	Homo sapiens CST gene for cerebroside sulfotransferase, exon 1, 2, 3, 4, 5
6902	10140		2.29	9.0E-13	N68653.1	EST_HUMAN	z26806.a1 Soares fetal liver spleen 1NF1.S Homo sapiens cDNA clone IMAGE:283651 3'
724	9988	19104	6.37	8.0E-13	U28185.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
724	9988	19105	6.37	8.0E-13	U29185.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
1808	11015	20208	1.99	8.0E-13	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (nrip) and survival motor neuron protein (smn) genes, complete cds
7123	16300		2.58	8.0E-13	U76027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FIP3 (FIP3) genes, complete cds
							Human gamma1 T-cell receptor beta chain TCRBV13S1, TCRBV6S8A2T, TCRBV5S8A3N2T, TCRBV13S8A2T, TCRBV6S8P, TCRBV6S3A2T, TCRBV13S8P, TCRBV6S3A1N1T, TCRBV5S2, TCRBV6S8A2T, TCRBV5S7P, TCRBV13S4, TCRBV6S2A1N1T, TCRBV6S4A2T, TCRBV6S4A1, TCRBV23S1A2T, TCRBV12P
8244	17373	26908	2.52	8.0E-13	U66060.1	NT	601463285F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3869813 5'
8838	17748		13.42	7.0E-13	BE778223.1	EST_HUMAN	POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE (PROTEIN-UDP ACETYL GALACTOSAMINYLTRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N-ACETYL GALACTOSAMINYLTRANSFERASE) (GALNAC-T)
9073	17699		19.47	7.0E-13	Q10473	SWISSPROT	Homo sapiens chromosome 21 segment HS21C007
2071	11271	20488	5.65	8.0E-13	AL163207.2	NT	y8204.r1 Soares placenta Nb2-HP Homo sapiens cDNA clone IMAGE:145769 5'
3294	12525		0.77	6.0E-13	R78338.1	EST_HUMAN	z177a12.a1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:728350 3' similar to contains Alu repetitive element; contains element MER22 repetitive element;
3375	12603		1.63	5.0E-13	AA435773.1	EST_HUMAN	MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (MLCK)
7438	16845	26137	2.89	5.0E-13	P07313	SWISSPROT	PM2-HT0224-221099-001-e11 HT0224 Homo sapiens cDNA
1833	11041		8.48	4.0E-13	AW378614.1	EST_HUMAN	Homo sapiens glyican 3 (GPC3) gene, partial cds and flanking repeat regions
2423	11814		3.52	4.0E-13	AF003529.1	EST_HUMAN	PM3-HT0520-230200-002-c08 HT0520 Homo sapiens cDNA
5484	14710	24068	4.77	4.0E-13	BE169131.1	EST_HUMAN	q132405.x1 NCI_CGAP_K045 Homo sapiens cDNA clone IMAGE:1898945 3' similar to contains Alu repetitive element;
7080	16257	25731	3.25	4.0E-13	A1289831.1	EST_HUMAN	z178g10.a1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:728514 3'
7728	16924	28433	2.08	4.0E-13	AA435819.1	EST_HUMAN	z178g10.a1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:728514 3'
7728	16924	28434	2.08	4.0E-13	AA435819.1	EST_HUMAN	Homo sapiens X-linked arylidic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
184	9463		5.11	3.0E-13	AF003528.1	NT	z178g10.a1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:781408 5'
875	10111		5.48	3.0E-13	AA430310.1	EST_HUMAN	Homo sapiens Xq pseudautosomal region; segment 2/2
2338	11631	20754	1.62	3.0E-13	AJ271736.1	NT	Homo sapiens chromosome 21 segment HS21C010
2441	11632		2.58	3.0E-13	AL163210.2	NT	OM3-FT0109-140700-242-H08 FT0100 Homo sapiens cDNA
2628	11810	21028	2.58	3.0E-13	BF372862.1	EST_HUMAN	

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3150	12385		2.42	3.0E-13	AA745844.1	EST_HUMAN	cb18d02.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1324035 3'
6422	15819	25083	8.11	3.0E-13	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
7288	16487		3.68	3.0E-13	A1064788.1	EST_HUMAN	HA0538 Human fetal liver cDNA library Homo sapiens cDNA
7616	16819	26314	3.1	3.0E-13	BE063508.1	EST_HUMAN	CMO-BT0281-031189-087-a03 BT0281 Homo sapiens cDNA
8128	17280	26803	2.87	3.0E-13	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
152	8434	18568	2.21	2.0E-13	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
243	9521	18952	1.34	2.0E-13	U23839.1	NT	Danio rerio fibroblast growth factor receptor 4 mRNA, complete cds
1277	10482	19051	5.93	2.0E-13	AF239710.1	NT	Homo sapiens DNA polymerase delta small subunit (POLD2) gene, exons 1 through 11 and complete cds
2085	12203	21338	0.79	2.0E-13	8924119	NT	Homo sapiens hypothetical protein PRO2130 (PRO2130), mRNA
2085	12203	21339	0.79	2.0E-13	8924119	NT	Homo sapiens hypothetical protein PRO2130 (PRO2130), mRNA
3249	12482	21614	1.03	2.0E-13	BF431889.1	EST_HUMAN	nab70f03.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE: 3'
3481	12705	21841	1.04	2.0E-13	AF108907.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
4086	13295		1.92	2.0E-13	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
5270	14433		2.68	2.0E-13	BE258449.1	EST_HUMAN	601111249F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3351829 5'
5718	14636	24332	4.51	2.0E-13	Q06852	SWISSPROT	GELL SURFACE GLYCOPROTEIN 1 PRECURSOR (OUTER LAYER PROTEIN B) (S-LAYER PROTEIN 1)
6004	15286	24718	6.56	2.0E-13	X16812.1	NT	Human PFKL gene (for liver-type 6-phosphofructokinase (EC 2.7.1.11) exon 2
7201	16378	25859	3.55	2.0E-13	5031808	NT	Homo sapiens mab-21 (C. elegans)-like 1 (MAB21L1) mRNA
8521	17552		10.13	2.0E-13	AW892155.1	EST_HUMAN	CMO-NN001-100300-274-e11 NN0001 Homo sapiens cDNA
286	8568	18701	1.54	1.0E-13	S74129.1	NT	FGF-1=fibroblast growth factor 1 [human, kidney, Genomic, 342 nt, segment 2 of 2]
898	10133	19295	4.82	1.0E-13	AJ007973.1	NT	Homo sapiens LGMD2B gene
1344	10558	19724	1.38	1.0E-13	X87344.1	NT	H. sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14 genes
1981	11194	20404	1.95	1.0E-13	AA720574.1	EST_HUMAN	hw21g02.s1 NCI_CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR.13 THR repetitive element;
4563	13787	22879	1.19	1.0E-13	BF340987.1	EST_HUMAN	602038008F1 NCI_CGAP_Bm84 Homo sapiens cDNA clone IMAGE:4185988 5'
7617	17132	26862	15.9	1.0E-13	BF108755.1	EST_HUMAN	7145e10.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3524443 3' similar to contains MER28.b2 MER29 repetitive element;

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8337	17435		1.5	1.0E-13	AV715377.1	EST_HUMAN	AV715377 DC8 Homo sapiens cDNA clone DC8AIE03 5'
9015	17887		2.04	1.0E-13	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
9161	17880		1.75	1.0E-13	X87578.1	NT	H. sapiens CD4 gene
338	9608	18734	3.04	9.0E-14	AA781159.1	EST_HUMAN	aj24c01.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391232 3' similar to contains MER19.11 MER19 repetitive element;
339	9807	18735	3.14	9.0E-14	AA781159.1	EST_HUMAN	aj24c01.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391232 3' similar to contains MER19.11 MER19 repetitive element;
2484	11655		3.37	9.0E-14	AW881577.1	EST_HUMAN	RC4-CT0322-080100-013-d09 CT0322 Homo sapiens cDNA
2710	11889	21106	6.2	9.0E-14	AB038182.1	NT	Homo sapiens TFF gene cluster for trefoil factor, complete cds
3075	12311	21432	5.07	9.0E-14	AW513288.1	EST_HUMAN	xc54h05.x1 NCI_CGAP_U1 Homo sapiens cDNA clone IMAGE:2707833 3'
3204	8608	18734	1.01	9.0E-14	AA781159.1	EST_HUMAN	aj24c01.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391232 3' similar to contains MER19.11 MER19 repetitive element;
3780	12898	22114	7.13	9.0E-14	D14547.1	NT	Human DNA, SINE repetitive element
4768	13957	23058	1.81	9.0E-14	AJ002153.1	NT	Segulus oedipus gene for seminal vesicle secreted protein semenogelin I
3832	13148		3.6	8.0E-14	R76289.1	EST_HUMAN	y172c03.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:144798 3'
6893	15589	25085	67.72	8.0E-14	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
6943	16087	25555	2.85	8.0E-14	AA219316.1	EST_HUMAN	zq17c10.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:829970 3'
7971	17160		5.08	8.0E-14	BE02558.1	EST_HUMAN	QV2-BT0258-281089-014-a01 BT0258 Homo sapiens cDNA
8738	17684	23954	1.58	8.0E-14	A1688118.1	EST_HUMAN	wc82h08.x1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2326143 3'
1608	11989		4.08	7.0E-14	AW151673.1	EST_HUMAN	x887e10.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2623148 3' similar to contains MER10.12 MER10 repetitive element;
372	8639	18771	11.58	8.0E-14	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
7018	16195	25870	3.82	8.0E-14	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
7018	16195	25871	3.82	8.0E-14	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
824	9889	18891	4.42	5.0E-14	Q63120	SWISSPROT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5 CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER 1 (MULTIDRUG RESISTANCE- ASSOCIATED PROTEIN 2) (CANALICULAR MULTIDRUG RESISTANCE PROTEIN)
5086	14268	23353	1.24	5.0E-14	AW079781.1	EST_HUMAN	xc03b05.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2575185 3' similar to contains L1.12 L1 repetitive element;
5458	14884	24034	5.3	5.0E-14	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
1131	11888		2.92	4.0E-14	P04928	SWISSPROT	S-ANTIGEN PROTEIN PRECURSOR
1843	11051	20242	5.65	4.0E-14	AJ007873.1	NT	Homo sapiens LGMD2B gene

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3734	12954		0.88	4.0E-14	AA046502.1	EST_HUMAN	z687a08.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:487858 5'
4279	13482	22579	2.22	4.0E-14	N46328.1	EST_HUMAN	yy73c12.s1 Soares_multiple_sclerosis_2NbHMSHP Homo sapiens cDNA clone IMAGE:278190 3' similar to contains L1.13 L1 repetitive element;
8082	18381		3.28	4.0E-14	A1896224.1	EST_HUMAN	wm08c03.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2435332 3' similar to contains Alu repetitive element;
957	10190	18344	0.85	3.0E-14	X95466.1	NT	R.norvegicus mRNA for CPG2 protein
7788	14488	23585	9.96	3.0E-14	AW265354.1	EST_HUMAN	xp45f12.x1 NCI_CGAP_HN11 Homo sapiens cDNA clone IMAGE:2743343 3' similar to contains Alu repetitive element; contains element MER9 repetitive element;
8892	18243		1.51	3.0E-14	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
395	9850	18785	3.21	2.0E-14	AJ271738.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
395	9850	18788	3.21	2.0E-14	AJ271738.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
687	11874	18072	8.95	2.0E-14	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2351	11544		1.78	2.0E-14	AW372868.1	EST_HUMAN	RC5-BT0377-091289-031-D12 BT0377 Homo sapiens cDNA
2427	11618		1.48	2.0E-14	7657629	NT	Homo sapiens rhabdoid tumor deletion region protein 1 (RTDR1), mRNA
2492	11682	20888	2.43	2.0E-14	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
2505	11683		1.08	2.0E-14	BE222432.1	EST_HUMAN	nv90g10.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3180738 3' similar to contains Alu repetitive element; contains OFR.11 OFR repetitive element;
5543	14767	24133	3.24	2.0E-14	U01317.1	NT	Human beta globin region on chromosome 11
6292	16473	24914	20.84	2.0E-14	BE158761.1	EST_HUMAN	IL2-HT0397-071289-024-D04 HT0397 Homo sapiens cDNA
6292	16473	24915	20.84	2.0E-14	BE158761.1	EST_HUMAN	IL2-HT0397-071289-024-D04 HT0397 Homo sapiens cDNA
7361	16577	20088	5.36	2.0E-14	AW139800.1	EST_HUMAN	UI-H-B1-adv-a-10-Q-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2718234 3'
8033	14767	24133	1.87	2.0E-14	U01317.1	NT	Human beta globin region on chromosome 11
1074	10288	19449	1.33	1.0E-14	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
1410	10623	19787	5.94	1.0E-14	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C088
1410	10623	19788	5.94	1.0E-14	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C088
1870	11174	20390	12.87	1.0E-14	L44140.1	NT	Homo sapiens chromosome X region from fibrin (FLN) gene to glucose-6-phosphate dehydrogenase (G6PD) gene, complete cds's
2151	11349	20565	5.32	1.0E-14	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2372	11565	20786	32.19	1.0E-14	AF001688.1	NT	Homo sapiens ribosomal protein L23A (RPL23A) gene, complete cds
2895	12133	21288	1.12	1.0E-14	P05227	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-II)
3132	12367	21487	5.56	1.0E-14	BF335227.1	EST_HUMAN	RC2-CT0432-310700-013-a09_1 CT0432 Homo sapiens cDNA
3132	12367	21488	5.56	1.0E-14	BF335227.1	EST_HUMAN	RC2-CT0432-310700-013-a09_1 CT0432 Homo sapiens cDNA
3895	13081	22197	2.03	1.0E-14	AA682894.1	EST_HUMAN	ae80c12.s1 Strategene schizo brain S11 Homo sapiens cDNA clone IMAGE:971360 3'
4468	13667	22768	2.01	1.0E-14	AW275552.1	EST_HUMAN	xp39h10.x1 NCI_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2763059 3'

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6576	14800	24173	2.32	1.0E-14	AF126145.1	NT	Bos taurus xenobiotic/medium-chain fatty acid:CoA ligase form XL-III mRNA, nuclear mRNA encoding mitochondrial protein, complete cds
5959	18087	24591	10.71	1.0E-14	11437150	NT	Homo sapiens prolamin (mouse) like 1 (PROML1), mRNA
5959	18087	24592	10.71	1.0E-14	11437150	NT	Homo sapiens prolamin (mouse) like 1 (PROML1), mRNA
1555	10769	19941	1.52	9.0E-15	7427522	NT	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), mRNA
2139	11337						Homo sapiens transcription factor (GHM) enhancer 3, JM11 protein, JMA4 protein, JMS protein, T54 protein, complete cds; and L-type calcium channel α
6002	14189	23279	1.12	9.0E-15	AF198779.1	NT	JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel α
6269	15470	24911	3.85	9.0E-15	BF335227.1	EST_HUMAN	RC2-CT0432-310700-013-609_1 CT0432 Homo sapiens cDNA
2763	9739		0.90	8.0E-15	P21416	SWISSPROT	GAG POLYPROTEIN [CONTAINS: CORE PROTEINS P15, P12, P30, P10]
7190	16367		3.7	7.0E-16	BE261482.1	EST_HUMAN	GM1148032F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3184023 5'
1001	10232	18387	8.38	6.0E-15	AW241968.1	EST_HUMAN	777d02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2700483 3' similar to contains
7850	18391		1.99	6.0E-15	AJ271736.1	NT	THR12 THR repetitive element;
418	9869	18809	8.63	5.0E-15	AW838943.1	EST_HUMAN	Homo sapiens Xq pseudautosomal region; segment 2/2
2718	11895	21112	2.92	6.0E-16	AL163208.2	NT	QV1-L T0036-150200-070-c10 L T0036 Homo sapiens cDNA
3445	12870		1.05	5.0E-15		EST_HUMAN	Homo sapiens chromosome 21 segment HS21C008
7267	16486		1.87	5.0E-15	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
433	9238	18400	3.42	4.0E-15	AW28817.1	EST_HUMAN	UI-H-BW0-qib-g-10-0-UI.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:2731219 3'
7628	15592	25053	2.78	4.0E-15	AV730056.1	EST_HUMAN	AV730056 HTF Homo sapiens cDNA clone HTFAVE06 5'
7628	15592	25054	2.78	4.0E-15	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
4200	13404		7.67	3.0E-15	AJ130894.1	NT	Homo sapiens mRNA for transcription factor
4948	14135		5.47	3.0E-15	AJ130894.1	NT	Homo sapiens mRNA for transcription factor
5054	14236	23323	4.65	3.0E-15	N89452.1	EST_HUMAN	LY1142F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone LY1142 5' similar to ANF(CARDIODILATIN)
5054	14236	23324	4.66	3.0E-15	P92485	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 6
6189	15380	24920	3.53	3.0E-15	AA078097.1	EST_HUMAN	7P01F03 Chromosome 7 Placental cDNA Library Homo sapiens cDNA clone 7P01F03
6189	15380	24921	3.53	3.0E-15	AA078097.1	EST_HUMAN	7P01F03 Chromosome 7 Placental cDNA Library Homo sapiens cDNA clone 7P01F03
7046	16223		2.34	3.0E-15	M27685.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds
					M27685.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds
					AA807128.1	EST_HUMAN	cc36a07.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1351764 3' similar to contains MER19.11
						EST_HUMAN	MER19 repetitive element;

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Table 4
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7374	18590	26079	3.8	3.0E-15	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
8748	18275		1.51	3.0E-15	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
254	9530	18661	5.23	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
373	9839	18772	4.08	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
373	9839	18773	4.08	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
1515	10729		1.55	2.0E-15	8923201	NT	Homo sapiens hypothetical protein FLJ20212 (FLJ20212), mRNA
3483	12707	21843	0.82	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
3483	12707	21844	0.82	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
4625	13819		2.81	2.0E-15	AI806335.1	EST_HUMAN	w070706.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2349923 3' similar to TR:Q81043 Q81043 NINEIN.;
6197	15378	24819	2.21	2.0E-15	AA704195.1	EST_HUMAN	z47603.s1 Soares_fetal_liver_spleen_1NFSL_S1 Homo sapiens cDNA clone IMAGE:460924 3'
8263	16434	24873	4.9	2.0E-15	W05084.1	EST_HUMAN	z47610.r1 Soares_fetal_liver_spleen_1NFSL_S1 Homo sapiens cDNA clone IMAGE:298875 5' similar to WP:F44F4.8 CE02227 TRANSPOSASE.;
8747	15942	25402	3.39	2.0E-15	D14547.1	NT	Human DNA, SINE repetitive element
7415	16827		3.67	2.0E-15	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
8108	12707	21843	2.56	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
9109	12707	21844	2.56	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
2730	11908		4.02	1.0E-15	AI689884.1	EST_HUMAN	b28h05.x1 NCJ_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2270745 3' similar to TR:Q13538 Q13539 MARINER TRANSPOSASE.;
2874	12211	21349	1.56	1.0E-15	BE043594.1	EST_HUMAN	h440602.y1 NCJ_CGAP_Ov34 Homo sapiens cDNA clone IMAGE:2869182 5'
3107	12342	21470	1.11	1.0E-15	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
4353	13555	22851	0.89	1.0E-15	BE182698.1	EST_HUMAN	RC3-HT0849-100500-022-505 HT0849 Homo sapiens cDNA
5922	15039	24441	1.78	1.0E-15	T95783.1	EST_HUMAN	ye40e10.s1 Soares_fetal_liver_spleen_1NFSL Homo sapiens cDNA clone IMAGE:120234 3' similar to contains MER6 repetitive element.;
6091	15292		1.87	1.0E-15	BE074217.1	EST_HUMAN	QV3-BT0569-270100-074-g05 BT0569 Homo sapiens cDNA
6807	15803	25258	3.75	1.0E-15	AI200876.1	EST_HUMAN	qf68h06.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1755227 3'

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6607	15903	25259	3.75	1.0E-15	AI200976.1	EST_HUMAN	qf68n06.k1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1765227 3'
6778	15974	25431	2.94	1.0E-15	4507208	NT	Homo sapiens spermidine synthase (SRM) mRNA
7395	16809	28100	6.95	1.0E-15	AF044083.1	NT	Homo sapiens major histocompatibility locus class III region
8182	18088	23808	5.74	1.0E-15	AI783944.1	EST_HUMAN	tr31c05.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2210912 3' similar to contains Alu repetitive element
4507	13703	22797	1.15	9.0E-16	4503168	NT	Homo sapiens cut (Drosophila)-like 1 (CCAT displacement protein) (CUTL1) mRNA
7665	16770	28261	2.85	9.0E-16	F06888.1	EST_HUMAN	HSC23F051 normalized infant brain cDNA Homo sapiens cDNA clone c-23f05
8130	18186		9.02	7.0E-16	T84149.1	EST_HUMAN	ye28c12.r1 Stratagene lung (#837210) Homo sapiens cDNA clone IMAGE:118082 5'
2108	11308		7.48	6.0E-16	AW972611.1	EST_HUMAN	EST384702 IMAGE resequences, MAGL Homo sapiens cDNA
1484	10687	19872	0.98	5.0E-16	AJ251154.1	NT	Mus musculus effector receptor cluster, OR37A, OR37B, OR37C, OR37E genes and OR37D pseudogene c880c04.s1 Soares_fetal_fetus_Nb2Hf8_9w Homo sapiens cDNA clone IMAGE:1623078 3' similar to contains element L1 repetitive element
2840	11823	21038	2.42	5.0E-16	AA982176.1	EST_HUMAN	601885734F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4104129 5'
8052	17188	28728	3.64	5.0E-16	BF217388.1	EST_HUMAN	Homo sapiens GTP binding protein 1 (GTPBP1), mRNA
8225	18003		12.84	5.0E-16	11418127	NT	QV1-JM0036-200300-116-g02 UM0036 Homo sapiens cDNA
2346	11639	20762	0.96	4.0E-16	AW797188.1	EST_HUMAN	QV1-JM0036-200300-115-g02 UM0036 Homo sapiens cDNA
2348	11639	20763	0.96	4.0E-16	AW797188.1	EST_HUMAN	MYELIN-OLIGODENDROCYTE GLYCOPROTEIN PRECURSOR
3434	12859	21790	5.03	4.0E-16	Q18653	SWISSPROT	PM4-BT0650-010400-002-g09 BT0650 Homo sapiens cDNA
4124	13330	22428	5.95	4.0E-16	BE083875.1	EST_HUMAN	PM4-BT0650-010400-002-g09 BT0650 Homo sapiens cDNA
4124	13330	22429	6.95	4.0E-16	BE083875.1	EST_HUMAN	PM4-BT0650-010400-002-g09 BT0650 Homo sapiens cDNA
6380	15500	25016	35.49	4.0E-16	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
7772	16987	28480	1.68	4.0E-16	AV730030.1	EST_HUMAN	AV730030 HTF Homo sapiens cDNA clone HTFAWA03 5'
8421	17483		1.39	4.0E-16	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
8514	17548		6.29	4.0E-16	C05947.1	EST_HUMAN	C05947 Human pancreas islet Homo sapiens cDNA clone hsc5355
8525	17655	23888	2.97	4.0E-16	6912459	NT	Homo sapiens Grb2-associated binder 2 (KIA00571), mRNA
8808	17728		1.45	4.0E-16	R18591.1	EST_HUMAN	yf8bb11.r1 Soares Infant brain INIB Homo sapiens cDNA clone IMAGE:30489 5'
130	8413	18548	1.45	3.0E-16	AW022862.1	EST_HUMAN	df45c01.y1 Marton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2486376 5'
130	8413	18549	1.45	3.0E-16	AW022862.1	EST_HUMAN	df45c01.y1 Marton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2486376 5'
472	9725		2.3	3.0E-16	AL048445.1	EST_HUMAN	DKFZp434P037_1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434P037 5'
482	9734		1.72	3.0E-16	AF135448.1	NT	Homo sapiens TSX (TSX) pseudogene, exon 5
1453	10698	18940	1.97	3.0E-16	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
2830	12188	21300	4.28	3.0E-16	P03200	SWISSPROT	ENVELOPE GLYCOPROTEIN GP340 (MEMBRANE ANTIGEN) (MA) [CONTAINS: GLYCOPROTEIN GP220]
3807	13123	22241	0.78	3.0E-16	T08168.1	EST_HUMAN	EST080860 Infant Brain, Bento Soares Homo sapiens cDNA clone HIBBA13 5' end

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4061	14148	23240	1.01	3.0E-16	AV661393.1	EST_HUMAN	AV661393 GLC Homo sapiens cDNA clone GLCGSA01 3'
6671	15868	25326	3.01	3.0E-16	AI002838.1	EST_HUMAN	em88h05.s1 Stratiogene schizo brain S11 Homo sapiens cDNA clone IMAGE:1884185 3' similar to contains THR.b2 THR repetitive element;
7118	16295	25777	6.55	3.0E-16	L78810.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
978	10211		1.32	2.0E-16	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C079
2850	11833		1.1	2.0E-16	J03061.1	NT	Human SSAN-related endogenous retroviral LTR-like element
4169	13363	22463	1.66	2.0E-16	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
8450	15847	25115	2.24	2.0E-16	AI732837.1	EST_HUMAN	nz47706.x5 NCI_CGAP_P12 Homo sapiens cDNA clone IMAGE:1280947 similar to TR:O54849 O54849 HYPOTHETICAL 42.9 KD PROTEIN. [2] TR:O08905 contains MER7.11 MER7 repetitive element;
7502	16709	28198	3.45	2.0E-16	5802145	NT	Homo sapiens ubiquitin carrier protein E2-C (UBCH10), mRNA
189	9468	18597	2.2	1.0E-16	AF200719.1	NT	Homo sapiens pituitary tumor transforming gene protein (PTTG) gene, complete cds
387	9681		32.18	1.0E-16	AA628592.1	EST_HUMAN	af39g11.s1 Soares fetal_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1034084 3' similar to contains OFR.12 OFR repetitive element;
1941	11145	20344	2.99	1.0E-16	BF327842.1	EST_HUMAN	QV0-BN0148-070700-283-a10 BN0148 Homo sapiens cDNA
5844	15061		25.98	1.0E-16	U45883.1	NT	Homo sapiens CCR8 chemokine receptor (CNKBR8) gene, complete cds
5913	15130	24539	3.2	1.0E-16	Q02779	SWISSPROT	MITOGEN-ACTIVATED PROTEIN KINASE KINASE 10 (MIXED LINEAGE KINASE 2) (PROTEIN KINASE MST)
6314	15061		7.17	1.0E-16	U45883.1	NT	Homo sapiens CCR8 chemokine receptor (CNKBR8) gene, complete cds
3719	12939	22056	2.63	9.0E-17	AW000048.1	EST_HUMAN	GM1-NN1003-200300-153-e01 NN1003 Homo sapiens cDNA
5974	15188		1.98	9.0E-17	AI392864.1	EST_HUMAN	tg22a11.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2108524 3' similar to contains MER28.12 MER28 repetitive element;
6498	15893		3.16	9.0E-17	AW150257.1	EST_HUMAN	tg48g12.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2830950 3' similar to contains OFR.12 OFR repetitive element;
7142	16319		2.25	9.0E-17	AF200718.1	NT	Homo sapiens pituitary tumor transforming gene protein (PTTG) gene, complete cds
1025	10251		1.34	8.0E-17	AW880701.1	EST_HUMAN	QV0-OT0032-080300-155-d01 OT0032 Homo sapiens cDNA
3970	13086		1.01	8.0E-17	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
5482	18056	24084	3.83	8.0E-17	BE172081.1	EST_HUMAN	MIR0-HT0559-080300-003-e04 HT0559 Homo sapiens cDNA
6198	15379		1.82	8.0E-17	AV730759.1	EST_HUMAN	AV730759 HTF Homo sapiens cDNA clone HTFAQB07 5'
1457	10670		4.26	7.0E-17	6763097	NT	Mus musculus apolipoprotein B editing complex 2 (ApoBec2), mRNA
5347	14577		3.44	7.0E-17	AF216650.1	NT	Homo sapiens putative MTAP (MTAP) mRNA, partial cds, alternatively spliced
5960	15175	24593	7.8	7.0E-17	AF228943.1	NT	Mus musculus WNT-2 gene, partial cds; putative ankyrin-related protein and cyclic fibrosis transmembrane conductance regulator (CFTR) genes, section 1 of 2 of the complete cds; and unknown gene

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
208	8489	18622	8.24	6.0E-17	AW883880.1	EST_HUMAN	RC1-HN0003-220300-021-b04 HN0003 Homo sapiens cDNA
5784	15011	24415	1.71	6.0E-17	AW682772.1	EST_HUMAN	h181404.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2878895 3' similar to contains L1.12 L1 repetitive element;
427	8282	18394	4.13	5.0E-17	T84110.1	EST_HUMAN	yc05108.r1 Stratiens lung (#337210) Homo sapiens cDNA clone IMAGE:79839 5'
8328	15506	24855	1.75	5.0E-17	T81043.1	EST_HUMAN	yd28604.r1 Soares fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:109327 5'
3814	12835	21855	0.85	4.0E-17	AA843697.1	EST_HUMAN	n188405.s1 NCI_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1058528 3'
8028	17183	28700	2.43	4.0E-17	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
8435	17501		2.34	4.0E-17	AI073546.1	EST_HUMAN	ov45604.x1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1840288 3' similar to TRQ16530
2068	11268	20482	1.45	3.0E-17	AW119123.1	EST_HUMAN	Q16530 PMS3 MRNA :contains MER10.12 MER10 repetitive element;
3157	12392		1.08	3.0E-17	P35410	SWISSPROT	xd39c09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2804784 3'
3821	12842	21861	1.16	3.0E-17	BE326522.1	EST_HUMAN	MAS-RELATED G PROTEIN-COUPLED RECEPTOR MRG
3821	12842	21862	1.16	3.0E-17	BE326522.1	EST_HUMAN	hw03504.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3181888 3'
6992	16170	25842	5.16	3.0E-17	AB026898.1	NT	hw03504.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3181888 3'
8398	17476		3.23	3.0E-17	11417968	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
358	9828	18756	4.54	2.0E-17	AI270080.1	EST_HUMAN	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
359	9828	18756	2.24	2.0E-17	AI270080.1	EST_HUMAN	qt63a08.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:1859922 3' similar to contains Alu repetitive element
896	10227		1.92	2.0E-17	AA722832.1	EST_HUMAN	qt63a08.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:1859922 3' similar to contains Alu repetitive element
2410	11602	20822	2.54	2.0E-17	Q28983	SWISSPROT	zq81c04.s1 Soares_fetal_heart1_NH-H19W Homo sapiens cDNA clone IMAGE:399751 3'
2410	11602	20823	2.54	2.0E-17	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
2890	12118	21249	6.89	2.0E-17	P12038	SWISSPROT	ZONADHESIN PRECURSOR
5378	14607	23717	1.9	2.0E-17	M27685.1	NT	NEUROFILAMENT TRIPLET H PROTEIN (200 KDA NEUROFILAMENT PROTEIN) (NEUROFILAMENT HEAVY POLYPEPTIDE) (NF-H)
5378	14607	23718	1.9	2.0E-17	M27685.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds
5774	14892		1.81	2.0E-17	AF050066.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds
7028	18208	25683	2.43	2.0E-17	BE298888.1	EST_HUMAN	Homo sapiens MHC class 1 region
7042	18219	25694	3.53	2.0E-17	AL163247.2	NT	600944890F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2860815 5'
7042	18218	25695	3.53	2.0E-17	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
7154	16331	25814	6.53	2.0E-17	D13991.1	NT	Homo sapiens chromosome 21 segment HS21C047
758	9889	19140	3.33	1.0E-17	P08183	SWISSPROT	Human CYP19 gene for aromatase cytochrome P-450, promoter region (containing two cis-acting transcriptional regulatory elements)
							MULTIDRUG RESISTANCE PROTEIN 1 (P-GLYCOPROTEIN 1)

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Table 4
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1893	10895		1.38	1.0E-17	AI271738.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
1738	10950	20133	5.09	1.0E-17	AL183207.2	NT	Homo sapiens chromosome 21 segment HS21C007
2086	11286	20489	1.89	1.0E-17	P02481	SWISSPROT	COLLAGEN ALPHA 1(III) CHAIN PRECURSOR
2304	11498	20718	3.54	1.0E-17	U78410.1	NT	Homo sapiens thrombospondin 2 (THBS2) gene, promoter region and exons 1A and 1B
3543	12768		0.83	1.0E-17	AF224689.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
4119	13325		8.44	1.0E-17	R08942.1	EST_HUMAN	y30607.t1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:128388 5'
7955	17094	26825	1.98	1.0E-17	Q28824	SWISSPROT	MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE (MLCK) [CONTAINS: TELOKIN]
2434	11625	20847	1.79	9.0E-18	AA174078.1	EST_HUMAN	zp18g12.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:609802 3'
3769	12887	22103	1.31	8.0E-18	4758977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
354	9622	18760	49.8	7.0E-18	AW316978.1	EST_HUMAN	xc10b04.x1 NCI CGAP Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb:120868 60S
354	9622	18761	49.8	7.0E-18	AW316978.1	EST_HUMAN	RIBOSOMAL PROTEIN L4 (HUMAN);
8836	9622	18750	4.04	7.0E-18	AW316978.1	EST_HUMAN	xc10b04.x1 NCI CGAP Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb:120868 60S
8836	9622	18761	4.04	7.0E-18	AW316978.1	EST_HUMAN	RIBOSOMAL PROTEIN L4 (HUMAN);
3264	12497	21627	1.38	8.0E-18	X71791.2	NT	xc10b04.x1 NCI CGAP Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb:120868 60S
4759	13950		3.42	6.0E-18	P52181	SWISSPROT	RIBOSOMAL PROTEIN L4 (HUMAN);
6542	15738		3.47	8.0E-18	11428155	NT	Rattus norvegicus partial Gdr/Pn-1 gene for gila-derived neuroprotease neadin I, enhancer region
7694	18893	26402	2.2	8.0E-18	AL183246.2	NT	PROTEIN-GLUTAMINE GAMMA-GLUTAMYL TRANSFERASE (TISSUE TRANSGLUTAMINASE)
7873	17082	26586	1.98	8.0E-18	X87344.1	NT	(TGASE C) (TGC)
8231	17360		2.73	8.0E-18	11428885	NT	Homo sapiens similar to high-mobility group (nonhistone chromosomal) protein 4 (H. sapiens) (LOC83448); mRNA
8671	17848	23977	1.73	8.0E-18	U87928.1	NT	mRNA
1156	10378	18530	17.47	5.0E-18	AI280214.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C048
4303	13504	22801	1.26	5.0E-18	10946685	NT	H. sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes
6311	14542	23811	1.95	5.0E-18	AF087813.1	NT	Homo sapiens similar to ribosomal protein L12 (H. sapiens) (LOC83081), mRNA
7551	16756	26249	4.21	5.0E-18	10242378	NT	Homo aconitase hydratase (ACO2) gene, exon 4
7551	16756	26250	4.21	5.0E-18	10242378	NT	qim65g11.x1 Soares placenta 8to9weeks_2NtHP8t8W Homo sapiens cDNA clone IMAGE:1893688 3' similar to contains Alu repetitive element;
							Mus musculus gasdermin (Gsdm), mRNA
							Human endogenous retrovirus HERV-P-T47D
							Homo sapiens lymphocyte activation-associated protein (LOC51088), mRNA
							Homo sapiens lymphocyte activation-associated protein (LOC51088), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8800	17725		5.65	5.0E-18	AW687182.1	EST_HUMAN	MR1-SN0035-060400-001-q11 SN0035 Homo sapiens cDNA
9161	17954		14.87	5.0E-18	AV650547.1	EST_HUMAN	AV650547 GLC Homo sapiens cDNA clone GLCGA02 3'
123	9408	18541	1.78	4.0E-18	BE044078.1	EST_HUMAN	h038h04.x1 NCI_CGAP_U1 Homo sapiens cDNA clone IMAGE:3039511 3' similar to contains MER29.b3
123	9408	18542	1.78	4.0E-18	BE044078.1	EST_HUMAN	h038h04.x1 NCI_CGAP_U1 Homo sapiens cDNA clone IMAGE:3039511 3' similar to contains MER29.b3
1891	10803	20080	18.8	4.0E-18	AA621814.1	EST_HUMAN	h024f11.s1 NCI_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1144845 3' similar to gb:M28328
1864	11081		1.02	4.0E-18	AI738592.1	EST_HUMAN	KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
2167	11365	20584	1.64	4.0E-18	Q06430	SWISSPROT	w03h08.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:2392085 3'
2167	11365	20585	1.64	4.0E-18	Q06430	SWISSPROT	N-ACETYLGLUCOSAMINIDE BETA-1,6-N-ACETYLGLUCOSAMINYLTRANSFERASE (N-ACETYLGLUCOSAMINYLTRANSFERASE)(I-BRANCHING ENZYME)(IGNT)
3774	12662	22107	0.61	4.0E-18	AI581586.1	EST_HUMAN	N-ACETYLGLUCOSAMINYLTRANSFERASE (N-ACETYLGLUCOSAMINYLTRANSFERASE)(I-BRANCHING ENZYME)(IGNT)
5376	14605	23714	2.33	4.0E-18	AD17565.1	EST_HUMAN	ACETYLGLUCOSAMINYLTRANSFERASE (I-BRANCHING ENZYME)(IGNT)
5376	14605	23715	2.33	4.0E-18	AD17565.1	EST_HUMAN	ACETYLGLUCOSAMINYLTRANSFERASE (I-BRANCHING ENZYME)(IGNT)
7575	16780	26275	7.21	4.0E-18	AA371807.1	EST_HUMAN	ar03b06.x1 Beta2ed colon HPLRB7 Homo sapiens cDNA clone IMAGE:2173139 3' similar to contains Alu repetitive element;
859	10085	19258	6.09	3.0E-18	AA814198.1	EST_HUMAN	ou23e08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1827138 3'
938	10171	19327	3.12	3.0E-18	BE088034.1	EST_HUMAN	ou23e08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1827138 3'
3927	13143	22260	1.29	3.0E-18	AL163247.2	NT	ou23e08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1827138 3'
6009	15259	24683	5.16	3.0E-18	BE001671.1	EST_HUMAN	EST63833 Pituitary gland, subtracted (prolactin/growth hormone) II Homo sapiens cDNA 5' end similar to EST containing O family repeat
8941	17819		5.72	3.0E-18	AW022015.1	EST_HUMAN	db22h11.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1324581 3' similar to SW:RS5_HUMAN
255	9531	19682	3.74	2.0E-18	AW836820.1	EST_HUMAN	P46782 40S RIBOSOMAL PROTEIN S6. ;
1161	10383		130.1	2.0E-18	BE256097.1	EST_HUMAN	CMO-BT0690-210300-288-g07 BT0690 Homo sapiens cDNA
3087	12523	21445	0.97	2.0E-18	Q39575	SWISSPROT	Homo sapiens chromosome 21 segment HS21C047
5400	14628		2.82	2.0E-18	AA668610.1	EST_HUMAN	PMO-BN0081-100300-001-b08 BN0081 Homo sapiens cDNA
5442	14668	23824	3.16	2.0E-18	D14547.1	NT	df31h12.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2485128 5'
5442	14668	23825	3.16	2.0E-18	D14547.1	NT	QV1-LT0038-150200-070-e07 LT0038 Homo sapiens cDNA
5786	15013	24417	3.75	2.0E-18	AW685853.1	EST_HUMAN	801114352F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3355044 5'
							DYNEIN GAMMA CHAIN, FLAGELLAR OUTER ARM
							ak53e07.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1408652 3' similar to TR:O14577
							O14577 BAC CLONE RG114A08 FROM TQ31, COMPLETE SEQUENCE. ;
							Human DNA, SINE repetitive element
							Human DNA, SINE repetitive element
							h04g01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2979984 3' similar to contains MER19.12 MER19 repetitive element ;

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7548	18761	26245	6.35	2.0E-18	AW470791.1	EST_HUMAN	ha33408.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2875489 3' similar to contains THR.b3 THR repetitive element;
8223	17353	26880	6.03	2.0E-18	AW151298.1	EST_HUMAN	xq47609.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2630728 3' similar to contains MER8.b2 MER8 repetitive element;
8600	10383		6.56	2.0E-18	BE256097.1	EST_HUMAN	801114352F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3355044 5'
4409	13609		0.91	1.0E-18	T95408.1	EST_HUMAN	ye43p05.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:120538 5' similar to contains L1 repetitive element;
4814	13808		0.94	1.0E-18	Y10198.1	NT	Homo sapiens PHEX gene
5389	14589	23677	2.61	1.0E-18	AV653405.1	EST_HUMAN	AV653405 GLC Homo sapiens cDNA clone GLCCKE11 3'
5475	14702	24057	3.08	1.0E-18	D00098.1	NT	Homo sapiens mRNA for Na,K-ATPase alpha-subunit, complete cds
5475	14702	24058	3.08	1.0E-18	D00098.1	NT	Homo sapiens mRNA for Na,K-ATPase alpha-subunit, complete cds
7040	16217	25682	6.88	1.0E-18	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
8548	17572	23993	2.92	1.0E-18	AF003529.1	NT	Homo sapiens glycocalyx 3 (GPC3) gene, partial cds and flanking repeat regions
552	9803	18830	5.11	9.0E-19	AA281861.1	EST_HUMAN	z111d08.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.12 MER19 repetitive element;
553	9803	18830	4	9.0E-19	AA281861.1	EST_HUMAN	z111d08.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.12 MER19 repetitive element;
6412	15009		3.42	9.0E-19	F08888.1	EST_HUMAN	HS2323F051 normalized infant brain cDNA Homo sapiens cDNA clone c-23f05
6678	15871	25330	3.24	9.0E-19	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
6678	15871	25331	3.24	9.0E-19	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
7687	16888	26394	4.7	9.0E-19	AB032869.1	NT	Homo sapiens mRNA for KIAA1143 protein, partial cds
8303	9803	18830	10.58	9.0E-19	AA281861.1	EST_HUMAN	z111d08.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.12 MER19 repetitive element;
1055	10281		1.04	8.0E-18	AW974902.1	EST_HUMAN	EST387007 IMAGE resequences, MAGN Homo sapiens cDNA
2210	11407	20631	1.9	7.0E-19	4758139	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 8 (RNA helicase, 54kD) (DDX8) mRNA
5851	15089	24478	2.02	7.0E-19	AF092090.1	NT	Rattus norvegicus cp151 mRNA, partial cds
8443	18382		2.85	7.0E-19	AA705694.1	EST_HUMAN	z160b01.s1 Soares fetal liver spleen 1NFLS_S1 Homo sapiens cDNA clone IMAGE:435145 3'
3781	12980		1.41	6.0E-19	AW852830.1	EST_HUMAN	PMD-CT0248-131099-001-g01 CT0248 Homo sapiens cDNA
4458	13658	22750	1.47	6.0E-19	P34988	SWISSPROT	OLFACTORY RECEPTOR 8 (M50)
4458	13658	22751	1.47	6.0E-19	P34988	SWISSPROT	OLFACTORY RECEPTOR 8 (M50)
4813	14002		1.34	6.0E-19	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2

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Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5050	14232	23317	1.01	6.0E-19	AL120817.1	EST_HUMAN	DKFZp782F192.1 782 (synonym: hmel2) Homo sapiens cDNA clone DKFZp782F192.5
5594	14818	24194	5.29	5.0E-19	Q00183	SWISSPROT	ZONA PELLUCIDA SPERM-BINDING PROTEIN B PRECURSOR (ZONA PELLUCIDA GLYCOPROTEIN ZP-X) (RC55)
8070	17205	28738	7.83	5.0E-19	AW183725.1	EST_HUMAN	x187b02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2684171 3' similar to contains element MSR1 repetitive element:
561	8811	18834	1.19	4.0E-19	AB007970.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501
2942	11825	21040	1.28	4.0E-19	BF687382.1	EST_HUMAN	602130910F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4287674 5'
3838	13053	22165	1	3.0E-19	Q28987	SWISSPROT	BETA-2 ADRENERGIC RECEPTOR
3838	13053	22168	1	3.0E-19	Q28987	SWISSPROT	BETA-2 ADRENERGIC RECEPTOR
4271	13474	22570	0.8	3.0E-19	O43900	SWISSPROT	LIM-ONLY PROTEIN 6 (TRIPLE LIM DOMAIN PROTEIN 6)
4271	13474	22571	0.6	3.0E-19	O43900	SWISSPROT	LIM-ONLY PROTEIN 6 (TRIPLE LIM DOMAIN PROTEIN 6)
4441	13841	22732	1.37	3.0E-19	AV708136.1	EST_HUMAN	AV708136 ADC Homo sapiens cDNA clone ADCAMA11 5'
6249	15430		2.23	3.0E-19	11432214	NT	Homo sapiens similar to aldo-keto reductase family 1, member B11 (aldose reductase-like) (H. sapiens) (LOC83222), mRNA
8697	17865		14.35	3.0E-19	AF165520.1	NT	Homo sapiens phorbol-in protein (PBI) mRNA, complete cds
2528	11714	20831	42.82	2.0E-19	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
4439	13639		1.65	2.0E-19	AI311783.1	EST_HUMAN	q081e02.x1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1915898 3' similar to TR:Q68389 Q68388 POL/ENV GENE:
6572	15768	25231	5.48	2.0E-19	AA012854.1	EST_HUMAN	zs34c09.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:360880 5'
8260	17387	26919	1.88	2.0E-19	BF330867.1	EST_HUMAN	RC3-BT0333-250800-114-R04 BT0333 Homo sapiens cDNA
8260	17387	26920	1.88	2.0E-19	BF330867.1	EST_HUMAN	RC3-BT0333-250800-114-R04 BT0333 Homo sapiens cDNA
488	9741		1.85	1.0E-19	BE408611.1	EST_HUMAN	601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5'
2130	11329	20548	1.23	1.0E-19	H30795.1	EST_HUMAN	y079g07.r1 Soares adult brain N2b4HB55Y Homo sapiens cDNA clone IMAGE:184188 5' similar to contains MER10 repetitive element:
2677	11859		1.79	1.0E-19	D38044.1	NT	Human gene for AII-receptor, exon 7-8
2800	12040		6.21	1.0E-19	4758977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
3379	12808	21740	1.3	1.0E-19	AA834987.1	EST_HUMAN	aj48b12.e1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1383631 3' similar to contains MER37.12
5700	14819	24313	2.41	1.0E-19	U12186.1	NT	Myxoid cystic curculius sodium/dicarboxylate cotransporter mRNA, partial cds
6898	15891		3.48	1.0E-19	T89920.1	EST_HUMAN	y072b02.r1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:123243 5' similar to contains OFR repetitive element:
7129	16308	25788	49.35	1.0E-19	AW812258.1	EST_HUMAN	RCO-ST0174-191099-031-B05 ST0174 Homo sapiens cDNA
7133	16310	25782	2.88	1.0E-19	N44631.1	EST_HUMAN	y01e09.r1 Soares melanocyte 2NblHM Homo sapiens cDNA clone IMAGE:272872 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8233	17302	26900	1.92	1.0E-19	U93163.1	NT	Homo sapiens MAGE-B2 (MAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1 (MAGE-B1) genes, complete cds
5954	15170	24594	2.54	8.0E-20	7657286	NT	Mus musculus keratin-associated protein 9-1 (Krtap9-1), mRNA
5954	15170	24594	2.54	8.0E-20	7657286	NT	Mus musculus keratin-associated protein 9-1 (Krtap9-1), mRNA
3243	12478	21809	0.6	7.0E-20	BF329455.1	EST_HUMAN	PM4-AN0098-050900-003-a04 AN0098 Homo sapiens cDNA
6086	14532	23556	6.05	7.0E-20	AL138120.1	EST_HUMAN	DKFZp547D092_r1 547 (synonym: tfrb1) Homo sapiens cDNA clone DKFZp547D092 5'
6824	15620	25279	10.98	7.0E-20	AA557657.1	EST_HUMAN	nl46c04.s1 NCI_CGAP_Pr4 Homo sapiens cDNA clone IMAGE:1043718 similar to contains MER29.b2 MER29 repetitive element;
6824	15620	26280	10.96	7.0E-20	AA557657.1	EST_HUMAN	nl46c04.s1 NCI_CGAP_Pr4 Homo sapiens cDNA clone IMAGE:1043718 similar to contains MER29.b2 MER29 repetitive element;
8205	17338		9.91	7.0E-20	6812633	NT	Homo sapiens ribosomal protein L13a (RPL13A), mRNA
3530	12753	21886	3.7	6.0E-20	P39188	SWISSPROT	ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY
4258	13461	22553	3.37	6.0E-20	BE622434.1	EST_HUMAN	601441231F1NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918231 5'
4595	13789		1.16	5.0E-20	AV725123.1	EST_HUMAN	AV725123 HTC Homo sapiens cDNA clone HTC8TA01 5'
6440	15637	25103	5.78	5.0E-20	W80525.1	EST_HUMAN	zh78c08.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:418181 3' similar to contains MER30.11 MER30 repetitive element;
6440	15637	25104	5.78	5.0E-20	W80525.1	EST_HUMAN	zh78c08.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:418181 3' similar to contains MER30.11 MER30 repetitive element;
1587	10811	19889	1.55	4.0E-20	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
8435	15632		6.61	4.0E-20	AI874352.1	EST_HUMAN	tz64g03.x1 NCI_CGAP_Ov35 Homo sapiens cDNA clone IMAGE:2283398 3'
2108	11307	20521	0.91	3.0E-20	U03988.1	NT	Human BXP21 gene
4182	13396	22498	1.28	3.0E-20	P23273	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN 114
4827	13821	22910	0.81	3.0E-20	AA037816.1	EST_HUMAN	zk36b12.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:484895 3' similar to contains L1.13 L1 repetitive element;
6753	15948		3.21	3.0E-20	D14547.1	NT	Human DNA, SINE repetitive element
7258	16478		2.1	3.0E-20	P11389	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE; ENDONUCLEASE]
8459	17515	24021	17.57	3.0E-20	BE888422.1	EST_HUMAN	601514180F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3915522 5'
840	10077		13.56	2.0E-20	AW303868.1	EST_HUMAN	x24a10.x1 NCI_CGAP_U4 Homo sapiens cDNA clone IMAGE:2761088 3' similar to SW:RS5_MOUSE P97461 40S RIBOSOMAL PROTEIN S5.;
1119	10343	18493	3.84	2.0E-20	AA516335.1	EST_HUMAN	ng68h08.s1 NCI_CGAP_Lip2 Homo sapiens cDNA clone IMAGE:940087 similar to TR:G1224068 G1224068 ORF2: FUNCTION UNKNOWN.;
1119	10343	18494	3.84	2.0E-20	AA516335.1	EST_HUMAN	ng68h08.s1 NCI_CGAP_Lip2 Homo sapiens cDNA clone IMAGE:940087 similar to TR:G1224068 G1224068 ORF2: FUNCTION UNKNOWN.;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2769	10077		10.39	2.0E-20	AW303898.1	EST_HUMAN	xr24e10.x1 NCI_CGAP_U4 Homo sapiens cDNA clone IMAGE:2761098 3' similar to SW:R35_MOUSE
4965	14152	23243	4.5	2.0E-20	Q26983	SWISSPROT	P97461 40S RIBOSOMAL PROTEIN S5.;
4965	14152	23244	4.5	2.0E-20	Q26983	SWISSPROT	ZONADHESIN PRECURSOR
5176	14364		2.31	2.0E-20	5174538	NT	ZONADHESIN PRECURSOR
6826	16020	25485	8.64	2.0E-20	D10083.1	NT	Homo sapiens melate dehydrogenase 1, NAD (soluble) (MDH1) mRNA
6826	16020	25486	8.64	2.0E-20	D10083.1	NT	Homo sapiens RGH1 gene, retrovirus-like element
8882	18088	23802	2.03	2.0E-20	H55371.1	EST_HUMAN	Homo sapiens RGH1 gene, retrovirus-like element
1981	11949	20393	4.81	1.0E-20	AA281961.1	EST_HUMAN	CHP220310 Chromosome 22 exon Homo sapiens cDNA clone C22_391 5'
4431	13631	22728	1.25	1.0E-20	BF115158.1	EST_HUMAN	z111d08.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.12
6820	18014	25479	2.76	1.0E-20	11418491	NT	repetitive element;
8086	17221	26757	3.06	1.0E-20	AF223391.1	NT	Homo sapiens Autosomal Highly Conserved Protein (AHCP), mRNA
8596	17603		2.02	1.0E-20	AA420453.1	EST_HUMAN	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
8308	17412		2.85	9.0E-21	AW698189.1	EST_HUMAN	nc80g08.r1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:745684 similar to contains L1.13 L1
8071	17208	26739	4.47	8.0E-21	AA809411.1	EST_HUMAN	repetitive element;
8473	17528		2.75	8.0E-21	O21330	SWISSPROT	RC3-NN0068-060500-021-b03 NN0068 Homo sapiens cDNA
2036	11237	20444	2.12	7.0E-21	P15800	SWISSPROT	cb71f08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1336835 3'
2036	11237	20445	2.12	7.0E-21	P15800	SWISSPROT	ATP SYNTHASE A CHAIN (PROTEIN 6)
4242	13445		6.6	7.0E-21	AA048502.1	EST_HUMAN	LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ) (LAMININ CHAIN B3)
6874	15869	25328	7.23	7.0E-21	D14718.1	NT	LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ) (LAMININ CHAIN B3)
							Human chromosomal protein HMGI related gene
7268	16905	25698	3.34	7.0E-21	AA723404.1	EST_HUMAN	z073d03.s1 Soares_fetal_heart_NbH19W Homo sapiens cDNA clone IMAGE:398981 3' similar to
7817	17010	26523	2.14	7.0E-21	7706868	NT	gb:M14338 VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN); contains THR.13 OFR
4081	13291	22390	0.95	8.0E-21	BE408811.1	EST_HUMAN	repetitive element;
833	10168	18323	0.75	5.0E-21	5802031	NT	Homo sapiens PTD013 protein (PTD013), mRNA
4357	13559	22654	3.53	5.0E-21	BE968839.1	EST_HUMAN	601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3633310 5'
4815	14004	23106	7.11	5.0E-21	4895474	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type 21 (PTPN21), mRNA
8389	17470		1.94	5.0E-21	AA393574.1	EST_HUMAN	601649871F1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:3933880 5'
							Homo sapiens melanoma antigen, family C, 1 (MAGEC1), mRNA
							z172c04.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:727878 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1707	10919	20104	1.53	4.0E-21	AA870713.1	EST_HUMAN	cc88e08.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1573094 3' similar to TR:Q16530 Q16530
6027	15235	24658	3.09	4.0E-21	AB019578.1	NT	PM53 MRNA ; contains ORF.11 ORF repetitive element;
1805	11014	20207	4.17	3.0E-21	AA218891.1	EST_HUMAN	Rattus norvegicus mRNA for rTIM, complete cds
2239	11434	20658	1.89	3.0E-21	AL183201.2	NT	zq15c06.s1 Strategene fetal retina 937202 Homo sapiens cDNA clone IMAGE:826771 3'
3045	12281	21403	3.89	3.0E-21	AJ007873.1	NT	Homo sapiens chromosome 21 segment HS21C001
5744	14963		2.05	3.0E-21	BF184739.1	EST_HUMAN	Homo sapiens LGMD2B gene
6113	15207	24628	6.82	3.0E-21	BF361093.1	EST_HUMAN	601844465F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4084945 5'
6869	16167	25639	14.95	3.0E-21	AW897760.1	EST_HUMAN	RC1-OT0083-100800-019-g08 OT0083 Homo sapiens cDNA
8881	18292	23688	6.77	3.0E-21	AL183213.2	NT	CM1-NN0063-280400-203-h08 NN0063 Homo sapiens cDNA
148	9430		18.59	2.0E-21	BE163247.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C013
943	10178	19329	0.75	2.0E-21	AB007857.2	NT	QV3-HT0458-170200-090-g12 HT0458 Homo sapiens cDNA
943	10178	19330	0.75	2.0E-21	AB007857.2	NT	Homo sapiens mRNA for KIAA0397 protein, partial cds
1222	10440		2.48	2.0E-21	BE064410.1	EST_HUMAN	Homo sapiens mRNA for KIAA0397 protein, partial cds
2802	11788	21006	2.87	2.0E-21	Q28983	SWISSPROT	RC4-BT0311-141189-011-h08 BT0311 Homo sapiens cDNA
2802	11788	21007	2.87	2.0E-21	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
4888	14076		0.95	2.0E-21	AW151873.1	EST_HUMAN	ZONADHESIN PRECURSOR
6583	15779	25239	2.42	2.0E-21	BE141785.1	EST_HUMAN	x467a10.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2823148 3' similar to contains MER10.12
6728	15821	25380	4.85	2.0E-21	AU138779.1	EST_HUMAN	QV0-HT0103-091189-050-g11 HT0103 Homo sapiens cDNA
7826	16827		2.09	2.0E-21	BE350127.1	EST_HUMAN	AU138779 PLACE1 Homo sapiens cDNA clone PLACE1005052 5'
7866	17056	26576	2.39	2.0E-21	BE973828.1	EST_HUMAN	h08g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3148258 3' similar to contains MER28.b3
7866	17056	26577	2.39	2.0E-21	BE973828.1	EST_HUMAN	MER28 repetitive element;
8708	17689		9.43	2.0E-21	AF176815.1	NT	601680636F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3951008 5'
1262	10477	19639	1.36	1.0E-21	AA557657.1	EST_HUMAN	601680636F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3951008 5'
1406	10619		2.37	1.0E-21	AF001264.1	EST_HUMAN	601680636F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3951008 5'
5889	15087		2.87	1.0E-21	AL079752.1	EST_HUMAN	Homo sapiens putative 8-hydroxyguanine DNA glycosylase gene, complete cds
6162	15345	24782	4.61	1.0E-21	AI223104.1	EST_HUMAN	h48c04.s1 NCI_CGAP_P14 Homo sapiens cDNA clone IMAGE:1043718 similar to contains MER29.b2
9107	17927		1.29	1.0E-21	AF046133.1	NT	MER29 repetitive element;
9281	18042	23826	2.96	1.0E-21	11435947	NT	ar68d12.x1 Barabead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2152343 3'
							DKFZp4340830 r1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp4340830 5'
							qg47605.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1838336 3' similar to gb:MB4241 QM
							PROTEIN (HUMAN);
							Homo sapiens chromosome Xp22 410-8
							Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4404	13604	22704	6.07	9.0E-22	A1702438.1	EST_HUMAN	t294a03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2286204 3' similar to TR:Q15408 Q15408
7372	16588	26077	5.14	9.0E-22	AV761874.1	EST_HUMAN	NEUTRAL PROTEASE LARGE SUBUNIT ;
8198	17330	26872	3.42	9.0E-22	AU140358.1	EST_HUMAN	AV761874 MDS Homo sapiens cDNA clone MDSCG05 5'
856	10189		3.77	8.0E-22	BE144748.1	EST_HUMAN	AU140358 PLACE2 Homo sapiens cDNA clone PLACE2000394 5'
671	8916	19043	7.04	7.0E-22	AL163248.2	NT	CMO-HT0179-281099-078-h06 HT0179 Homo sapiens cDNA
4288	13471	22584	2.26	7.0E-22	Q61838	SWISSPROT	Homo sapiens chromosome 21 segment HS21C046
5063	14243	23330	1	7.0E-22	AB008681.1	NT	ALPHA-2-MACROGLOBULIN PRECURSOR (ALPHA2M)
6728	16824	26363	5.03	7.0E-22	M78590.1	EST_HUMAN	Homo sapiens gene for activin receptor type IIB, complete cds
6863	16141	25810	3.07	7.0E-22	AF008680.1	NT	EST00738 Fetal brain, Stratagene (cat#836208) Homo sapiens cDNA clone HFBGF07
6539	15735		2.7	6.0E-22	AW029123.1	EST_HUMAN	Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region
5884	15101	24512	3.17	5.0E-22	AL163303.2	NT	wx05g07.x1 NCI_CGAP_Ges4 Homo sapiens cDNA clone IMAGE:2542812 3'
7173	16350	25828	5.76	5.0E-22	U60822.1	NT	Homo sapiens chromosome 21 segment HS21C103
8942	17820		2.41	5.0E-22	BF476511.1	EST_HUMAN	Human dystrophin (DMD) gene, exons 7, 8 and 9, and partial cds
3615	12838		0.97	4.0E-22	AJ271735.1	NT	naa27b08.x1 NCI_CGAP_P28 Homo sapiens cDNA clone IMAGE:3255888 3' similar to contains Alu repetitive element
7310	16528	26019	2.62	4.0E-22	BF216030.1	EST_HUMAN	Homo sapiens Xq pseudautosomal region; segment 1/2
8113	17831		1.88	4.0E-22	AL163209.2	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
986	10169		1	3.0E-22	AI469879.1	EST_HUMAN	601882813F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095434 5'
2534	11722	20839	3.24	3.0E-22	AI859038.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C009
3653	12874		1.38	3.0E-22	D14718.1	NT	tm14h10.x1 NCI_CGAP_Cot14 Homo sapiens cDNA clone IMAGE:2158811 3' similar to gb:L18593 HIGH AFFINITY INTERLEUKIN-8 RECEPTOR B (HUMAN); contains L1.1 L1 repetitive element ;
4814	14003	23105	2.9	3.0E-22	AI080125.1	EST_HUMAN	wf68604.x1 NCI_CGAP_Bim25 Homo sapiens cDNA clone IMAGE:2429839 3' similar to SW:RL21_HUMAN
1823	11127		3.44	2.0E-22	N24942.1	EST_HUMAN	P48778 60S RIBOSOMAL PROTEIN L21. ;
2489	11679	20898	1.17	2.0E-22	P24916	SWISSPROT	Human chromosomal protein HMG1 related gene
3368	12825	21758	3.95	2.0E-22	8394043	NT	qb28cd07.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:1687680 3' similar to contains MER12.12 MER12 repetitive element ;
4211	13414	22508	1.48	2.0E-22	AW817784.1	EST_HUMAN	wk73d05.s1 Soares_melanocyte_2NbHM Homo sapiens cDNA clone IMAGE:267369 3'
5742	14961	24361	3.5	2.0E-22	BF082118.1	EST_HUMAN	IMMEDIATE EARLY GENE 13 PROTEIN PRECURSOR
6893	16171	25843	2.51	2.0E-22	AI276522.1	EST_HUMAN	Homo sapiens protein kinase, AMP-activated, gamma 3 non-catalytic subunit (PRKAG3), mRNA
8234	17363	26801	2.32	2.0E-22	AW418880.1	EST_HUMAN	PM1-ST0262-261198-001-d12 ST0262 Homo sapiens cDNA
8271	17819	23872	1.45	2.0E-22	AL163280.2	NT	RCO-TN0079-150900-025-h12 TN0079 Homo sapiens cDNA
							q17b108.x1 Soares_NbHMPu_S1 Homo sapiens cDNA clone IMAGE:1878288 3' similar to contains
							MER29.13 MER29 repetitive element ;
							ha24f04.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2874655 3'
							Homo sapiens chromosome 21 segment HS21C080

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal:	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1844	11062	20243	1.67	1.0E-22	AW86517.1	EST_HUMAN	PM4-SN0020-010400-008-h02 SN0020 Homo sapiens cDNA
2046	11734	20851	1.88	1.0E-22	U50871.1	NT	Human familial Alzheimer's disease (STM2) gene, complete cds
3388	12615	21748	1.63	1.0E-22	D14547.1	NT	Human DNA, SINE repetitive element
9182	17881		6.27	9.0E-23	AW80280.1	EST_HUMAN	IL2-JM0076-070400-061-F11 UM0076 Homo sapiens cDNA
3548	12768	21897	0.65	8.0E-23	AF198349.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
3282	12513		2.13	7.0E-23	AV647246.1	EST_HUMAN	AV647246 GLC Homo sapiens cDNA clone GLCAW007 3'
7609	16812	26308	4.68	7.0E-23	5031952	NT	Homo sapiens Ndc58 (D. melanogaster)-like protein (NOT68L) mRNA
3412	12838		1.55	6.0E-23	AF198333.1	NT	Rattus norvegicus RIM1B (Rim1B) mRNA, complete cds
4254	13457	22549	1.11	6.0E-23	AL163249.2	NT	Homo sapiens chromosome 21 segment HS210049
8412	17488	24008	2.85	6.0E-23	AF224689.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
8412	17488	24009	2.85	6.0E-23	AF224689.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
8617	17614	23887	4.22	6.0E-23	A1209130.1	EST_HUMAN	q659c03.x1 Scores: testis_NHT Homo sapiens cDNA clone IMAGE:1839460 3' similar to SW:MV10_MOUSE P23249 PROTEIN MOV-10. ;
5414	14842	23774	4.25	5.0E-23	U82671.2	NT	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), catractin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and LI>
5789	18084	24388	4.03	5.0E-23	AF179818.1	NT	Pongo pygmaeus olfactory receptor (PPY116) gene, partial cds
6287	18084	24388	3.15	5.0E-23	AF179818.1	NT	Pongo pygmaeus olfactory receptor (PPY116) gene, partial cds
6410	16007	25073	3.27	3.0E-23	AA130165.1	EST_HUMAN	z65g09.r1 Scores: pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:503088 5' similar to contains MER28.12 MER29 repetitive element ;
6839	16044	25508	4.41	3.0E-23	Z70684.1	NT	Human endogenous retroviral element HC2
6839	16044	25509	4.41	3.0E-23	Z70684.1	NT	Human endogenous retroviral element HC2
7172	16349		2.65	3.0E-23	AW807927.1	EST_HUMAN	RC3-NN0066-270400-011-h01 NN0066 Homo sapiens cDNA
672	9917	19048	6.01	2.0E-23	AJ288880.1	NT	Homo sapiens KIAA0851 gene (partial), X13 gene and LZTFL1 gene
1161	11844		2.89	2.0E-23	M5270.1	NT	Human matrix Gla protein (MGP) gene, complete cds
2748	11827	21141	1.06	2.0E-23	P22105	SWISSPROT	TENASCIN-X PRECURSOR (TN-X) (HEXABRACHION-LIKE)
2748	11827	21142	1.06	2.0E-23	P22105	SWISSPROT	TENASCIN-X PRECURSOR (TN-X) (HEXABRACHION-LIKE)
3350	12578		1.34	2.0E-23	A1201458.1	EST_HUMAN	q673f11.x1 NCI CGAP P128 Homo sapiens cDNA clone IMAGE:1943767 3' similar to TR:Q13537 Q13537
3697	12817		4.49	2.0E-23	BE165980.1	EST_HUMAN	MER3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA
3654	13169	22283	3.05	2.0E-23	H59931.1	EST_HUMAN	Y118a02.r1 Scores: fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:205418 5'
3654	13169	22284	3.05	2.0E-23	H59931.1	EST_HUMAN	Y118a02.r1 Scores: fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:205418 5'

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
							Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
8418	15815		8.05	2.0E-23	AF280107.1	NT	
8395	17474		4.45	2.0E-23	M32858.1	NT	
8951	17825		1.87	2.0E-23	AF008660.1	NT	Human alcohol dehydrogenase gamma subunit (ADH3) gene, exon 1
9079	18295		1.78	2.0E-23	AU133831.1	EST_HUMAN	Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region
4527	13723	22819	1.69	1.0E-23	AL163252.2	NT	AU133831 OVARI1 Homo sapiens cDNA clone OVARC1000948 5'
4777	13968		1.63	1.0E-23	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C052
5973	15187		2.6	1.0E-23	BE378471.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C010
6582	15778	25238	2.4	1.0E-23	AA448097.1	EST_HUMAN	601238455F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608653 5'
550	9809		1.82	9.0E-24	AA663213.1	EST_HUMAN	zw62c06.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:782688 5' similar to contains PTR5.12
4949	13943	22633	1.06	8.0E-24	P23289	SWISSPROT	PTR5 repetitive element;
4949	13943	22634	1.06	8.0E-24	P23289	SWISSPROT	ab75a08.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:852758 3' similar to
3853	13069		1.26	7.0E-24	AW837854.1	EST_HUMAN	TR:E19822 E19822 CA PROTEIN.;
7234	18455		2.37	7.0E-24	AW303317.1	EST_HUMAN	OLFACTORY RECEPTOR-LIKE PROTEIN I3
713	9865		2.33	6.0E-24	AB001421.1	NT	OLFACTORY RECEPTOR-LIKE PROTEIN I3
848	10085	18244	16.07	8.0E-24	AL163249.2	NT	QV0-DT0047-170200-122-408 DT0047 Homo sapiens cDNA
3947	13163	22278	8.91	6.0E-24	AJ228043.1	NT	kv17803.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813405 3' similar to contains Alu repetitive element; contains MER19.12 MER19 repetitive element;
5628	14852	24235	3.4	4.0E-24	AA594178.1	EST_HUMAN	Macaca fasciata mRNA for Testis-Specific Protein Y (TSPY), complete cds
7735	16932	26440	2.1	4.0E-24	BE544822.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C048
8794	17721	23982	2.81	4.0E-24	AB028018.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
9053	17924	23875	1.87	4.0E-24	11418318	NT	nm31105.s1 NCI_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1085528 3' similar to SW:POL_MLVRK
6901	18058	25528	2.35	3.0E-24	AL163252.2	NT	P31795 POL POLYPROTEIN;
8876	17773	23942	2.46	3.0E-24	BF127762.1	EST_HUMAN	601078812F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3464488 5'
2315	11509	20730	2.19	2.0E-24	AA167539.1	EST_HUMAN	Homo sapiens mRNA for KIAA1083 protein, partial cds
3781	12869		0.88	2.0E-24	AW886189.1	EST_HUMAN	Homo sapiens G-2 and S-phase expressed 1 (GTSE1), mRNA
8714	18339		9.69	2.0E-24	M28877.1	NT	Homo sapiens chromosome 21 segment HS21C052
1671	10884	20068	2.13	1.0E-24	7708340	NT	601810449F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4053398 5'
2633	11816		1.53	1.0E-24	AW1820194.1	EST_HUMAN	zp11109.r1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:808181 5'
2685	12222	21355	1.19	1.0E-24	D88423.1	NT	RC3-NN0068-090500-021-503 NN0068 Homo sapiens cDNA
							Human O family dispersed repeat element
							Homo sapiens CGI-127 protein (LOC51848), mRNA
							QV0-ST0284-100400-185-c10 ST0294 Homo sapiens cDNA
							Mus musculus mRNA for HGT keratin, partial cds

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Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4266	13459		2.16	1.0E-24	AF143313.1	NT	Homo sapiens PTEN (PTEN) gene, exon 2
6312	16493	24939	3.94	1.0E-24	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
6439	15636	25102	3.19	1.0E-24	AW601164.1	EST_HUMAN	CHMO-NIN1010-130300-281-407 NIN1010 Homo sapiens cDNA
9288	18048		1.24	1.0E-24	BE677411.1	EST_HUMAN	7d83103.x1 Lupsaki_dorsal_root_ganglion Homo sapiens cDNA clone IMAGE:3278605 3' similar to contains MER10.13 MER10 repetitive element;
8194	17328	26868	1.83	9.0E-25	7708707	NT	Homo sapiens putative secreted protein (SIG11), mRNA
5020	14207	23292	3.45	7.0E-25	AA483944.1	EST_HUMAN	ne92e10.s1 NCI_CGAP_Kid1 Homo sapiens cDNA clone IMAGE:911754 similar to contains MER1.b2 MER1 repetitive element;
6535	15731	25195	4.4	7.0E-25	AA488648.1	EST_HUMAN	ne08a09.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:880408 3' similar to contains THR.b2 THR repetitive element;
8196	17327	26869	10.9	7.0E-25	AA583540.1	EST_HUMAN	nf25h06.s1 NCI_CGAP_P11 Homo sapiens cDNA clone IMAGE:914843 similar to SW.R14A_YEAST P36105 PROBABLE 60S RIBOSOMAL PROTEIN L14EA.;
6085	14531		4.79	8.0E-25	W87623.1	EST_HUMAN	zh65h07.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:418989 5'
6394	16584	25021	10.69	6.0E-25	7305360	NT	Mus musculus obagelin (Obag), mRNA
7893	17053	28574	4.51	5.0E-25	AW979107.1	EST_HUMAN	EST391217 MAGE resequences, MAGP Homo sapiens cDNA
1448	10661	19838	3.01	4.0E-25	T88107.1	EST_HUMAN	yes5h04.r1 Soares_fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:121763 5'
3380	12807		2.84	4.0E-25	AW887871.1	EST_HUMAN	PM3-OT0093-280200-001-g07 OT0093 Homo sapiens cDNA
4307	13508		3.15	4.0E-25	BE170957.1	EST_HUMAN	QV3-HT0543-140400-149-e11 HT0543 Homo sapiens cDNA
3292	12523	21654	3.43	3.0E-25	8923321	NT	Homo sapiens hypothetical protein FLJ20344 (FLJ20344), mRNA
3292	12623	21656	3.43	3.0E-25	8923321	NT	Homo sapiens hypothetical protein FLJ20344 (FLJ20344), mRNA
4916	14104	23197	0.71	3.0E-25	P28822	SWISSPROT	KALLISTATIN PRECURSOR (KALLIKREIN INHIBITOR) (PROTEASE INHIBITOR 4)
5255	14428	23504	0.97	3.0E-25	H52187.1	EST_HUMAN	yr60b11.r1 Soares_fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:208661 5' similar to contains MER8 repetitive element;
6577	15773	25234	4.44	3.0E-25	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
7601	16804	26289	2.11	3.0E-25	AA579013.1	EST_HUMAN	nf30h10.s1 NCI_CGAP_P11 Homo sapiens cDNA clone IMAGE:915331 similar to contains L1.11 L1 repetitive element;
1355	10570	19735	3.68	2.0E-25	5032158	NT	Homo sapiens transducin (beta)-like 1 (TBL1) mRNA
2274	11488	20690	8.59	2.0E-25	BE88018.1	EST_HUMAN	601311330F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913087 5'
2784	11688	20914	6.4	2.0E-25	P17008	SWISSPROT	40S RIBOSOMAL PROTEIN S16
4172	13376	22475	1.92	2.0E-25	P17008	SWISSPROT	40S RIBOSOMAL PROTEIN S16
4172	13378	22478	1.92	2.0E-25	P17008	SWISSPROT	40S RIBOSOMAL PROTEIN S16
7006	16184	25656	3.35	2.0E-25	AL449573.1	EST_HUMAN	AL449573 Homo sapiens Testis (Starvides GS) Homo sapiens cDNA
368	9635	18788	1.02	1.0E-25	AL040226.1	EST_HUMAN	DKFZp434f0313_r1 434 (synonym: h063) Homo sapiens cDNA clone DKFZp434f0313 5'
1255	10471		3.27	1.0E-25	9635487	NT	Human endogenous retrovirus, complete genome

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2388	11591	20809	2.1	1.0E-25	Q06055	SWISSPROT	ATP SYNTHASE LIPID-BINDING PROTEIN P2 PRECURSOR (ATPASE PROTEIN 9) (SUBUNIT C)
4875	14083	23158	3.1	1.0E-25	BE182737.1	EST_HUMAN	PM1-HT0454-080100-002-H09 HT0454 Homo sapiens cDNA
5996	18070	24709	2.88	1.0E-25	AA582690.1	EST_HUMAN	nn54h11.s1 NC1 CGAP_K048 Homo sapiens cDNA clone IMAGE:1087749 3'
6428	15628	25091	5.51	1.0E-25	AA708078.1	EST_HUMAN	z88g04.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:384822 3' similar to contains PTR5.13 PTR5 repetitive element.
7541	18748	26240	3.92	1.0E-26	U63163.1	NT	Homo sapiens IMAGE-B2 (IMAGE-B2), IMAGE-B3 (IMAGE-B3), IMAGE-B4 (IMAGE-B4), and IMAGE-B1 (IMAGE-B1) genes, complete cds
8408	17484	26597	1.54	1.0E-25	D14547.1	NT	Human DNA, SINE repetitive element
8409	17484	26598	1.54	1.0E-25	D14547.1	NT	Human DNA, SINE repetitive element
8234	18008		1.31	1.0E-26	X51766.1	NT	Human lambda-immunoglobulin constant region complex (germline)
2445	11638	20857	1.4	9.0E-28	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
8272	18107		2.48	9.0E-28	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
6532	14758		1.92	8.0E-28	D14547.1	NT	Human DNA, SINE repetitive element
1556	10770	18942	2.5	7.0E-26	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
3958	13173	22288	1.42	7.0E-28	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
4141	13347	22448	2.19	7.0E-28	AW340163.1	EST_HUMAN	hd02e12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2808388 3'
8172	17304		9.82	7.0E-28	AA115895.1	EST_HUMAN	zn30d08.r1 Stratagene neuroepithelium NT2RAM1 937234 Homo sapiens cDNA clone IMAGE:548943 5' similar to gb:M14338 VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN);
8999	17859		1.79	7.0E-28	AW954559.1	EST_HUMAN	EST386628 IMAGE resequences, MAGC Homo sapiens cDNA
2192	11389	20612	2.57	6.0E-28	AF028308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and tyrosinogen gene families
3320	12549	21883	1.57	6.0E-28	AA208131.1	EST_HUMAN	zq52h04.r1 Stratagene neuroepithelium (8837231) Homo sapiens cDNA clone IMAGE:845271 5'
8180	17312	20854	6.07	6.0E-28	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1185	10408	18560	3.11	5.0E-28	AI708235.1	EST_HUMAN	as38h08.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2319519 3' similar to WP:F49C12.11 CE03371
1185	10406	18561	3.11	5.0E-28	AI708235.1	EST_HUMAN	as38h08.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2319519 3' similar to WP:F49C12.11 CE03371
6883	16074		3.97	4.0E-28	7657870	NT	Homo sapiens upstream binding transcription factor, RNA polymerase I (UBTF), mRNA
7253	16473	26865	4.16	4.0E-28	BE268187.1	EST_HUMAN	601191345F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535210 5'
7889	17059	26580	1.65	4.0E-28	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
1730	10842	20124	1.37	3.0E-28	D14547.1	NT	Human DNA, SINE repetitive element
1972	11178	20382	1.31	3.0E-28	AL045855.2	EST_HUMAN	DKFZp434088_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434088 5'

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Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2000	11203		3.1	3.0E-26	AA115895.1	EST_HUMAN	zn30008.r1 Stratagene neurophilum NT2RAM1 837234 Homo sapiens cDNA clone IMAGE:548943 5' similar to gb:M14338 VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN);
3760	12879	22094	1.44	3.0E-26	AA152464.1	EST_HUMAN	zn3010.r1 Stratagene colon (#837204) Homo sapiens cDNA clone IMAGE:588427 5' similar to TR:G885374 G885374 THYROID RECEPTOR INTERACTOR;
3760	12879	22095	1.44	3.0E-26	AA152464.1	EST_HUMAN	zn3010.r1 Stratagene colon (#837204) Homo sapiens cDNA clone IMAGE:588427 5' similar to TR:G885374 G885374 THYROID RECEPTOR INTERACTOR;
6048	15218	24638	9.41	3.0E-26	BF245458.1	EST_HUMAN	601884983F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4083278 5'
7313	16531		1.99	3.0E-26	AF036405.1	NT	Homo sapiens MLL (MLL) gene, exons 1-3, and partial cds
8102	17238	26772	2.54	3.0E-26	AW875651.1	EST_HUMAN	QV2-PT0012-040400-124-e05 PT0012 Homo sapiens cDNA
8102	17238	26773	2.54	3.0E-26	AW875651.1	EST_HUMAN	QV2-PT0012-040400-124-e05 PT0012 Homo sapiens cDNA
8128	17283	26807	10.41	3.0E-26	AA583173.1	EST_HUMAN	nn37d05.s1 NCI_CGAP_G05 Homo sapiens cDNA clone IMAGE:1086057 3' similar to contains OFR.t1 OFR repetitive element;
8183	17674		1.58	3.0E-26	AW073434.1	EST_HUMAN	xa57b09.x1 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2570873 3' similar to contains MER30.t1 MER30 repetitive element;
888	9831	18082	8.9	2.0E-26	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21O082
1834	11042		3.51	2.0E-26	AL038099.2	EST_HUMAN	DKFZp568L171_s1 568 (synonym: hfrk2) Homo sapiens cDNA clone DKFZp568L171 3'
3187	12432	21568	4.94	2.0E-26	X86894.1	NT	Musculus mRNA for astrocytic phosphoprotein, PEA-15
7338	16554		3.33	2.0E-26	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
7771	18888	26479	4.24	2.0E-26	AB01412.1	EST_HUMAN	tc89a01.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2185416 3' similar to contains Alu repetitive element; contains element MER20 MER20 repetitive element;
7858	17085		2.02	2.0E-26	AF055066.1	NT	Homo sapiens MHC class 1 region
8622	17663		2.84	2.0E-26	AB037859.1	NT	Homo sapiens mRNA for KIAA1438 protein, partial cds
8733	18284	23683	1.44	2.0E-26	11435947	NT	Homo sapiens chromosome 12 open reading frame 3 (G12ORF3), mRNA
134	9417	18551	11.48	1.0E-26	BE170371.1	EST_HUMAN	QV4-HT0538-020300-123-e02 HT0538 Homo sapiens cDNA
2014	11216	20425	1.53	1.0E-26	AL038363.2	EST_HUMAN	DKFZp434H1910_r1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434H1910 5'
2529	11717	20634	1.71	1.0E-26	BE814985.1	EST_HUMAN	MR2-BN0114-240500-030-g07 BN0114 Homo sapiens cDNA
2647	11830		22.1	1.0E-26	AF261085.1	NT	Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GADPH) mRNA, complete cds
6014	15284		2.88	1.0E-26	BE165980.1	EST_HUMAN	MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA
7469	16877		3.11	1.0E-26	AL038487.1	EST_HUMAN	DKFZp568C2148_r1 568 (synonym: hfrk2) Homo sapiens cDNA clone DKFZp568C2148 5'
8780	18357		2.07	1.0E-26	H55093.1	EST_HUMAN	CHR220032 Chromosome 22, exon Homo sapiens cDNA clone C22_45 5'
8855	18107		3.98	9.0E-27	U93163.1	NT	Homo sapiens IMAGE-B2 (IMAGE-B2), IMAGE-B3 (IMAGE-B3), IMAGE-B4 (IMAGE-B4), and IMAGE-B1 (IMAGE-B1) genes, complete cds
8275	17398		5.28	9.0E-27	BF445556.1	EST_HUMAN	naa03c07.x1 NCI_CGAP_Pt28 Homo sapiens cDNA clone IMAGE:3253844 3' similar to contains OFR.t1 OFR repetitive element;

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10	9308	18408	2.21	8.0E-27	A1831462.1	EST_HUMAN	wj48c04.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2408150 3' similar to contains THR.b2
584	9814		5.13	8.0E-27	AL163227.2	NT	TH-R repetitive element;
1420	10633	19801	58.1	8.0E-27	AW162737.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C027
1420	10633	19802	58.1	8.0E-27	AW162737.1	EST_HUMAN	au87h08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783285 3' similar to gb:K00558
2133	11331	20551	1.68	8.0E-27	AW684778.1	EST_HUMAN	TUBULIN ALPHA-1 CHAIN (HUMAN);
3148	12383	21518	3.14	8.0E-27	P12238	SWISSPROT	au87h08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783285 3' similar to gb:K00558
3327	12558	21693	0.88	8.0E-27	AF181897.1	NT	TUBULIN ALPHA-1 CHAIN (HUMAN);
6077	14523		8.24	8.0E-27	BE928560.1	EST_HUMAN	PM2-SN0018-220300-002-407 SN0018 Homo sapiens cDNA
6104	15108	24616	2.83	8.0E-27	N84970.1	EST_HUMAN	ADP-ATP CARRIER PROTEIN, LIVER ISOFORM T2 (ADP/ATP TRANSLOCASE 3) (ADENINE
690	9833		1.34	7.0E-27	Z70894.1	NT	NUCLEOTIDE TRANSLOCATOR 3) (ANT 3)
5122	14301		2.35	7.0E-27	AW628172.1	EST_HUMAN	Homo sapiens WRN (WRN) gene, complete cds
7335	16551		4.9	7.0E-27	AJ271735.1	NT	MR4-BT0398-250800-204-006 BT0398 Homo sapiens cDNA
6926	17809		1.82	7.0E-27	AV723365.1	EST_HUMAN	J1751F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J1751 5' similar to
7314	19532	28021	25.43	6.0E-27	M26897.1	NT	REPETITIVE ELEMENT L1
7145	16322	25803	3.44	5.0E-27	BF688814.1	EST_HUMAN	Human endogenous retroviral element HC2
7145	16322	25804	3.44	5.0E-27	BF688814.1	EST_HUMAN	h51h12.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2875879 3' similar to TR:O76040
8130	17284	26808	2.76	4.0E-27	X89211.1	NT	O76040 ORF2: FUNCTION UNKNOWN.;
2008	11211	20421	7.24	3.0E-27	X60958.1	NT	Homo sapiens Xq pseudocentromeric region; segment 122
4257	13480	22552	1.33	3.0E-27	BE071924.1	EST_HUMAN	AV723365 HTB Homo sapiens cDNA clone HTBAHE02 5'
5362	14592	23698	6.3	3.0E-27	AA077705.1	EST_HUMAN	Human nuclear protein (B23) mRNA, complete cds
6956	16108	25574	3.1	3.0E-27	BF035327.1	EST_HUMAN	602121491F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4278527 5'
8287	18045		1.79	3.0E-27	AW502868.1	EST_HUMAN	602121491F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4278527 5'
43	9339	18446	20.19	2.0E-27	AF054187.1	NT	H1 sapiens DNA for endogenous retroviral like element
1890	11067		35.81	2.0E-27	AA565345.1	EST_HUMAN	R.nattus RYA3 mRNA for a potential ligand-binding protein
3073	12309		12.63	2.0E-27	AW628172.1	EST_HUMAN	PMO-BT0527-090100-001-d11 BT0527 Homo sapiens cDNA
							7B44C08 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B44C08
							601458331F1 NIH_MGC_86 Homo sapiens cDNA clone IMAGE:3862088 5'
							UI-HF-BNO-alk-q-12-Q-UI-1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077879 5'
							Homo sapiens alpha NAC mRNA, complete cds
							hk01b10.s1 NCI_CGAP_P111 Homo sapiens cDNA clone IMAGE:1000899 similar to gb:M17888 80S
							ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN);
							h51h12.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2875879 3' similar to TR:O76040
							O76040 ORF2: FUNCTION UNKNOWN.;

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3180	12425	21558	1.36	2.0E-27	AF111167.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
3180	12425	21559	1.36	2.0E-27	AF111167.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
6844	16033		2.26	2.0E-27	AA551927.1	EST_HUMAN	nt08h05.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943737 similar to contains L1.13 L1 repetitive element;
7528	16733	26223	3.41	2.0E-27	AU121685.1	EST_HUMAN	AU121685 MAMMA1 Homo sapiens cDNA clone MAMMA1000748 5'
8021	11067		18.89	2.0E-27	AA565345.1	EST_HUMAN	nk01b10.s1 NCI_CGAP_P11 Homo sapiens cDNA clone IMAGE:1000699 similar to gb.M17888 60S
442	8698		2.08	1.0E-27	AL163248.2	NT	ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN); Homo sapiens chromosome 21 segment HS21C048
1004	10235	19388	1.34	1.0E-27	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
4057	13287		1.07	1.0E-27	BE360127.1	EST_HUMAN	h09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3148256 3' similar to contains MER28.b3 MER29 repetitive element;
5800	15117	24529	5.8	1.0E-27	8005855	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
6026	15234	24656	1.89	1.0E-27	F30158.1	EST_HUMAN	HSPD20481 HM3 Homo sapiens cDNA clone s4000085G10
6026	16234	24657	1.89	1.0E-27	F30158.1	EST_HUMAN	HSPD20481 HM3 Homo sapiens cDNA clone s4000085G10
6760	16955		2.91	1.0E-27	BE079760.1	EST_HUMAN	RC8-BT0827-140200-011-E08 BT0827 Homo sapiens cDNA
8959	16177	25848	3.53	1.0E-27	D87449.1	NT	Human mRNA for KIAA0280 gene, partial cds
8193	17328	26870	3.61	1.0E-27	AF111093.1	NT	Bos taurus letraphlin 3 splice variant bibah mRNA, complete cds
139	9420		1.89	9.0E-28	BE348398.1	EST_HUMAN	hwi7c11.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3183188 3' similar to TR:Q07314 Q07314
316	9587	18718	2.2	9.0E-28	AU126280.1	EST_HUMAN	SECRETED NEUREXIN III-ALPHA-C PRECURSOR, [3] TR:Q07280 TR:Q07313;
8355	17448		6.41	9.0E-28	BF377868.1	EST_HUMAN	CM2-TN0140-070900-372-g01 TN0140 Homo sapiens cDNA
8899	18204		2.25	8.0E-28	AW157571.1	EST_HUMAN	au83h08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782811 3' similar to TR:O60302 O60302 KIAA0555 PROTEIN, contains element MER22 repetitive element;
1188	10410	19584	20.71	7.0E-28	AU142750.1	EST_HUMAN	AU142750 Y79AA1 Homo sapiens cDNA clone Y79AA1000824 5'
7742	16838	26447	10.67	7.0E-28	11417868	NT	Homo sapiens gamma-glutamyltransferase-like activity 1 (GGTLA1), mRNA
8314	17418		2.77	7.0E-28	AV735348.1	EST_HUMAN	AV735348 CB Homo sapiens cDNA clone CBFAK12 5'
8971	17841		3.8	8.0E-28	AA504562.1	EST_HUMAN	aa80e03.r1 NCI_CGAP_GC81 Homo sapiens cDNA clone IMAGE:825340 5' similar to contains Alu repetitive element/contains element PTR5 repetitive element;
323	9584		2.63	5.0E-28	AI921003.1	EST_HUMAN	wc18c07.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2455892 3' similar to contains THR.b1 THR repetitive element;
3895	13189	22307	1.47	5.0E-28	R78762.1	EST_HUMAN	y88f10.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:148443 5'

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Table 4
Single Exon Probes Expressed In HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2588	11774	20894	2.43	4.0E-28	AW195068.1	EST_HUMAN	xn33c09.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2895604 3' similar to SW:GG95_HUMAN
2833	12171	21304	1.12	4.0E-28	4505316	NT	Q08379 GOLGIN-85 ;
3072	12308	21430	4.2	4.0E-28	BE409100.1	EST_HUMAN	Homo sapiens myosin phosphatase, target subunit 1 (MYPT1), mRNA
5271	14444	23515	12.18	4.0E-28	AF218927.1	NT	801300703F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3835305 5'
6222	15403	24844	2.04	4.0E-28	AI198941.1	EST_HUMAN	Homo sapiens diacylglycerol kinase beta (DGK1) gene, exon 23
7441	16849		4.32	4.0E-28	AF028308.1	NT	qf68f10.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1755019 3' similar to gb:M19503 LINE-1
7576	16781		24.75	4.0E-28	AB038241.1	NT	REVERSE TRANSCRIPTASE HOMOLOG (HUMAN);
7594	15403	24844	3.74	4.0E-28	AI198941.1	EST_HUMAN	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families
1280	10505		1.95	3.0E-28	AF155382.1	NT	Felis catus GAPDH mRNA for glyceraldehyde-3-phosphate dehydrogenase, complete cds
6727	15922	25381	2.47	3.0E-28	BF354030.1	EST_HUMAN	qf68f10.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1755019 3' similar to gb:M19503 LINE-1
7609	16714	26202	1.85	3.0E-28	U53588.1	NT	REVERSE TRANSCRIPTASE HOMOLOG (HUMAN);
8778	17706		2.07	3.0E-28	AI831991.1	EST_HUMAN	Homo sapiens metalloproteinase-like, disintegrin-like, cysteine-rich protein 2 epsilon (ADAM22) mRNA, complete cds
8970	17840	23912	1.53	3.0E-28	11430460	NT	MR3-HT0713-280500-013-008 HT0713 Homo sapiens cDNA
8970	17840	23913	1.53	3.0E-28	11430460	NT	Homo sapiens MHC class 1 region
88	9381	18511	7.51	2.0E-28	BE082187.1	EST_HUMAN	wj98f07.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2410885 3' similar to contains Alu repetitive element; contains element HGR repetitive element;
1173	10394	19546	10.56	2.0E-28	Y11107.3	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
2438	11630	20851	1.92	2.0E-28	AI348034.1	EST_HUMAN	RC1-BT0254-220300-019-c05 BT0254 Homo sapiens cDNA
5802	15019		6.05	2.0E-28	BF212805.1	EST_HUMAN	Homo sapiens ITGB4 gene for Integrin beta 4 subunit, exons 3-41
6953	16131		4.38	2.0E-28	AW972305.1	EST_HUMAN	qp35b06.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1910483 3' similar to contains L1.b2 L1 repetitive element;
8137	17270	26815	2.58	2.0E-28	AF224689.1	NT	601814190F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4048751 5'
8758	17687		1.37	2.0E-28	H08378.1	EST_HUMAN	601814190F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4048751 5'
1472	10695	19860	2.38	1.0E-28	D38044.1	NT	EST_HUMAN
2188	11383	20807	5.07	1.0E-28	BF333238.1	EST_HUMAN	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
4568	13780		2.28	1.0E-28	U09410.1	NT	y79c09.r1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:44300 5'
8414	15611		6.26	1.0E-28	11428885	NT	Human gene for Ah-receptor, exon 7-9
8469	15888		3.16	1.0E-28	8922783	NT	QV1-BT0821-120900-360-b03 BT0821 Homo sapiens cDNA
							Human zinc finger protein ZNF131 mRNA, partial cds
							Homo sapiens similar to ribosomal protein L12 (H. sapiens) (LOC83081), mRNA
							Homo sapiens hypothetical protein FLJ10968 (FLJ10968), mRNA

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Table 4
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6848	16037	25501	4.97	1.0E-28	AA308744.1	EST_HUMAN	EST179615 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to similar to retroviral LTR
7030	16207	25984	3.28	1.0E-28	4758431	NT	Homo sapiens gamma-glutamyltransferase-like activity 1 (GGT1A1), mRNA
7030	16207	25985	3.28	1.0E-28	4758431	NT	Homo sapiens gamma-glutamyltransferase-like activity 1 (GGT1A1), mRNA
8319	17422		3.88	1.0E-28	AA054182.1	EST_HUMAN	zf51c01.1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:380448 5'
9106	18091		1.83	1.0E-28	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
9211	18313	23563	3.18	9.0E-29	AW663987.1	EST_HUMAN	h19g06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2878288 3'
8873	17770		3.8	8.0E-29	Q00130	SWISSPROT	HYPOTHETICAL GENE 50 PROTEIN
1582	10785	18972	1.61	7.0E-28	AW869447.1	EST_HUMAN	EST378521 MAGE resequences, MAGI Homo sapiens cDNA
9284	18030		6.86	7.0E-29	AJ132352.1	NT	Rattus norvegicus mRNA for 45 kDa secretory protein, partial
602	9849	18988	15.71	6.0E-29	A1638748.1	EST_HUMAN	wp69601.x1 NCI_CGAP_Bim25 Homo sapiens cDNA clone IMAGE:2468885 3' similar to TR:O15475
8628	17621		5.29	6.0E-29	BE940436.1	EST_HUMAN	O15475 UNNAMED HERV-H PROTEIN ; contains LTR7 b1 LTR7 repetitive element ;
8719	17873		1.47	6.0E-29	BF668087.1	EST_HUMAN	RC3-UT0082-210800-021-c05 UT0082 Homo sapiens cDNA
6022	14209		1.78	6.0E-29	AL163203.2	NT	60218-092F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300079 5'
6680	15885		9.84	5.0E-29	AW887541.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C003
							RC3-OT0091-170300-011-c12 OT0091 Homo sapiens cDNA
3188	12433		2.82	4.0E-29	A1752387.1	EST_HUMAN	cn15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn15c02 random
5659	14882		7.39	4.0E-29	BE164830.1	EST_HUMAN	QV1-HT0471-280300-121-e05 HT0471 Homo sapiens cDNA
6698	15894	25355	5.52	4.0E-29	J04888.1	NT	Human 90 kD heat shock protein gene, complete cds
4408	13608	22708	1.67	3.0E-29	AB042297.1	NT	Homo sapiens PTS gene for 9-pyruvoylthiopyridine synthase, complete cds
4744	13635	23039	1.07	3.0E-29	BF393236.1	EST_HUMAN	QV1-BT0821-120900-360-b03 BT0821 Homo sapiens cDNA
6854	16042	25608	2.62	3.0E-29	AW303317.1	EST_HUMAN	xv17R03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813405 3' similar to contains Alu repetitive element; contains MER19.12 MER19 repetitive element ;
6828	16121		2.61	3.0E-29	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
7818	17011	26524	2.7	3.0E-29	AA403053.1	EST_HUMAN	z162b01.1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:726889 5' similar to TR:G1335789
8518	17550		1.58	3.0E-29	D63882.1	NT	G1335789 GAG-POL POLYPROTEIN ;
489	9751	18678	1.54	2.0E-29	AF084869.1	NT	Human HsLIM15 mRNA for HsLIM15, complete cds
489	9751	18679	1.54	2.0E-29	AF084869.1	NT	Homo sapiens envelope protein RIC-8 (env) gene, complete cds
							Homo sapiens envelope protein RIC-8 (env) gene, complete cds
1519	10733	19803	6.77	2.0E-29	A1963604.1	EST_HUMAN	wr65d10.x1 NCI_CGAP_UH1 Homo sapiens cDNA clone IMAGE:2492563 3' similar to TR:O15548 O15548
							HERV-E ENVELOPE GLYCOPROTEIN ;
1519	10733	19804	6.77	2.0E-29	A1963604.1	EST_HUMAN	wr65d10.x1 NCI_CGAP_UH1 Homo sapiens cDNA clone IMAGE:2492563 3' similar to TR:O15548 O15548
							HERV-E ENVELOPE GLYCOPROTEIN ;

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4284	13487	22558	1.91	2.0E-29	AL163288.2	NT	Homo sapiens chromosome 21 segment HS21C088
6914	16102	25568	4.35	2.0E-29	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
6914	16102	25569	4.35	2.0E-29	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
7147	16324	25808	4.53	2.0E-29	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
7147	16324	25807	4.53	2.0E-29	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
8012	17152		1.9	2.0E-29	11425108	NT	Homo sapiens chromosome 21 segment HS21C048
8047	17183		2.01	2.0E-29	AW880701.1	EST_HUMAN	Homo sapiens splicing factor similar to dnal (SPF31), mRNA
8284	17391		1.8	2.0E-29	AL163227.2	NT	QV0-OT0032-080300-155-d01 OT0032 Homo sapiens cDNA
6714	15909	25368	11.38	1.0E-29	AW883880.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C027
6820	15137	24548	3.11	9.0E-30	AA761215.1	EST_HUMAN	RC1-HN0003-220300-021-b04 HN0003 Homo sapiens cDNA n220c07 s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1288332 3' similar to contains MER4.b1 MER4 repetitive element;
8398	17475		4.04	9.0E-30	11422745	NT	Homo sapiens zinc/iron regulated transporter-like (ZIRT1), mRNA
6787	15014		9.51	8.0E-30	F08688.1	EST_HUMAN	HSC23F051 normalized infant brain cDNA Homo sapiens cDNA clone c-23105
6560	15746	25206	3.85	8.0E-30	AA363873.1	EST_HUMAN	EST97317 Thymus 1 Homo sapiens cDNA 5' end similar to EST containing O family repeat
1604	10717		1.52	7.0E-30	BE091133.1	EST_HUMAN	PM4-BT0724-150400-004-d11 BT0724 Homo sapiens cDNA
1743	10655	20138	1.39	6.0E-30	D25303.1	NT	Human mRNA for integrin alpha subunit, complete cds
3163	12388	21520	2.68	8.0E-30	BE008026.1	EST_HUMAN	QV0-BN0147-280400-214-f12 BN0147 Homo sapiens cDNA
9235	14488		2.32	6.0E-30	X61765.1	NT	Human lambda-immunoglobulin constant region complex (germline) repetitive element;
3888	13203	22311	40.02	5.0E-30	A1398892.1	EST_HUMAN	tg92p03.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2118276 3' similar to contains Alu
6285	18132		6.38	6.0E-30	U87831.1	NT	Human aconitase hydratase (ACO2) gene, exon 7
7484	16672		3.56	5.0E-30	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
7714	16913	28421	7.8	5.0E-30	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
7714	16913	28422	7.8	5.0E-30	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
2111	11310	20523	2.02	4.0E-30	AW837471.1	EST_HUMAN	QV3-DT0043-080200-080-c08 DT0043 Homo sapiens cDNA
2111	11310	20524	2.02	4.0E-30	AW837471.1	EST_HUMAN	QV3-DT0043-080200-080-c08 DT0043 Homo sapiens cDNA
6748	16941	26401	4.27	4.0E-30	AW812488.1	EST_HUMAN	CM1-ST0181-091189-035-08 ST0181 Homo sapiens cDNA qq83c05.x1 Scores_total (cdus_Nb2-IF8_gw Homo sapiens cDNA clone IMAGE:1638920 3' similar to contains MER28.b2 MER28 repetitive element;
1180	10382		1.64	3.0E-30	A1398551.1	EST_HUMAN	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 1-8
3740	12860	22075	0.64	3.0E-30	AF128883.1	NT	TRANSCRIPTION FACTOR AP-2
7759	16955	28463	2.59	3.0E-30	P34056	SWISSPROT	CM0-CT0307-310100-158-h03 CT0307 Homo sapiens cDNA
681	9924	18055	0.91	2.0E-30	AW857315.1	EST_HUMAN	HSC23F051 normalized infant brain cDNA Homo sapiens cDNA clone c-23105
1092	10316		2.41	2.0E-30	F08688.1	EST_HUMAN	
1473	10886	18881	4.84	2.0E-30	BE175877.1	EST_HUMAN	RCS-HT0582-110400-013-H08 HT0582 Homo sapiens cDNA

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Table 4
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2675	11857	21072	8.46	2.0E-30	BE765232.1	EST_HUMAN	IL2-NT0101-280700-116-E04 NT0101 Homo sapiens cDNA
2870	12108	21237	8.13	2.0E-30	AF114158.1	NT	Homo sapiens Y-linked zinc finger protein (ZFY) gene, complete cds
3771	12889	22105	1.85	2.0E-30	AW206581.1	EST_HUMAN	U1-H-B11-efo-c-12-Q-J1.s1 NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2722558 3'
4787	13976	23078	1.85	2.0E-30	BE288945.1	EST_HUMAN	801118860F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028438 5'
4787	13978	23080	1.85	2.0E-30	BE288945.1	EST_HUMAN	801118860F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028438 5'
6833	15829	25291	6.69	2.0E-30	C18839.1	EST_HUMAN	C18839 Human placenta cDNA (TF-ujwara) Homo sapiens cDNA clone GEN-570C01 5'
6885	15860	26318	2.21	2.0E-30	BE670817.1	EST_HUMAN	7a37c12.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284862 3' similar to SW-DHSA_HUMAN P31040 SUCCINATE DEHYDROGENASE [UBIQUINONE] FLAVOPROTEIN SUBUNIT PRECURSOR ;
6885	15860	26319	2.21	2.0E-30	BE670817.1	EST_HUMAN	7a37c12.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284862 3' similar to SW-DHSA_HUMAN P31040 SUCCINATE DEHYDROGENASE [UBIQUINONE] FLAVOPROTEIN SUBUNIT PRECURSOR ;
7072	16249	25722	2.78	2.0E-30	AW871588.1	EST_HUMAN	EST383857 MAGC resequences, MAGL Homo sapiens cDNA
7102	16279	25759	5.8	2.0E-30	AW470791.1	EST_HUMAN	ha33408.x1 NCL_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2875489 3' similar to contains THR.b3 THR repetitive element ;
291	8565	18638	18.27	1.0E-30	C18839.1	EST_HUMAN	C18839 Human placenta cDNA (TF-ujwara) Homo sapiens cDNA clone GEN-570C01 5'
544	9795	18819	3.42	1.0E-30	AW468887.1	EST_HUMAN	MER1.13 MER1 MER1 repetitive element ;
723	9865	18103	2.66	1.0E-30	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
2179	11376	20588	19.88	1.0E-30	AA694377.1	EST_HUMAN	ac77b08.s1 Stratiogene lung (#837210) Homo sapiens cDNA clone IMAGE:888589 3'
2425	11816	20838	2.33	1.0E-30	BF547728.1	EST_HUMAN	802022560F1 NCL_CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4157991 5'
2882	12200	21334	1.51	1.0E-30	5803091	NT	Homo sapiens methionine aminopeptidase; eIF-2-associated p87 (MNPEP), mRNA
3019	12255	21384	0.81	1.0E-30	AA315045.1	EST_HUMAN	EST188868 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end
6386	15566	25023	2.19	1.0E-30	BF183230.1	EST_HUMAN	80188832F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040694 5'
9037	18228		0.1	1.0E-30	H55593.1	EST_HUMAN	CHR220332 Chromosome 22 exon Homo sapiens cDNA clone C22_728 5'
3748	12888	22082	0.91	8.0E-31	TT3025.1	EST_HUMAN	yc65e08.r1 Stratiogene liver (#837224) Homo sapiens cDNA clone IMAGE:85570 5'
3748	12888	22083	0.91	8.0E-31	TT3025.1	EST_HUMAN	yc65e08.r1 Stratiogene liver (#837224) Homo sapiens cDNA clone IMAGE:85570 5'
1084	10308	19461	2.7	8.0E-31	8923389	NT	Homo sapiens hypothetical protein FLJ20420 (FLJ20420), mRNA
2376	11568		13.17	8.0E-31	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C008
718	8960		1.45	7.0E-31	AA372637.1	EST_HUMAN	EST84555 Colon adenocarcinoma IV Homo sapiens cDNA 5' end
2628	11811	21028	2.27	7.0E-31	BE326517.1	EST_HUMAN	hw05a11.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182012 3'
2628	11811	21029	2.27	7.0E-31	BE326517.1	EST_HUMAN	hw05a11.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182012 3'
8871	17769	23840	2.52	7.0E-31	X31755.1	NT	Human lambda-immunoglobulin constant region complex (germline)

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Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3658	12870		2.63	6.0E-31	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
6508	15705		6.07	6.0E-31	AF055086.1	NT	Homo sapiens MHC class 1 region
7324	16540	26029	2.02	6.0E-31	AU119105.1	EST_HUMAN	AU119105 HEMBA1 Homo sapiens cDNA clone HEMBA1005050 5'
8455	17512	24020	1.93	6.0E-31	AW372868.1	EST_HUMAN	RCS-BT0377-081288-031-D12 BT0377 Homo sapiens cDNA
8594	18152		2.61	6.0E-31	BE894488.1	EST_HUMAN	601433087F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918524 5'
197	9477	18609	1.74	5.0E-31	M60894.1	NT	Homo sapiens type I DNA topoisomerase gene, exon 8
197	9477	18810	1.74	5.0E-31	M60894.1	NT	Homo sapiens type I DNA topoisomerase gene, exon 8
6812	15808		9.55	5.0E-31	BF056540.1	EST_HUMAN	7408704.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:3443478 3' similar to TR:Q13537 Q13537 SIMILAR TO POGO ELEMENT; contains L1.1 L1 repetitive element;
803	9850		4.69	4.0E-31	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
1590	10803	19978	0.85	4.0E-31	Q10473	SWISSPROT	POLYPEPTIDE N-ACETYL GALACTOSAMINYL TRANSFERASE (PROTEIN-JDP ACETYL GALACTOSAMINYL TRANSFERASE) (UDP-GALNAc:POLYPEPTIDE, N- ACETYL GALACTOSAMINYL TRANSFERASE) (GALNAc-T1)
1787	10897		2.49	4.0E-31	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
2742	11821		1.88	4.0E-31	6730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
8834	17824		1.25	4.0E-31	AJ230125.1	NT	Homo sapiens GGT1 gene, exon 1
8019	17871		1.44	4.0E-31	AB008881.1	NT	Homo sapiens gene for activin receptor type IIB, complete cds
2555	11742	20680	5.53	3.0E-31	6005971	NT	Homo sapiens SEC83, endoplasmic reticulum translocan component (S. cerevisiae) like (SEC83L), mRNA
6228	16407	24849	7.95	3.0E-31	4828853	NT	Homo sapiens NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 8 (18kD, ASH1) (NDUFB8) mRNA
6512	15708		2.89	3.0E-31	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C008
6951	16120	25597	3.74	3.0E-31	D14523.1	NT	Horse mRNA for ferritin L-chain, complete cds
7228	16447	25937	2.86	3.0E-31	P11174	SWISSPROT	40S RIBOSOMAL PROTEIN S15 (RIG PROTEIN)
7712	16911		7.41	3.0E-31	BF036327.1	EST_HUMAN	601458531F1 NIH_MGC_86 Homo sapiens cDNA clone IMAGE:36d2085 5'
1883	11080	20281	1.04	2.0E-31	AW538171.1	EST_HUMAN	QV2-LT0051-280300-111-103 LT0051 Homo sapiens cDNA
2308	11502	20724	2.54	2.0E-31	AL118245.1	EST_HUMAN	DKFZp781G1513_r1 781 (synonym: hamy2) Homo sapiens cDNA clone DKFZp781G1513 5'
2404	11598	20816	4.8	2.0E-31	AA458824.1	EST_HUMAN	aa88f11.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:638413 3' similar to contains THR.12 THR repetitive element;
5542	14788	24132	2.77	2.0E-31	BE350127.1	EST_HUMAN	h08g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element;
6795	15980		2.34	2.0E-31	AA87764.1	EST_HUMAN	m08704.s1 NCI_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1161055 3' similar to TR:Q13537 Q13537 MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE.;

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6830	16024	25489	4.65	2.0E-31	7681535	NT	Homo sapiens B9 protein (B9), mRNA
7098	16275	25754	3	2.0E-31	BE408811.1	EST_HUMAN	601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5'
7098	16275	25755	3	2.0E-31	BE408811.1	EST_HUMAN	601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5'
8565	17585		2.14	2.0E-31	AF148512.1	NT	Homo sapiens hexokinase II gene, promoter region
8712	18380		2.48	2.0E-31	AI114527.1	EST_HUMAN	HA1110 Human fetal liver cDNA library Homo sapiens cDNA
16	9312	18415	7.1	1.0E-31	U83183.1	NT	Homo sapiens MAGE-B2 (MAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1 (MAGE-B1) genes, complete cds
1638	10852	20030	6.69	1.0E-31	O85371	SWISSPROT	OLFACTORY RECEPTOR 2C1
1638	10852	20031	6.69	1.0E-31	O85371	SWISSPROT	OLFACTORY RECEPTOR 2C1
1638	10852	20032	6.69	1.0E-31	O85371	SWISSPROT	OLFACTORY RECEPTOR 2C1
4637	13831	22918	1.87	1.0E-31	AL134376.1	EST_HUMAN	DKFZp547B235_1 547 (synonym: hfbt1) Homo sapiens cDNA clone DKFZp547B235 5'
4637	13831	22919	1.87	1.0E-31	AL134376.1	EST_HUMAN	DKFZp547B235_1 547 (synonym: hfbt1) Homo sapiens cDNA clone DKFZp547B235 5'
5322	14554	23624	3.51	1.0E-31	AW391678.1	EST_HUMAN	MR3-ST0220-161288-028-008_1 ST0220 Homo sapiens cDNA
5728	14944	24340	2.11	1.0E-31	AF048727.1	NT	Homo sapiens minisatellite cab1 repeat region
7490	16697	26182	2.54	1.0E-31	AI086434.1	EST_HUMAN	q121103 x1 NC1_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:1750709 3' similar to TR:Q18595 Q18595 FRATAXIN ;
8257	17384	28917	6.47	1.0E-31	AW303317.1	EST_HUMAN	xv1703.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813405 3' similar to contains Alu repetitive element; contains MER19.12 MER19 repetitive element ;
5950	15186	24578	2.53	8.0E-32	AV723978.1	EST_HUMAN	AV723978 HTB Homo sapiens cDNA clone HTBAA601 5'
2045	11246	20456	7.85	8.0E-32	AI056770.1	EST_HUMAN	ac15609.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1675384 3'
4878	14064	23159	0.96	7.0E-32	P52591	SWISSPROT	NUCLEAR ENVELOPE PORE MEMBRANE PROTEIN POM 121 (PORE MEMBRANE PROTEIN OF 121 KD) (P145)
8838	17683		3.22	7.0E-32	X17283.1	NT	Human chromosome 22 Immunoglobulin V(K) gene, part, with 5' breakpoint between orphon and neighbouring non-amplified region
1041	10287	19418	48.91	5.0E-32	AF118827.1	NT	Homo sapiens PRO1181 mRNA, complete cds
939	10172		2.6	4.0E-32	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C046
8338	15516	24962	3.11	4.0E-32	11432574	NT	Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA
6338	15516	24963	3.11	4.0E-32	11432574	NT	Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA
462	9715	18850	3.57	3.0E-32	Y17293.1	NT	Homo sapiens FLI-1 gene, partial
1454	10687	19841	10.88	3.0E-32	AV731500.1	EST_HUMAN	AV731500 HTF Homo sapiens cDNA clone HTFAK07 5'
6875	16086	25534	6.4	3.0E-32	AV758634.1	EST_HUMAN	AV758634 BM Homo sapiens cDNA clone BMFBFBH12 5'
6875	16086	25535	6.4	3.0E-32	AV758634.1	EST_HUMAN	AV758634 BM Homo sapiens cDNA clone BMFBFBH12 5'
7489	16706	26182	9.12	3.0E-32	AA77621.1	EST_HUMAN	z05a07.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:448500 3' similar to contains THR13 THR repetitive element ;

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Table 4
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8588	17587		5.38	3.0E-32	BE278086.1	EST_HUMAN	601156285F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3139701 5'
8950	14491	23579	3.58	3.0E-32	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (MLL T4) mRNA
8950	14491	23580	3.58	3.0E-32	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (MLL T4) mRNA
9112	17930		2.92	3.0E-32	BE278086.1	EST_HUMAN	601156285F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3139701 5'
5963	15081	24493	5.72	2.0E-32	Z38133.1	NT	H. sapiens mRNA for myosin
5963	15081	24494	5.72	2.0E-32	Z38133.1	NT	H. sapiens mRNA for myosin
9228	18008	23847	1.47	2.0E-32	AV738449.1	EST_HUMAN	AV738449 CB Homo sapiens cDNA clone CBFBIA08 5'
9228	18008	23848	1.47	2.0E-32	AV738449.1	EST_HUMAN	AV738449 CB Homo sapiens cDNA clone CBFBIA08 5'
2638	11819		1.51	1.0E-32	D84430.1	NT	Homo sapiens mRNA for phenylalanyl RNA synthetase, complete cds
3059	12295		1.32	1.0E-32	BE743299.1	EST_HUMAN	601573207F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3834433 5'
6106	15200	24818	6.28	1.0E-32	11439788	NT	Homo sapiens chromosome 11 open reading frame 8 (C11ORF8), mRNA
6653	15848	26307	7.33	1.0E-32	AA720574.1	EST_HUMAN	hw21g02.s1 NCI_CGAP: GC80 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR.13 THR repetitive element;
3456	12681		5.61	9.0E-33	BE327112.1	EST_HUMAN	hw07c05.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182216 3' similar to TR:O88539 O88539 WW DOMAIN BINDING PROTEIN 11;
5637	15054		3.19	9.0E-33	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
6712	15907	25368	2.29	9.0E-33	BF347229.1	EST_HUMAN	602021164F1 NCI_CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4156670 5'
7378	16594		7.28	9.0E-33	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
63	9359	18480	4.34	7.0E-33	5031738	NT	Homo sapiens short-chain alcohol dehydrogenase family member (HEP27) mRNA
63	9359	18481	4.34	7.0E-33	5031738	NT	Homo sapiens short-chain alcohol dehydrogenase family member (HEP27) mRNA
2127	11328	20544	2.68	7.0E-33	AI590115.1	EST_HUMAN	hw2b09.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2178809 3' similar to contains OFR.11 OFR repetitive element;
2611	11785		9	7.0E-33	AV730058.1	EST_HUMAN	AV730058 HTF Homo sapiens cDNA clone HTFAVE08 5'
3208	12442		18.28	7.0E-33	AW971307.1	EST_HUMAN	EST383398 MAGL Homo sapiens cDNA
4472	13070	22781	0.96	7.0E-33	AA157467.1	EST_HUMAN	z550601.1 Strabagene endothelial cell 637223 Homo sapiens cDNA clone IMAGE:590328 5'
7405	16817	26107	4.81	7.0E-33	BF347229.1	EST_HUMAN	602021164F1 NCI_CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4156670 5'
7800	16893	26508	2.26	7.0E-33	AW971568.1	EST_HUMAN	EST3833657 MAGL Homo sapiens cDNA
8545	17570	23691	5.15	7.0E-33	AA601418.1	EST_HUMAN	hw10h01.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100881 3' similar to contains L1.1 L1 repetitive element;
3717	12937		1.15	6.0E-33	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
6847	16942	26303	4.52	6.0E-33	JO4038.1	NT	Human glyceraldehyde-3-phosphate dehydrogenase (GAPDH) gene, complete cds

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8681	15876	25335	3.6	6.0E-33	11429188	NT	Homo sapiens similar to RAD23 (S. cerevisiae) homolog B (H. sapiens) (LOC83277), mRNA
1747	10859		1.81	5.0E-33	BF373515.1	EST_HUMAN	QV1-FT0169-100700-271-902 FT0169 Homo sapiens cDNA
1846	11054		1.22	5.0E-33	11141884	NT	Homo sapiens solute carrier family 5 (cholesterol transporter), member 7 (SLC5A7), mRNA
1863	11070	20260	4	5.0E-33	4507208	NT	Homo sapiens spermidine synthase (SRM) mRNA
1883	11070	20261	4	5.0E-33	4507208	NT	Homo sapiens spermidine synthase (SRM) mRNA
2237	11432		3.28	5.0E-33	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
4035	13245	22348	0.68	5.0E-33	AB014588.1	NT	Homo sapiens mRNA for KIAA0689 protein, partial cds
8343	17440		1.31	5.0E-33	11433063	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), mRNA
1136	10356		1.64	4.0E-33	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
2095	11285	20507	2.46	4.0E-33	4758897	NT	Homo sapiens RAB1, member RAS oncogene family (RAB1) mRNA
2384	11577		2.74	4.0E-33	AA626821.1	EST_HUMAN	ab51b11.1 Stratagene lung carcinoma 837218 Homo sapiens cDNA clone IMAGE:844317 5' similar to contains Alu repetitive element; contains MER28 b2 MER28 repetitive element;
2510	11688	20916	16.8	4.0E-33	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
4480	13878	22768	1.55	4.0E-33	AW293349.1	EST_HUMAN	U1-H-B12-ah1-c03-0-U1.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2727149 3'
5397	14826	23739	24.3	4.0E-33	AA053053.1	EST_HUMAN	z171e08.1 Stratagene colon (#637204) Homo sapiens cDNA clone IMAGE:510038 5' similar to gb:X12671_ma1 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1 (HUMAN);
1097	10321		6.43	3.0E-33	BE950127.1	EST_HUMAN	h109g01.x1 NCI_CGAP_K1d13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER28.b3 MER28 repetitive element;
1088	10321		3.04	3.0E-33	BE350127.1	EST_HUMAN	h109g01.x1 NCI_CGAP_K1d13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER28.b3 MER28 repetitive element;
2413	12016		2.64	3.0E-33	AV847851.1	EST_HUMAN	AV847851 GLC Homo sapiens cDNA clone GLC8CF09 3'
17	8313		0.77	2.0E-33	AI160188.1	EST_HUMAN	qb67g03.x1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:1705204 3' similar to contains OFR.11 OFR repetitive element;
104	9319		2.52	2.0E-33	AI160188.1	EST_HUMAN	qb67g03.x1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:1705204 3' similar to contains OFR.11 OFR repetitive element;
4411	13611		4.41	2.0E-33	BE158039.1	EST_HUMAN	MRO-HT0405-160300-202-408 HT0405 Homo sapiens cDNA
5008	14163	23282	25.82	2.0E-33	AA626883.1	EST_HUMAN	ab51g11.1 Stratagene lung carcinoma 837218 Homo sapiens cDNA clone IMAGE:844388 5' similar to gb:X00734_cds1 TUBULIN BETA-5 CHAIN (HUMAN);
5125	14304	23393	1.41	2.0E-33	11421332	NT	Homo sapiens hypothetical protein SIRP-b2 (SIRP-b2), mRNA
5125	14304	23394	1.41	2.0E-33	11421332	NT	Homo sapiens hypothetical protein SIRP-b2 (SIRP-b2), mRNA
5838	15055	24462	1.83	2.0E-33	AI277492.1	EST_HUMAN	qb6d01.x1 Soares_NhMPu_S1 Homo sapiens cDNA clone IMAGE:1890161 3'
8	8304		1.67	1.0E-33	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7867	17057	26578	2	1.0E-33	AW898818.1	EST_HUMAN	QV3-BN0047-230200-102-503 BN0047 Homo sapiens cDNA
8167	17286	26842	5.99	1.0E-33	U60822.1	NT	Human dystrophin (DMD) gene, exons 7, 8 and 9, and partial cds
8841	17750		2	1.0E-33	AI927191.1	EST_HUMAN	wo88c08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2482410 3'
9024	8304		5.11	1.0E-33	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
9059	17880	23888	1.63	1.0E-33	AV727809.1	EST_HUMAN	AV727809 HTC Homo sapiens cDNA clone HTCCNC12 5'
9248	18017		2.54	9.0E-34	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
2137	11335	20553	1.18	8.0E-34	8922751	NT	Homo sapiens hypothetical protein FLJ10900 (FLJ10900), mRNA
1448	10658	19834	2.78	7.0E-34	T70846.1	EST_HUMAN	y415a05.r1 Soares fetal liver spleen 1N1FLS Homo sapiens cDNA clone IMAGE:108320 5'
8018	17813		2.89	7.0E-34	H12888.1	EST_HUMAN	y14c10.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:148722 5'
477	9728	18862	1.31	6.0E-34	U10891.1	NT	Human G2 protein mRNA, partial cds
477	9728	18863	1.31	6.0E-34	U10891.1	NT	Human G2 protein mRNA, partial cds
8418	17480	24010	1.7	6.0E-34	U03686.1	NT	Mus musculus DAB/2J hair-specific (hac1-1) gene
1846	11083		3.27	6.0E-34	7708500	NT	Homo sapiens Npw38-binding protein Npw38P (LOC51729), mRNA
6084	14274	23357	4.37	6.0E-34	U30883.1	NT	Human splicing factor SRP55-1 (SRP-55) mRNA, complete cds
6736	15831	23391	2.28	5.0E-34	AF078778.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
7247	18487	25958	2.25	5.0E-34	AB037836.1	NT	Homo sapiens mRNA for KIAA1435 protein, partial cds
7808	18689		1.91	5.0E-34	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C008
1987	11171	20377	2.12	4.0E-34	AI804687.1	EST_HUMAN	tt94c08.x1 NCI_CGAP_P728 Homo sapiens cDNA clone IMAGE:2249194 3'
2879	11851	21075	0.84	4.0E-34	8922807	NT	Homo sapiens hypothetical protein FLJ10889 (FLJ10889), mRNA
3137	12372	21503	1.09	4.0E-34	5803188	NT	Homo sapiens splicing factor 3a, subunit 3, 60kD (SF3A3), mRNA
7711	18910		5.68	3.0E-34	BF035327.1	EST_HUMAN	601458531F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3882086 5'
1495	10708	19881	11.67	1.0E-34	P12236	SWISSPROT	ADP ATP CARRIER PROTEIN, LIVER ISOFORM T2 (ADP/ATP TRANSLOCASE 3) (ADENINE NUCLEOTIDE TRANSLOCATOR 3) (ANT 3)
3654	12875	21983	1.4	1.0E-34	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
4047	13257	22358	0.98	1.0E-34	AY008397.1	NT	Homo sapiens WNT3 precursor (WNT3) mRNA, complete cds
4047	13257	22359	0.98	1.0E-34	AY008397.1	NT	Homo sapiens WNT3 precursor (WNT3) mRNA, complete cds
4476	13674		5.59	1.0E-34	BE071414.1	EST_HUMAN	RC2-BT0508-240400-016-H08 BT0508 Homo sapiens cDNA
5728	14047	24344	2.28	1.0E-34	BE874052.1	EST_HUMAN	601484430F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886968 5'
5728	14047	24345	2.28	1.0E-34	BE874052.1	EST_HUMAN	601484430F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886968 5'
6861	16168	25641	10.13	1.0E-34	AL036835.1	EST_HUMAN	DKFZp564A1563_r1 564 (synonym: hfrb2) Homo sapiens cDNA clone DKFZp564A1563 5'
8804	18316		2.28	1.0E-34	AA807097.1	EST_HUMAN	cc31c11.s1 NCI_CGAP_GC81 Homo sapiens cDNA clone IMAGE:1351318 3' similar to gbX68203 TYROSINE-PROTEIN KINASE RECEPTOR FLT4 PRECURSOR (HUMAN);

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9050	17922		4.53	1.0E-34	AL103210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3824	12845	21884	1.17	9.0E-35	AW583302.1	EST_HUMAN	hh77b08.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2888787 5'
230	8508		17.95	8.0E-35	6031190	NT	Homo sapiens prohibitin (PHB) mRNA
1709	10821	20108	3.14	8.0E-35	BF588937.1	EST_HUMAN	nas33a08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3288134 3' similar to TR:O75912
1708	10821						O75912 DIACYLGLYCEROL KINASE IOTA. ;
4883	14071	20107	3.14	8.0E-35	BF589937.1	EST_HUMAN	nas33a08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3288134 3' similar to TR:O75912
7281	16500	25883	2.31	8.0E-35	BE378480.1	EST_HUMAN	O75912 DIACYLGLYCEROL KINASE IOTA. ;
8535	17580		3.51	8.0E-35	BF589282.1	EST_HUMAN	nas33a08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3288134 3' similar to TR:O75912
6887	15085	24488	1.82	7.0E-35	11425417	NT	nas33a08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3288134 3' similar to TR:O75912
1417	10830	19788	1.02	6.0E-35	AA757115.1	EST_HUMAN	O75912 DIACYLGLYCEROL KINASE IOTA. ;
1837	11141	20337	1.3	6.0E-35	6005975	NT	nas33a08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3288134 3' similar to TR:O75912
4030	13240	22344	0.89	6.0E-35	AW287191.1	EST_HUMAN	nas33a08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3288134 3' similar to TR:O75912
8427	15024	25088	5.25	6.0E-35	6005921	NT	nas33a08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3288134 3' similar to TR:O75912
143	8425	18558	70.88	5.0E-35	AF154830.1	NT	nas33a08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3288134 3' similar to TR:O75912
1884	10898	20083	1.86	5.0E-35	X63382.1	NT	nas33a08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3288134 3' similar to TR:O75912
2738	11917	21131	2.17	5.0E-35	AB007886.2	NT	nas33a08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3288134 3' similar to TR:O75912
2870	12208	21344	1.15	5.0E-35	6812839	NT	nas33a08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3288134 3' similar to TR:O75912
4403	13603	22703	1.74	5.0E-35	AF023288.1	NT	nas33a08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3288134 3' similar to TR:O75912
8523	16719		3.88	5.0E-35	BE880892.1	EST_HUMAN	nas33a08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3288134 3' similar to TR:O75912
7733	16830		3.48	5.0E-35	AA001788.1	EST_HUMAN	nas33a08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3288134 3' similar to TR:O75912
1436	10850	18824	34.03	4.0E-35	BE267807.1	EST_HUMAN	nas33a08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3288134 3' similar to TR:O75912
1788	10888	20163	8.81	4.0E-35	H91193.1	EST_HUMAN	nas33a08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3288134 3' similar to TR:O75912
4819	14008		0.83	4.0E-35	AF003528.1	NT	nas33a08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3288134 3' similar to TR:O75912
6138	14314		0.89	4.0E-35	BE408102.1	EST_HUMAN	nas33a08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3288134 3' similar to TR:O75912
6189	15351		1.9	4.0E-35	BE350127.1	EST_HUMAN	nas33a08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3288134 3' similar to TR:O75912
8628	15824	25288	7.14	4.0E-35	AL046596.1	EST_HUMAN	nas33a08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3288134 3' similar to TR:O75912
1558	10772	18945	48.18	3.0E-35	BE268182.1	EST_HUMAN	nas33a08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3288134 3' similar to TR:O75912

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2289	11494		3.28	3.0E-35	AF22492.1	NT	Homo sapiens phospholipid scramblase 1 gene, complete cds
6359	14589	23865	24.94	3.0E-35	BF433100.1	EST_HUMAN	7n25a09.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3565381 3' similar to TR:Q8QZH7
6359	14589	23866	24.84	3.0E-35	BF433100.1	EST_HUMAN	Q9QZH7 F-BOX PROTEIN FBL2 ;
108	11959	18528	1.05	2.0E-35	N88965.1	EST_HUMAN	7n25a09.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3565381 3' similar to TR:Q8QZH7
1198	10418	19570	0.8	2.0E-35	T11909.1	EST_HUMAN	Q8QZH7 F-BOX PROTEIN FBL2 ;
2184	11381	20605	6.37	2.0E-35	AB018413.1	NT	K6932F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone K6932 5' similar to REPETITIVE ELEMENT
2844	11827	21042	1.22	2.0E-35	AW685005.1	EST_HUMAN	A971F Heart Homo sapiens cDNA clone A971
3283	12514	21844	1.02	2.0E-35	6912459	NT	Homo sapiens mRNA for Gab2, complete cds
3283	12514	21845	1.02	2.0E-35	6912459	NT	h18a12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2070188 3' similar to SW:TR12_HUMAN Q14688 THYROID RECEPTOR INTERACTING PROTEIN 12 ;
3532	12755		1.11	2.0E-35	AB020702.1	NT	Homo sapiens Grib2-associated binder 2 (KIAA0571), mRNA
3688	13104	22221	0.69	2.0E-35	BE247575.1	EST_HUMAN	Homo sapiens Grib2-associated binder 2 (KIAA0571), mRNA
3688	13104	22222	0.69	2.0E-35	BE247575.1	EST_HUMAN	Homo sapiens mRNA for KIAA0895 protein, partial cds
4673	13887	24063	2.75	2.0E-35	H49239.1	EST_HUMAN	TCBAP2E4328 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4328
5481	14708	24063	2	2.0E-35	BF332417.1	EST_HUMAN	TCBAP2E4328 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4328
7378	16592	26080	5.53	2.0E-35	X59417.1	NT	y18a12.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:274079 5'
8289	12514	21844	1.22	2.0E-35	6912459	NT	QV0-BT0701-210490-189-b04 BT0701 Homo sapiens cDNA
8289	12514	21845	1.22	2.0E-35	6912459	NT	H. sapiens PROS-27 mRNA
8470	17823	24023	1.28	2.0E-35	BE904978.1	EST_HUMAN	Homo sapiens Grib2-associated binder 2 (KIAA0571), mRNA
8470	17823	24024	1.28	2.0E-35	BE904978.1	EST_HUMAN	Homo sapiens Grib2-associated binder 2 (KIAA0571), mRNA
9026	17878		8.58	2.0E-35	AL163210.2	NT	601496774F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3888689 5'
9144	11959	18528	2	2.0E-35	N88965.1	EST_HUMAN	601496774F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3888689 5'
48	8345	18455	4.75	1.0E-35	AA631949.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C010
48	8345	18456	4.75	1.0E-35	AA631949.1	EST_HUMAN	K6932F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone K6932 5' similar to REPETITIVE ELEMENT
760	10001	19147	72.69	1.0E-35	AW388473.1	EST_HUMAN	hmfr16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
760	10001	19148	72.69	1.0E-35	AW388473.1	EST_HUMAN	hmfr16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
919	10154		2.05	1.0E-35	T87847.1	EST_HUMAN	IL2-ST0162-131099-008-d12 ST0162 Homo sapiens cDNA
							IL2-ST0162-131099-008-d12 ST0162 Homo sapiens cDNA
							y493a01.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:115752 5' similar to SP:A44282 A44282 RETROVIRUS-RELATED POLYPROTEIN - HUMAN ;

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2507	11895	20913	1.56	1.0E-35	7705894	NT	Homo sapiens hypothetical protein (LOC51233), mRNA
2723	11802	21118	1.21	1.0E-36	BE350127.1	EST_HUMAN	h08g01.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER28.b3
2723	11802	21118	1.21	1.0E-35	BE350127.1	EST_HUMAN	MER29 repetitive element;
3108	12343	21471	1.33	1.0E-35	6006030	NT	h08g01.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER28.b3
3127	12392	21491	1.95	1.0E-35	AV650422.1	EST_HUMAN	Homo sapiens transcription elongation factor B (SIII), polypeptide 1-like (TCEB1L) mRNA
3127	12392	21492	1.95	1.0E-35	AV650422.1	EST_HUMAN	AV650422 GLC Homo sapiens cDNA clone GLCCE06 3'
4414	13614	22709	4.84	1.0E-35	7856905	NT	AV650422 GLC Homo sapiens cDNA clone GLCCE06 3'
4414	13614	22710	4.84	1.0E-35	7856905	NT	Mus musculus activin receptor interacting protein 1 (Arip1-pending), mRNA
6833	18076	25592	3.9	1.0E-35	AU158595.1	EST_HUMAN	Mus musculus activin receptor interacting protein 1 (Arip1-pending), mRNA
6833	18076	25593	3.9	1.0E-35	AU158595.1	EST_HUMAN	AU158595 PLAC3 Homo sapiens cDNA clone PLACE3000382 3'
8237	17368		4.28	1.0E-35	A1525119.1	EST_HUMAN	AU158595 PLAC3 Homo sapiens cDNA clone PLACE3000382 3'
8321	18273		2.31	1.0E-35	11418274	NT	primm-7.D01.r bvtumor Homo sapiens cDNA 5'
8337	17662		2.05	1.0E-35	11418110	NT	Homo sapiens fibulin 1 (FBLN1), mRNA
8815	17803		2.34	1.0E-35	BE792832.1	EST_HUMAN	Homo sapiens casein kinase 1, epsilon (GSKN1E), mRNA
2881	12119	21250	1.79	7.0E-36	AW657579.1	EST_HUMAN	601584833F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3936985 5'
3082	12318		5.8	7.0E-36	4557498	NT	GM1-CT0316-081299-083-d07 CT0315 Homo sapiens cDNA
6360	15540	24884	6.98	7.0E-36	U08672.1	NT	Homo sapiens C-terminal binding protein 2 (CTBP2) mRNA
6360	15540	24885	5.98	7.0E-36	U08672.1	NT	Human carcinoembryonic antigen gene family member 12 (CGM12) gene, exons L and LN
8704	17668	23948	2.64	7.0E-36	AF052051.1	NT	Human carcinoembryonic antigen gene family member 12 (CGM12) gene, exons L and LN
1973	11177	20383	1.77	6.0E-36	7708822	NT	Homo sapiens glutathione transferase A4 gene, exon 1
2382	11575		5.88	6.0E-36	AB035346.1	NT	Homo sapiens ninjurin 2 (NINJ2), mRNA
3618	12839	21958	0.66	6.0E-36	BF515101.1	EST_HUMAN	Homo sapiens TGL9 gene, exon 12
5353	14583	23659	6.31	6.0E-36	AI435169.1	EST_HUMAN	UI-H-BW1-amy-c-12-0-JL.s1 NCL_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3083542 3'
6125	15309	24742	3.34	6.0E-36	AW780143.1	EST_HUMAN	h03b06.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2126195 3' similar to gb:M11949 PANCREATIC SECRETORY TRYPSIN INHIBITOR PRECURSOR (HUMAN);
8081	17218	26750	2.20	6.0E-36	AI380499.1	EST_HUMAN	h008h02.x1 NCL_CGAP_Co14 Homo sapiens cDNA clone IMAGE:3036827 3' similar to SW:IMA2_HUMAN
135	9418	19552	9.88	5.0E-36	AJ271735.1	NT	P32282 IMPORTIN ALPHA-2 SUBUNIT;
2709	11887	21104	47.02	5.0E-36	BE388438.1	EST_HUMAN	h05c09.x1 NCL_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2107024 3' similar to contains MER9.b2
3390	12811	21831	2.13	5.0E-36	AL163209.2	NT	MER9 repetitive element;
4798	13987	23093	2.18	5.0E-36	5728728	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
							Homo sapiens Xq pseudautosomal region; segment 1/2
							601285567F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607289 5'
							Homo sapiens chromosome 21 segment HS21C009
							Homo sapiens API5-like 1 (API5L1), mRNA

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Table 4
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4768	13987	23094	2.18	5.0E-36	5728728	NT	Homo sapiens APIS-like 1 (API5L1), mRNA
8287	9418	19552	4.4	5.0E-36	AJ271735.1	NT	Homo sapiens Xa pseudocautosomal region; segment 1/2
8593	17602	24008	2.39	5.0E-36	11417882	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
1232	10450	19606	1.85	4.0E-36	BE010038.1	EST_HUMAN	PM3-BN0176-100400-001-g04 BN0176 Homo sapiens cDNA
1444	10657	19833	1.45	4.0E-36	P10288	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE; ENDONUCLEASE]
1622	10835	20011	1.15	4.0E-36	BE382574.1	EST_HUMAN	601298574F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3628388 5'
2189	11386		5.46	4.0E-36	AW247772.1	EST_HUMAN	2820020.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820020 5'
3328	12557	21694	0.79	4.0E-36	BE389289.1	EST_HUMAN	601282266F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604168 5'
3328	12557	21695	0.79	4.0E-36	BE389289.1	EST_HUMAN	601282266F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604168 5'
5181	14340	23429	0.59	4.0E-36	AA805361.1	EST_HUMAN	ok05b11.1.1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1608909 3' similar to SW:03HL_RAT_P29268 3-HYDROXYISOBUTYRATE DEHYDROGENASE PRECURSOR;
5891	14911	24305	2.59	4.0E-36	11497041	NT	Homo sapiens a disintegrin and metalloproteinase domain 22 (ADAM22), transcript variant 3, mRNA
6359	15539	24993	1.69	4.0E-36	M3320.1	NT	Human platelet Glycoprotein IIb (GP1Ib) gene, exons 2-29
7559	18784	26255	2.9	4.0E-36	AA400370.1	EST_HUMAN	zu09c10.1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:743250 5'
8609	17607		1.56	4.0E-36	11420518	NT	Homo sapiens nuclear factor of activated T-cells, cytoplasmic 2 (NFATC2), mRNA
8857	18158		3.54	4.0E-36	AV753629.1	EST_HUMAN	AV753629 TP Homo sapiens cDNA clone TFGABH01 5'
9265	18032		1.38	4.0E-36	D25217.2	NT	Homo sapiens mRNA for KIAA0027 protein, partial cds
703	8945	19081	2.65	3.0E-36	AF089810.1	NT	Homo sapiens neuroxin III-alpha gene, partial cds
1480	10702	19878	0.98	3.0E-36	AF110239.1	NT	Homo sapiens calcium/calmodulin-stimulated cyclic nucleotide phosphodiesterase (PDE1A) gene, partial cds
1489	10702	19877	0.98	3.0E-36	AF110239.1	NT	Homo sapiens calcium/calmodulin-stimulated cyclic nucleotide phosphodiesterase (PDE1A) gene, partial cds
2262	11457	20675	3.92	3.0E-36	7682401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
4605	13702	22798	8.01	3.0E-36	10181139	NT	Mus musculus junctophilin 1 (Jp1-pending), mRNA
7871	16870	26373	1.79	3.0E-36	BF036327.1	EST_HUMAN	601458531F1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:3662088 5'
3134	12369	21500	6.47	2.0E-36	BE259287.1	EST_HUMAN	601106343F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3342708 5'
4978	14165	23255	23.75	2.0E-36	AW880376.1	EST_HUMAN	QV0-O10030-240300-174-h04 OT0030 Homo sapiens cDNA
5434	14661	23801	2.36	2.0E-36	AF287747.1	NT	Mus musculus p47-phox gene, complete cds
5591	14815	24189	3.46	2.0E-36	T08756.1	EST_HUMAN	EST06848 Infant Brain, Bento Soares Homo sapiens cDNA clone HIBBJ28 5' end
5915	15132	24541	13.08	2.0E-36	T69628.1	EST_HUMAN	yc44a07.r1 Strategene liver (#837224) Homo sapiens cDNA clone IMAGE:83508 5'
895	10130	19292	1.73	1.0E-36	BE409310.1	EST_HUMAN	601300938F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635480 5'
2113	11312	20527	1.28	1.0E-36	BE146523.1	EST_HUMAN	RC1-HT0217-131189-021-h07 HT0217 Homo sapiens cDNA
2113	11312	20528	1.28	1.0E-36	BE146523.1	EST_HUMAN	RC1-HT0217-131189-021-h07 HT0217 Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2188	11388	20586	1.21	1.0E-36	BF673761.1	EST_HUMAN	602138493F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4272888 5'
3318	12548		1.63	1.0E-36	AF156862.1	NT	Homo sapiens human endogenous retrovirus W proC8-19 protease (pro) gene, partial cds
5746	14863		5.34	1.0E-36	AI987714.1	EST_HUMAN	wb37c12.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2307882 3' similar to contains Alu repetitive element;
6445	15642	25108	4.87	1.0E-36	AA148034.1	EST_HUMAN	z051a12.r1 Stratagene endothelial cell 837223 Homo sapiens cDNA clone IMAGE:590398 5'
6445	15642	25109	4.87	1.0E-36	AA148034.1	EST_HUMAN	z051a12.r1 Stratagene endothelial cell 837223 Homo sapiens cDNA clone IMAGE:590398 5'
7115	16282	25773	5.47	1.0E-36	BF384169.1	EST_HUMAN	QV3-NN1023-010600-199-H01 NN1023 Homo sapiens cDNA
7621	16728	26217	3.97	1.0E-36	AW887636.1	EST_HUMAN	CM3-NN0061-140400-147-H12 NN0081 Homo sapiens cDNA
7819	17134	26684	4.03	1.0E-36	AW504143.1	EST_HUMAN	UI-HF-BN0-ale-c-03-0-UJ.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078277 5'
8488	17521		4.59	1.0E-36	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
8944	17821		3.71	1.0E-36	AL103213.2	NT	Homo sapiens chromosome 21 segment HS21C013
9209	17982		2.95	1.0E-36	AF202723.1	NT	Homo sapiens Sad1 unc-84 domain protein 2 (SUN2) mRNA, partial cds
9248	16426	24869	2.31	9.0E-37	AW008277.1	EST_HUMAN	ws80b07.x1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2504245 3'
9248	16429	24870	2.31	9.0E-37	AW008277.1	EST_HUMAN	ws80b07.x1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2504245 3'
8745	17680		2.13	9.0E-37	W22618.1	EST_HUMAN	73D4 Human retina cDNA Tsp5091-cleaved sublibrary Homo sapiens cDNA not directional
3330	12559	21697	0.89	8.0E-37	4757679	NT	Homo sapiens chimerin (chimerin) 2 (CHN2) mRNA
5584	14808	24181	3.76	8.0E-37	BE350127.1	EST_HUMAN	h108g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146258 3' similar to contains MER29.b3
5584	14808	24182	3.76	8.0E-37	BE350127.1	EST_HUMAN	MER29 repetitive element;
5604	14828	24204	4.96	8.0E-37	AW840840.1	EST_HUMAN	MER29 repetitive element;
6423	15620	25084	8.42	8.0E-37	X87344.1	NT	RC1-CN0008-210100-012-a09_1 CN0008 Homo sapiens cDNA
1281	10508		3.81	7.0E-37	AL042800.1	EST_HUMAN	H. sapiens DNA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes
7342	16558	26046	9.31	7.0E-37	AI817700.1	EST_HUMAN	DKFZp434E0422_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434E0422 5'
7471	16870	26161	4.11	7.0E-37	AI536702.1	EST_HUMAN	wk25b11.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2413341 3' similar to contains PTR5.12
9080	17904		3.34	6.0E-37	AF202723.1	NT	PTR5 repetitive element;
5705	14924	24317	4.29	5.0E-37	AA307123.1	EST_HUMAN	hm87g03.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2185140 3' similar to contains L1.b3 L1 repetitive element;
5705	14924	24318	4.29	5.0E-37	AA307123.1	EST_HUMAN	Homo sapiens Sad1 unc-84 domain protein 2 (SUN2) mRNA, partial cds
7494	16701		5.03	6.0E-37	7657117	NT	EST1178035 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
8463	17518		6.75	5.0E-37	AF149773.1	NT	EST1178035 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
2388	11561	20798	4.76	4.0E-37	AA702764.1	EST_HUMAN	Homo sapiens glycine C-acetyltransferase (2-amino-3-ketobutyrate-CoA ligase) (GCAT), mRNA
							Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
							z190b04.s1 Soares_fetal_liver_spleen_1NFLS S1 Homo sapiens cDNA clone IMAGE:448015 3'

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7602	16805	26300	1.77	4.0E-37	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
7602	16805	26301	1.77	4.0E-37	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
1884	11187	20397	2.81	3.0E-37	AL048958.1	EST_HUMAN	DKFZp434L2418_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434L2418
1884	11187	20398	2.81	3.0E-37	AL048958.1	EST_HUMAN	DKFZp434L2418_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434L2418
2478	11688		4.67	3.0E-37	AW061150.1	EST_HUMAN	EST1373222 IMAGE resequences, MAGF Homo sapiens cDNA
2820	12158		3.85	3.0E-37	AW061150.1	EST_HUMAN	EST1373222 IMAGE resequences, MAGF Homo sapiens cDNA
388	9880	18817	0.74	2.0E-37	D89790.1	NT	Homo sapiens mRNA for AML1, complete cds
388	9880	18818	0.74	2.0E-37	D89790.1	NT	Homo sapiens mRNA for AML1, complete cds
1088	10312	19465	2.82	2.0E-37	AU131202.1	EST_HUMAN	AU131202 NT2RP3 Homo sapiens cDNA clone NT2RP3002168 5'
1088	10312	19468	2.82	2.0E-37	AU131202.1	EST_HUMAN	AU131202 NT2RP3 Homo sapiens cDNA clone NT2RP3002168 5'
1803	11137	20333	4.55	2.0E-37	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
3871	13087	22203	6.5	2.0E-37	4503210	NT	Homo sapiens cytochrome P450, subfamily XXVIIA (steroid 27-hydroxylase, cerebrotendinous xanthomatosis), polypeptide 1 (CYP27A1b) mRNA
4231	13434	22528	1.04	2.0E-37	4826885	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 1 (DDX1) mRNA
5855	15171	24588	3.38	2.0E-37	AA348720.1	EST_HUMAN	EST152831 Fetal heart II Homo sapiens cDNA 5' end
6477	15674	25145	3.78	2.0E-37	BF204032.1	EST_HUMAN	601869157F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4111408 5'
8094	17228	26786	20.18	2.0E-37	AF176013.1	NT	Homo sapiens J domain containing protein 1 isoform b (JDP1) mRNA, complete cds
8908	18021		3.29	2.0E-37	11417972	NT	Homo sapiens pascadillo (zabrafish) homolog 1, containing BRCT domain (PES1), mRNA
9262	18021		3.91	2.0E-37	11417972	NT	Homo sapiens pascadillo (zabrafish) homolog 1, containing BRCT domain (PES1), mRNA
2057	11258	20473	4.06	1.0E-37	AL163281.2	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C081
3181	12398		1.04	1.0E-37	AW862082.1	EST_HUMAN	RC3-CT0347-210400-018-H03 CT0347 Homo sapiens cDNA
3838	13154	22271	1.05	1.0E-37	AF189011.1	NT	Homo sapiens ribonuclease III (RN3) mRNA, complete cds
4959	14146	23238	2.15	1.0E-37	BF371719.1	EST_HUMAN	QVO-FN0180-280700-318-c10 FN0180 Homo sapiens cDNA
6893	15888	25348	3.8	1.0E-37	AA171406.1	EST_HUMAN	zp21802.1 Stratiogene neuroepithelium (#837231) Homo sapiens cDNA clone IMAGE:810059 5' similar to contains L1.12 L1 repetitive element :
7288	16307	25988	6.46	1.0E-37	M22878.1	NT	Human somatic cytochrome c (HC1) processed pseudogene, complete cds
8768	17722		2.73	1.0E-37	BE771814.1	EST_HUMAN	GM3-F10068-140700-243-407 F10068 Homo sapiens cDNA
5564	14788	24159	1.78	9.0E-38	10048482	NT	Rattus norvegicus multidomain presynaptic cytomatrix protein Piccolo (LOC56768), mRNA
1229	10447	19603	1.67	8.0E-38	11436955	NT	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
2462	11653	20875	1.28	8.0E-38	BF348221.1	EST_HUMAN	602018401F1 NCI_CGAP_Brm87 Homo sapiens cDNA clone IMAGE:4153992 5'
2149	11347	20564	9.62	7.0E-38	AW972825.1	EST_HUMAN	EST1384920 IMAGE resequences, MAGL Homo sapiens cDNA
4208	13411	22505	0.7	7.0E-38	H18092.1	EST_HUMAN	yn51807.1 Soares adult brain N255HB55Y Homo sapiens cDNA clone IMAGE:171973 5'
3007	12243	21374	2.28	6.0E-38	BF030303.1	EST_HUMAN	601455722F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:38589348 5'
8322	17424		7.1	6.0E-38	11435947	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7787	16882	26495	2.23	2.0E-38	AA595480.1	EST_HUMAN	nc34g03.a1 NCI_CGAP_P123 Homo sapiens cDNA clone IMAGE:1102812 3' similar to TR:E212316 E212316 NADP DEPENDENT LEUKOTRIENE B4 12-HYDROXYDEHYDROGENASE.;
7787	16882	26496	2.23	2.0E-38	AA595480.1	EST_HUMAN	nc34g03.a1 NCI_CGAP_P123 Homo sapiens cDNA clone IMAGE:1102812 3' similar to TR:E212316 E212316 NADP DEPENDENT LEUKOTRIENE B4 12-HYDROXYDEHYDROGENASE.;
8024	17161	26698	6.35	2.0E-38	BE712780.1	EST_HUMAN	QV2-HT0698-080800-283-a05 HT0698 Homo sapiens cDNA
8153	17285	26828	3.85	2.0E-38	AF190501.1	NT	Homo sapiens leucine-rich repeat-containing G protein-coupled receptor 6 (LGR6) mRNA, partial cds
8153	17285	26829	3.85	2.0E-38	AF190501.1	NT	Homo sapiens leucine-rich repeat-containing G protein-coupled receptor 6 (LGR6) mRNA, partial cds
8376	17461		8.04	2.0E-38	AV726988.1	EST_HUMAN	AV726988 HTC Homo sapiens cDNA clone HTCA007 5'
8377	17462		2.07	2.0E-38	AB012723.1	NT	Homo sapiens gene for kinesin-like protein, complete cds
8681	17651		1.59	2.0E-38	M55630.1	NT	Human topoisomerase I pseudogene 2
8683	17661	23982	3.6	2.0E-38	H55841.1	EST_HUMAN	CH2220580 Chromosome 22 exon Homo sapiens cDNA clone C22_788 5'
8757	17698		1.99	2.0E-38	S74608.1	NT	E1 beta-pyruvate dehydrogenase beta (promoter) [human, placenta, Genomic, 1280 nt]
8243	18014		2.44	2.0E-38	11418248	NT	Homo sapiens sulfotransferase-related protein (SULTX3), mRNA
1101	10325		2.54	1.0E-38	AA401570.1	EST_HUMAN	z162b02.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:742639 5' similar to contains element MER19 repetitive element;
1098	11172	20378	2.74	1.0E-38	4885288	NT	Homo sapiens guanine nucleotide binding protein-like 1 (GNL1), mRNA
1098	11191	20401	1.19	1.0E-38	7881989	NT	Homo sapiens KIAA0173 gene product (KIAA0173), mRNA
2458	11648	20871	4.36	1.0E-38	AF270831.1	NT	Homo sapiens cyclin K (CCNK) gene, exon 7
2576	11782	20983	1.1	1.0E-38	4758371	NT	Homo sapiens fibrinogen-like 1 (FGL1), mRNA
4137	13343	22444	0.98	1.0E-38	AB037863.1	NT	Homo sapiens mRNA for KIAA1442 protein, partial cds
4310	13511	22805	0.87	1.0E-38	4505018	NT	Homo sapiens low density lipoprotein receptor-related protein 8 (LRP8) mRNA, and translated products
4315	13518	22810	1.58	1.0E-38	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4315	13518	22811	1.56	1.0E-38	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4597	13791	22882	1.02	1.0E-38	8922543	NT	Homo sapiens hypothetical protein FLJ10800 (FLJ10800), mRNA
5872	14882	24284	4.04	1.0E-38	7305360	NT	Mus musculus otogelin (Otog), mRNA
5872	14892	24285	4.04	1.0E-38	7305360	NT	Mus musculus otogelin (Otog), mRNA
6254	15435	24874	2.8	1.0E-38	AB014512.1	NT	Homo sapiens mRNA for KIAA0812 protein, partial cds
8881	16072	25541	8.97	1.0E-38	BE350127.1	EST_HUMAN	h09g01.x1 NCI_CGAP_K1f13 Homo sapiens cDNA clone IMAGE:3148256 3' similar to contains MER28.b3 MER29 repetitive element;
8122	17258	26798	1.81	1.0E-38	7682109	NT	Homo sapiens KIAA0428 gene product (KIAA0428), mRNA
8534	18087		1.97	1.0E-38	AL183294.2	NT	Homo sapiens chromosome 21 segment HS21C084

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Single Exon Probes Expressed In HELA Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
56	9353	18469	5.86	8.0E-39	4502312	NT	Homo sapiens ATPase, H+ transporting, lysosomal (vacuolar proton pump) 16kD (ATP8C) mRNA
1398	10812	19776	1.29	8.0E-39	4758229	NT	Homo sapiens estrogen receptor-binding fragment-associated gene 9 (EBAG9) mRNA
1797	11008		2.74	8.0E-39	A1823404.1	EST_HUMAN	wh53f10.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2384491 3' similar to TR:P87890 P87890 POL PROTEIN ;
2063	11284	20477	5.62	7.0E-39	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
7368	16800	28088	2.68	6.0E-39	BF331829.1	EST_HUMAN	QV1-BT0631-040900-357-02 BT0631 Homo sapiens cDNA
9152	17855		2.33	6.0E-39	BE870394.1	EST_HUMAN	7e34c03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284356 3' similar to WP:R151.6 CE00828 ;
1016	10244	18398	3.22	6.0E-39	AF003528.1	NT	Homo sapiens X-linked arylidic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
2942	12180	21314	8.37	5.0E-39	A1750154.1	EST_HUMAN	a18b004.x1 Barstead cotan HPLRB7 Homo sapiens cDNA clone IMAGE:2374063 3' similar to TR:Q15408 Q15408 NEUTRAL PROTEASE LARGE SUBUNIT ; contains LTR7.1 LTR7 repetitive element ;
8945	17764		2.06	5.0E-39	11420289	NT	Homo sapiens hypothetical protein FLJ10803 (FLJ10803), mRNA
557	8807	18932	97.11	4.0E-39	AB015910.1	NT	Chlorocebus aethiops mRNA for ribosomal protein S4X, complete cds
3548	12771	21899	0.94	4.0E-39	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
8963	17765		3.91	4.0E-39	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
8983	17848		2.14	4.0E-39	BE836452.1	EST_HUMAN	QV0-FN0063-280600-278-c08 FN0063 Homo sapiens cDNA
49	9348	18457	19.73	3.0E-39	AA631949.1	EST_HUMAN	fmfc16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
49	9348	18458	19.73	3.0E-39	AA631949.1	EST_HUMAN	fmfc16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
49	9348	18459	19.73	3.0E-39	AA631949.1	EST_HUMAN	fmfc16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
8368	17455	28583	6.17	3.0E-39	A1084557.1	EST_HUMAN	α63a10.s1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1660988 3' similar to SW:GTR5_RAT P43427 GLUCOSE TRANSPORTER TYPE 5, SMALL INTESTINE ;
8368	17455	28584	6.17	3.0E-39	A1084557.1	EST_HUMAN	α63a10.s1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1660988 3' similar to SW:GTR5_RAT P43427 GLUCOSE TRANSPORTER TYPE 5, SMALL INTESTINE ;
8413	17487		5.85	3.0E-39	H37903.1	EST_HUMAN	y951c08.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:180954 3'
907	10142		8.08	2.0E-39	BE408203.1	EST_HUMAN	601301607F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3636289 5'
922	10157		13.75	2.0E-39	A1525119.1	EST_HUMAN	pramine-7.D01.r bvtumor Homo sapiens cDNA 5'
1039	10265		3.85	2.0E-39	AF000573.1	NT	Homo sapiens homocitrate 1,2-dioxygenase gene, complete cds
1516	10730		98	2.0E-39	AW372318.1	EST_HUMAN	PMO-BT0340-211288-003-402 BT0340 Homo sapiens cDNA
1943	11147	20347	2.64	2.0E-39	AA720574.1	EST_HUMAN	hw21g02.s1 NCI_CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR.13 THR repetitive element ;
2592	11778	20997	1.47	2.0E-39	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
4387	13598	22699	1.65	2.0E-39	BF370207.1	EST_HUMAN	RC4-FN0037-280700-011-a10 FN0037 Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5437	14684	23817	4.29	2.0E-39	AA508880.1	EST_HUMAN	ng88f03.s1 NCL_CGAP_P16 Homo sapiens cDNA clone IMAGE:541883
6242	15423	24884	2.22	2.0E-39	AA080887.1	EST_HUMAN	zn06f02.r1 Stratiogene hNT neuron (#837233) Homo sapiens cDNA clone IMAGE:546651 5'
7970	17149	26885	2.7	2.0E-39	D86984.1	NT	Human mRNA for KIAA0209 gene, partial cds
1502	10715	19887	3.01	1.0E-39	AJ006345.1	NT	Homo sapiens KVLQT1 gene
1502	10715	19888	3.01	1.0E-39	AJ006345.1	NT	Homo sapiens KVLQT1 gene
1517	10731	19890	6.07	1.0E-39	7657020	NT	Homo sapiens DKFZp434P211 protein (DKFZP434P211), mRNA
4663	13857	22855	7.37	1.0E-39	AW951985.1	EST_HUMAN	EST384085 MAGC resequences, MAGB Homo sapiens cDNA
4663	13857	22856	7.37	1.0E-39	AW951985.1	EST_HUMAN	EST384085 MAGC resequences, MAGB Homo sapiens cDNA
4713	13904	23004	11.24	1.0E-39	7657020	NT	Homo sapiens DKFZp434P211 protein (DKFZP434P211), mRNA
5519	14744	24111	4.29	1.0E-39	AJ278170.1	NT	Mus musculus mRNA for neuronal interacting factor X1 (NIX1) (Nix1 gene)
5519	14744	24112	4.29	1.0E-39	AJ278170.1	NT	Mus musculus mRNA for neuronal interacting factor X1 (NIX1) (Nix1 gene)
6008	15258		1.72	1.0E-39	11438738	NT	Homo sapiens tubby like protein 3 (TULP3), mRNA
6240	15421	24882	2.06	1.0E-39	D78132.1	NT	Homo sapiens mRNA for ras-related GTP-binding protein, complete cds
8791	17718		1.28	1.0E-39	U07000.1	NT	Human breakpoint cluster region (BCR) gene, complete cds
562	8812	18935	1.44	9.0E-40	5803210	NT	Homo sapiens UDP-glucose pyrophosphorylase 2 (UGP2), mRNA
1242	10458	19616	12.31	9.0E-40	4755145	NT	Homo sapiens AE-binding protein 1 (AEBP1) mRNA
1242	10458	19617	12.31	9.0E-40	4755145	NT	Homo sapiens AE-binding protein 1 (AEBP1) mRNA
1450	10663	18636	1.29	9.0E-40	4507512	NT	Homo sapiens tissue inhibitor of metalloproteinase 3 (Soreby fundus dystrophy, pseudoinflammatory) (TIMP3) mRNA
3768	12868	22102	0.8	9.0E-40	4503764	NT	Homo sapiens fragile X mental retardation 1 (FMR1) mRNA
3950	14468	22279	4.18	9.0E-40	AB033070.1	NT	Homo sapiens mRNA for KIAA1244 protein, partial cds
4502	13541	22632	0.6	9.0E-40	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
3008	12242	21373	0.86	8.0E-40	AA078195.1	EST_HUMAN	7H15A04 Chromosome 7 HeLa cDNA Library Homo sapiens cDNA clone 7H15A04
3868	13114		7.24	8.0E-40	BE396541.1	EST_HUMAN	601288958F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3619168 5'
6363	15563	25019	2.32	7.0E-40	U60325.1	NT	Human DNA polymerase gamma mRNA, nuclear gene encoding mitochondrial protein, complete cds
6363	15563	25020	2.32	7.0E-40	U60325.1	NT	Human DNA polymerase gamma mRNA, nuclear gene encoding mitochondrial protein, complete cds
7473	16681	26164	2.72	7.0E-40	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
2686	11867	21080	5.57	6.0E-40	AA361275.1	EST_HUMAN	EST70527 T-cell lymphoma Homo sapiens cDNA 5' end similar to zinc finger protein family
2686	11867	21081	5.57	6.0E-40	AA361275.1	EST_HUMAN	EST70527 T-cell lymphoma Homo sapiens cDNA 5' end similar to zinc finger protein family
5632	14856		2.07	6.0E-40	BE504768.1	EST_HUMAN	hz40g01.x1 NCL_CGAP_GC8 Homo sapiens cDNA clone IMAGE:3210480 3'

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Table 4
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6057	15228	24845	4.82	6.0E-40	11439783	NT	Homo sapiens fatty acid desaturase 1 (FADS1), mRNA
6057	15228	24846	4.82	6.0E-40	11439783	NT	Homo sapiens fatty acid desaturase 1 (FADS1), mRNA
7004	16241	25715	10.56	6.0E-40	AV653028.1	EST_HUMAN	AV653028 GLC Homo sapiens cDNA clone GLCDGF04 3'
7084	16241	25716	10.56	6.0E-40	AV653028.1	EST_HUMAN	AV653028 GLC Homo sapiens cDNA clone GLCDGF04 3'
2565	11761	20971	3.15	5.0E-40	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
1842	11050	20241	2.09	4.0E-40	A1686005.1	EST_HUMAN	t891b01.x1 NCL_CGAP_P128 Homo sapiens cDNA clone IMAGE:2248873 3' similar to TR:O73505 O73505 POL PROTEIN.;
2078	11278		4.83	4.0E-40	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
4383	13584	22888	9.15	4.0E-40	7882117	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
6480	15857	25128	4.42	4.0E-40	AA742808.1	EST_HUMAN	nv34e10.t1 NCL_CGAP_Br4 Homo sapiens cDNA clone IMAGE:1222122
6787	15882	25442	2.71	4.0E-40	BE009416.1	EST_HUMAN	PMO-BN0167-070500-002-h12 BN0167 Homo sapiens cDNA
6787	15882	25443	2.71	4.0E-40	BE009416.1	EST_HUMAN	PMO-BN0167-070500-002-h12 BN0167 Homo sapiens cDNA
7304	16522	26013	1.88	4.0E-40	AW841585.1	EST_HUMAN	RC1-CN0017-120200-012-e04 CN0017 Homo sapiens cDNA
4114	13321	22421	0.89	3.0E-40	A1825849.1	EST_HUMAN	wh12r07.x1 NCL_CGAP_Kdt1 Homo sapiens cDNA clone IMAGE:2380548 3'
4889	14077		0.93	3.0E-40	AA055118.1	EST_HUMAN	zf18r09.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:377163 3'
6951	15167	24580	7.57	3.0E-40	11417342	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A), mRNA
6991	15787	25246	5.04	3.0E-40	5454167	NT	Homo sapiens HBV associated factor (XAP4) mRNA
7255	16475	25867	1.91	3.0E-40	D86984.1	NT	Human mRNA for KIAA0209 gene, partial cds
7583	16787	26281	1.91	3.0E-40	BE350127.1	EST_HUMAN	h08g01.x1 NCL_CGAP_K1d13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3
7816	17008	26522	14.52	3.0E-40	6005813	NT	MER29 repetitive element;
330	9600		5.88	2.0E-40	A1223036.1	EST_HUMAN	Homo sapiens serine threonine protein kinase (NDR), mRNA
804	10043		8.66	2.0E-40	AW303868.1	EST_HUMAN	qg52r08.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1838847 3'
1783	11002		1.97	2.0E-40	AV731601.1	EST_HUMAN	x24e10.x1 NCL_CGAP_U4 Homo sapiens cDNA clone IMAGE:2761098 3' similar to SW:RS5_MOUSE P97461 40S RIBOSOMAL PROTEIN S5.;
1803	11109	20302	3.35	2.0E-40	4506188	NT	AV731601 HTF Homo sapiens cDNA clone HTFAZE06 5'
1803	11109	20303	3.35	2.0E-40	4506188	NT	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 7 (PSMA7) mRNA, and translated products
2039	11240	20448	1.44	2.0E-40	A1868502.1	EST_HUMAN	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 7 (PSMA7) mRNA, and translated products
2135	11333	20552	1.8	2.0E-40	5453502	NT	w80a11.x1 NCL_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2514716 3' similar to TR:Q81828 Q81828 ZINC FINGER PROTEIN.;
							Homo sapiens adenyl cyclase-associated protein 2 (CAP2) mRNA

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Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3090	12326	21449	4.72	2.0E-40	5453592	NT	Homo sapiens adenyl cyclase-associated protein 2 (CAP2) mRNA
4922	14110	23208	1.88	2.0E-40	AL183280.2	NT	Homo sapiens chromosome 21 segment HS21C080
4922	14110	23207	1.88	2.0E-40	AL183280.2	NT	Homo sapiens chromosome 21 segment HS21C080
893	10128		1.72	1.0E-40	AA225989.1	EST_HUMAN	nc08a08.s1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:1007608
2584	11770	20890	4.35	1.0E-40	BF036881.1	EST_HUMAN	601460375F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3863863 5'
2848	11829		2.98	1.0E-40	BE018348.1	EST_HUMAN	bb78a10.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3048570 5' similar to TR:Q9Z158 Q9Z158
3267	12500		1.01	1.0E-40	4507142	NT	SYNTAXIN 17.1
4611	13805	22896	5.6	1.0E-40	4508012	NT	Homo sapiens sorting nexin 3 (SNX3) mRNA
6120	15304	24738	2.37	1.0E-40	AA573201.1	EST_HUMAN	Homo sapiens zinc finger protein 200 (ZNF200) mRNA, and translated products
6120	15304	24737	2.37	1.0E-40	AA573201.1	EST_HUMAN	h4204.s1 NCI_CGAP_AA1 Homo sapiens cDNA clone IMAGE:995167 3'
7491	16888	28183	6.81	1.0E-40	AU149345.1	EST_HUMAN	h4204.s1 NCI_CGAP_AA1 Homo sapiens cDNA clone IMAGE:995167 3'
8909	18232		6.76	1.0E-40	BF334112.1	EST_HUMAN	AU149345 NT2RM4 Homo sapiens cDNA clone NT2RM4002122 3'
3791	13009	22124	0.81	9.0E-41	W01596.1	EST_HUMAN	MR2-CT0222-21 1099-002-610 CT0222 Homo sapiens cDNA
8430	15630	26095	2.36	8.0E-41	AL163203.2	NT	z38a02.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:294602 5'
838	11979	19233	1.42	7.0E-41	A1934364.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C003
838	11979	19234	1.42	7.0E-41	A1934364.1	EST_HUMAN	wp04h04.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2463895 3'
4680	13854	22951	1.12	7.0E-41	BE389582.1	EST_HUMAN	wp04h04.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2463895 3'
4690	13854	22952	1.12	7.0E-41	BE389582.1	EST_HUMAN	601282077F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3603955 5'
5281	14434	23508	7.39	7.0E-41	11431114	NT	601282077F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3603955 5'
6658	14881	24270	3.45	7.0E-41	11419208	NT	Homo sapiens hypothetical protein (FLJ10688), mRNA
7972	17151	26888	1.68	7.0E-41	4768445	NT	Homo sapiens a disintegrin and metalloproteinase domain 22 (ADAM22), mRNA
8250	18229		5.86	7.0E-41	11417872	NT	Homo sapiens guanine nucleotide binding protein 10 (GNG10) mRNA
285	9659	18683	1.26	6.0E-41	AB037183.1	NT	Homo sapiens pascadillo (zabrafish) homolog 1, containing BRCT domain (PES1), mRNA
2081	11281	20497	1.72	6.0E-41	7857042	NT	Homo sapiens DSCR5p mRNA, complete cds
1771	10881	20171	2.49	5.0E-41	T62628.1	EST_HUMAN	Homo sapiens Down syndrome candidate region 1 (DSCR1), mRNA
5901	15118		2.22	5.0E-41	BE067042.1	EST_HUMAN	yc03e10.s1 Stratiogene lung (#837210) Homo sapiens cDNA clone IMAGE:79826 3'
386	9651		1.87	4.0E-41	BE156318.1	EST_HUMAN	PM4-BT0341-251198-002-F11 BT0341 Homo sapiens cDNA
1106	10330	18480	1.12	4.0E-41	AU119344.1	EST_HUMAN	QV0-HT0367-150200-114-g09 HT0367 Homo sapiens cDNA
							AU119344 HEMBA1 Homo sapiens cDNA clone HEMBA1005583 5'
1414	10627	19783	16.08	4.0E-41	A1027117.1	EST_HUMAN	ow45e06.s1 Soares parathyroid tumor NbhPA Homo sapiens cDNA clone IMAGE:1649784 3' similar to TR:O00597 O00597 CYTOCHROME C-LIKE POLYPEPTIDE, contains LTR5.b1 LTR5 repetitive element;

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1414	10627	19794	18.08	4.0E-41	A1027117.1	EST_HUMAN	ow45608.s1 Soares_parathyroid_tumor_NhrHPA Homo sapiens cDNA clone IMAGE:1649784 3' similar to TR:000597 000597 CYTOCHROME C-LIKE POLYPEPTIDE; contains LTR5.b1 LTR5 repetitive element;
1427	10640	19811	2.73	4.0E-41	AB008681.1	NT	Homo sapiens gene for activin receptor type IIB, complete cds
1612	10925	20000	5.77	4.0E-41	A1500408.1	EST_HUMAN	hm86c04.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2165958 3' similar to contains OFR.b1 OFR repetitive element;
2841	12080	21204	4.37	4.0E-41	AJ229041.1	NT	Homo sapiens 859 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
2841	12080	21205	4.37	4.0E-41	AJ229041.1	NT	Homo sapiens 859 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
4126	13332	22430	2.46	4.0E-41	X92885.1	NT	H. sapiens DNase I hypersensitive site (HSS-3) enhancer element
5879	15098		1.77	4.0E-41	AV758295.1	EST_HUMAN	AV758295 BM Homo sapiens cDNA clone BMFBHC08 5'
6990	16168	25640	4.92	4.0E-41	BF304883.1	EST_HUMAN	601888096F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4122119 5'
8174	17308		10.3	4.0E-41	AV710480.1	EST_HUMAN	AV710480 Gu Homo sapiens cDNA clone CUAAGC07 5'
8988	16121		1.78	4.0E-41	AV708431.1	EST_HUMAN	AV708431 ADC Homo sapiens cDNA clone ADCARE02 5'
9188	17977	23858	1.4	4.0E-41	BE887118.1	EST_HUMAN	601508315F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3910059 5'
955	10188	19343	2.08	3.0E-41	AB030178.1	NT	Homo sapiens PAD-H19 mRNA for peptidylarginine deiminase type II, complete cds
4327	13528	22622	3.69	3.0E-41	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
6438	14665	23818	7.72	3.0E-41	X87688.1	NT	H. sapiens mRNA for putative p64 CLCP protein
5925	15042	24448	1.7	3.0E-41	AB037808.1	NT	Homo sapiens mRNA for KIAA1387 protein, partial cds
8220	17350	26868	1.82	3.0E-41	AJ229041.1	NT	Homo sapiens 859 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
8698	17762		1.85	3.0E-41	BF125922.1	EST_HUMAN	601762940F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4028081 5'
1792	10757	19831	29.38	2.0E-41	U43701.1	NT	Human ribosomal protein L23a mRNA, complete cds
1828	11132	20327	1.52	2.0E-41	AA331940.1	EST_HUMAN	EST35818 Embryo, 8 week I Homo sapiens cDNA 5' end
2185	11382	20808	1.27	2.0E-41	D86982.1	NT	Human mRNA for KIAA0207 gene, complete cds
2233	11428	20654	5.68	2.0E-41	X89831.1	NT	G.gorilla DNA for ZNF80 gene homolog
2780	10757	19831	18.14	2.0E-41	U43701.1	NT	Human ribosomal protein L23a mRNA, complete cds
3300	12631	21683	38.49	2.0E-41	AA449549.1	EST_HUMAN	z08804.r1 Soares_tetus_Nb2Hf8_9w Homo sapiens cDNA clone IMAGE:785839 5'
4624	13618	22808	1.43	2.0E-41	AL163287.2	NT	Homo sapiens chromosome 21 segment HS21C087
4624	13618	22809	1.43	2.0E-41	AL163287.2	NT	Homo sapiens chromosome 21 segment HS21C087
6368	15548	25001	6.72	2.0E-41	AF038404.1	NT	Homo sapiens homolog of Nedd5 (hNedd5) mRNA, complete cds
6487	15894	25161	2.25	2.0E-41	M96944.1	NT	Human B-cell specific transcription factor (BSAP) mRNA, complete cds
6487	15894	25162	2.25	2.0E-41	M96944.1	NT	Human B-cell specific transcription factor (BSAP) mRNA, complete cds
8020	17159	26865	3.94	2.0E-41	AA372637.1	EST_HUMAN	EST84555 Cdon adenocarcinoma IV Homo sapiens cDNA 5' end
3171	12408	21540	1.16	1.0E-41	BE669735.1	EST_HUMAN	601445847F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3848803 5'

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Table 4
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3171	12408	21541	1.16	1.0E-41	BE869735.1	EST_HUMAN	601445647F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:3849803 5'
4564	13758	22855	10.99	1.0E-41	6879468	NT	Mus musculus tubulin alpha 8 (Tubef), mRNA
8462	17517		2.67	1.0E-41	11526291	NT	Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA
468	9722	18853	8.13	8.0E-42	AF003530.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
2078	11279	20495	2.22	8.0E-42	AB026888.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
8508	18236		28.5	8.0E-42	AA493896.1	EST_HUMAN	nm07602.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943588 similar to TR:G434304 G434304 367BP EXPRESSED SEQUENCE TAG MRNA;
8528	18109		1.24	8.0E-42	AW088062.1	EST_HUMAN	xc87a04.x1 NCI_CGAP_Bm35 Homo sapiens cDNA clone IMAGE:2582174 3' similar to contains OFR.12
940	10173		3.09	7.0E-42	AL163285.2	NT	OFR repetitive element;
6838	16043	25507	2.35	7.0E-42	AI204358.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C085
1823	11031	20224	16.63	8.0E-42	AF012872.1	NT	qf58g12.x1 Scores testis NIH Homo sapiens cDNA clone IMAGE:1754278 3'
1823	11031	20225	16.63	6.0E-42	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
2253	11448		2.87	6.0E-42	AW238658.1	EST_HUMAN	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
133	9416		5.67	5.0E-42	AJ271795.1	NT	xp28f08.x1 NCI_CGAP_HN10 Homo sapiens cDNA clone IMAGE:2741786 3' similar to contains L1.1 L1 repetitive element;
444	9898	18834	1.43	5.0E-42	BE217913.1	EST_HUMAN	Homo sapiens Xq pseudautosomal region; segment 1/2
493	9748		3.16	5.0E-42	5730038	NT	h931e11.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3175052 3'
494	9747		2.81	5.0E-42	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
5968	15280	24712	2.51	5.0E-42	11417857	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
6168	15348	24768	1.74	5.0E-42	AF071569.1	NT	Homo sapiens myotubularin related protein 3 (MTMR3), mRNA
7569	16774	20267	2.28	5.0E-42	8923182	NT	Homo sapiens multifunctional calcium/calmodulin-dependent protein kinase II delta2 isoform mRNA, complete cds
761	10002	19149	18.41	4.0E-42	AF055088.1	NT	Homo sapiens hypothetical protein FLJ20163 (FLJ20163), mRNA
761	10002	19150	18.41	4.0E-42	AF055088.1	NT	Homo sapiens MHC class I region
1073	10298	19448	2.86	4.0E-42	AF169011.1	NT	Homo sapiens MHC class I region
4176	13390	22481	1.79	4.0E-42	X59417.1	NT	Homo sapiens ribonuclease III (RN3) mRNA, complete cds
4235	13438	22631	5.6	4.0E-42	4506496	NT	H. sapiens PROS-27 mRNA
4582	13776	22869	16.6	4.0E-42	4508008	NT	Homo sapiens regulatory factor X, 4 (influences HLA class II expression) (RFX4) mRNA
5188	14372	23459	1.04	4.0E-42	AW818635.1	NT	Homo sapiens zinc finger protein 177 (ZNF177) mRNA
7242	16482	25951	1.78	4.0E-42	AW818630.1	EST_HUMAN	Homo sapiens DKFZP564O2082 protein (DKFZP564O2082), mRNA
7242	16482	25952	1.78	4.0E-42	AW818630.1	EST_HUMAN	RC1-ST0278-040400-018-h11 ST0278 Homo sapiens cDNA
7951	17090	26820	3.51	4.0E-42	BF035327.1	EST_HUMAN	RC1-ST0278-040400-018-h11 ST0278 Homo sapiens cDNA
							601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3882088 5'

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Table 4
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1478	10680	18868	2.54	2.0E-42	BF376834.1	EST_HUMAN	RCO-TN0078-110800-024-g07 TN0078 Homo sapiens cDNA
2350	11549	20770	1.77	2.0E-42	AV690218.1	EST_HUMAN	AV690218 GKC Homo sapiens cDNA clone GKCCBB08 5'
2375	11568		3.58	2.0E-42	AW888344.1	EST_HUMAN	RC3-NN0070-270400-011-h10 NN0070 Homo sapiens cDNA
2380	11582	20769	24.12	2.0E-42	AW250059.1	EST_HUMAN	2818283.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2818283 3'
5554	14778	24145	17	2.0E-42	AW955388.1	EST_HUMAN	EST387438 MAGC resequences, MAGC Homo sapiens cDNA
5554	14778	24146	17	2.0E-42	AW955388.1	EST_HUMAN	EST387438 MAGC resequences, MAGC Homo sapiens cDNA
8228	17358	26897	2	2.0E-42	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
741	9881	19124	1.41	1.0E-42	X57147.1	NT	Human endogenous retrovirus pHE.1 (ERV9)
1049	10275	19428	1.78	1.0E-42	AW285809.1	EST_HUMAN	UI-H-B11-aff-e-04-Q-JJ.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2721871 3'
1109	10333	19483	1.58	1.0E-42	AJ251818.1	NT	Homo sapiens partial C9 gene for complement component C9, exon 1
1109	10333	19484	1.58	1.0E-42	AJ251818.1	NT	Homo sapiens partial C9 gene for complement component C9, exon 1
1249	11889	19628	12.22	1.0E-42	AF087166.1	NT	Homo sapiens NADH-ubiquinone oxidoreductase AGGG subunit precursor homolog mRNA, nuclear gene encoding mitochondrial protein, complete cds
1249	11889	19629	12.22	1.0E-42	AF087166.1	NT	Homo sapiens NADH-ubiquinone oxidoreductase AGGG subunit precursor homolog mRNA, nuclear gene encoding mitochondrial protein, complete cds
1875	10887	20073	1.1	1.0E-42	11423219	NT	Homo sapiens rec (LOC51201), mRNA
2508	11898	20915	2.09	1.0E-42	5174458	NT	Homo sapiens major histocompatibility complex, class II, DM alpha (HLA-DMA) mRNA
2918	12157	21292	10.03	1.0E-42	4505524	NT	Homo sapiens origin recognition complex, subunit 5 (yeast homolog)-like (ORC5L) mRNA, and translated products
3688	12909	22028	2.23	1.0E-42	7662027	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
3777	12895	22111	1.02	1.0E-42	5031610	NT	Homo sapiens Golgi vesicular membrane trafficking protein p18 (BET1) mRNA
3900	13116	22233	1.09	1.0E-42	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C087
4232	13435	22529	2.23	1.0E-42	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
4768	13949	23050	2.4	1.0E-42	5803122	NT	Homo sapiens chromosome 21 segment HS21C080
4758	13949	23051	2.4	1.0E-42	5803122	NT	Homo sapiens proteasome inhibitor (PI31), mRNA
4788	13977	23081	6.15	1.0E-42	4508758	NT	Homo sapiens proteasome inhibitor (PI31), mRNA
4887	14075	23173	1.22	1.0E-42	AB033114.1	NT	Homo sapiens gamma-galactosyltransferase 3 (B4GALT3) mRNA
7562	16767	26258	1.67	1.0E-42	11437455	NT	Homo sapiens mRNA for KIAA1288 protein, partial cds
7104	18281	25761	6.25	9.0E-43	4757869	NT	Homo sapiens chromatin-specific transcription elongation factor, 140 kDa subunit (FACTP140), mRNA
7607	18810	26305	3.42	9.0E-43	AA435719.1	EST_HUMAN	Homo sapiens chromodomain protein, Y chromosome-like (CDYL) mRNA
658	9804	18030	14.02	8.0E-43	AV736824.1	EST_HUMAN	z178a07.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728532 3'
658	9804	19031	14.02	8.0E-43	AV736824.1	EST_HUMAN	AV736824 CB Homo sapiens cDNA clone CBLAKH08 5'
707	9949	18085	4.54	8.0E-43	8923278	NT	AV736824 CB Homo sapiens cDNA clone CBLAKH08 5'
							Homo sapiens hypothetical protein FLJ20297 (FLJ20297), mRNA

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
707	9949	19088	4.54	8.0E-43	8923278	NT	Homo sapiens hypothetical protein FLJ20287 (FLJ20287), mRNA
707	9949	19087	4.54	8.0E-43	8923278	NT	Homo sapiens hypothetical protein FLJ20287 (FLJ20287), mRNA
3620	12841	21860	8	7.0E-43	AW248442.1	EST_HUMAN	2822251.5 prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822251 5'
6707	15802		6.35	7.0E-43	A1938748.1	EST_HUMAN	wp6801.1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2468985 3' similar to TR:O16475 O15475 UNNAMED HERV-H PROTEIN ; contains LTR7.b1 LTR7 repetitive element ;
1351	10568		18.5	6.0E-43	AA491880.1	EST_HUMAN	ne72d08.s1 NCI_CGAP_Ew1 Homo sapiens cDNA clone IMAGE:808803 similar to gb:L05095 60S RIBOSOMAL PROTEIN L30 (HUMAN);
2652	11740		2.84	6.0E-43	AV708201.1	EST_HUMAN	AV708201 ADC Homo sapiens cDNA clone ADCACC10 5'
5783	15010	24414	2.46	6.0E-43	9655873	NT	Homo sapiens ATP-binding cassette, sub-family C (CFTR/MRP), member 3 (ABCC3), transcript variant MRP3B, mRNA
6045	15213	24633	1.97	6.0E-43	AW468887.1	EST_HUMAN	Ind30b04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910891 3' similar to contains MER1.13 MER1 MER1 repetitive element ;
7888	16883		6.52	6.0E-43	AL118158.1	EST_HUMAN	DKFZp781L1712_r1 781 (synonym: hamy2) Homo sapiens cDNA clone DKFZp781L1712 5'
140	9422		2.31	5.0E-43	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
509	9781	18887	2.47	6.0E-43	AA382780.1	EST_HUMAN	EST86033 Testis 1 Homo sapiens cDNA 5' end
2788	12039	21161	1.47	5.0E-43	AV732578.1	EST_HUMAN	AV732578 HTF Homo sapiens cDNA clone HTFANC08 5'
6888	16080	26557	5	5.0E-43	AA465288.1	EST_HUMAN	sa33d08.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:815055 5'
7187	16384	25844	2.95	5.0E-43	A173244.1	EST_HUMAN	o062c10.x5 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1568810 3' similar to TR:P90591 P90591 PV14 GENE. ;
7348	16584	28053	5.41	5.0E-43	AW863007.1	EST_HUMAN	MR2-SNO007:280400-004-c02 SNO007 Homo sapiens cDNA
7642	16747	26241	1.88	5.0E-43	W28011.1	EST_HUMAN	5584 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
7883	16428	25816	2.28	5.0E-43	X15804.1	NT	Human mRNA for alpha-actinin Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
980	11943	19387	9.87	4.0E-43	AF003528.1	NT	Homo sapiens protocadherin beta 6 (PCDHB6), mRNA
6131	15316		2.02	4.0E-43	11416703	NT	q78a02.x1 NCI_CGAP_K1d3 Homo sapiens cDNA clone IMAGE:1885354 3' similar to contains MER10.13 MER10 repetitive element ;
6519	15715	25180	4.94	4.0E-43	A1244341.1	EST_HUMAN	q78a02.x1 NCI_CGAP_K1d3 Homo sapiens cDNA clone IMAGE:1885354 3' similar to contains MER10.13 MER10 repetitive element ;
6518	15715	25181	4.94	4.0E-43	A1244341.1	EST_HUMAN	ycf2h10.r1 Soares fetal liver spleen 1N1FLS Homo sapiens cDNA clone IMAGE:113827 5'
7852	17042	26556	1.73	4.0E-43	T77380.1	EST_HUMAN	yp08b05.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:31383 5' similar to contains MER10 repetitive element ;
8438	17502		3.09	4.0E-43	R20950.1	EST_HUMAN	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
1221	10439		2.8	3.0E-43	AF223391.1	NT	

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Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1870	10883	20087	4.5	3.0E-43	X87869.1	NT	H. sapiens gene encoding La autoantigen
3547	12770	21888	1.47	3.0E-43	S69002.1	NT	AML1-EVI-1=AML1-EVI-1 fusion protein (rearranged translocation) [human, leukemic cell line SKH1, mRNA Mutant, 5938 nt]
4277	13480	22578	1.1	3.0E-43	AA548154.1	EST_HUMAN	nk5508.s1 NCL CGAP_P77 Homo sapiens cDNA clone IMAGE:1017419
5975	15189	24808	4.19	3.0E-43	U65487.1	NT	Human ribosomal RNA upstream binding transcription factor (UBTF) gene, partial cds
6513	15708		8.19	3.0E-43	AA458824.1	EST_HUMAN	sa88f11.s1 Stratagene fetal retina 837202 Homo sapiens cDNA clone IMAGE:838413 3' similar to contains THR12 THR repetitive element;
6724	15919	25378	2.48	3.0E-43	7661721	NT	Homo sapiens hypothetical protein (HSA011916), mRNA
8218	17347	26887	2.04	3.0E-43	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
188	9467		10.09	2.0E-43	AI190764.1	EST_HUMAN	qd81c09.x1 Soares_NHT Homo sapiens cDNA clone IMAGE:1733968 3' similar to contains PTR7.3
6563	16769		7.03	2.0E-43	U43701.1	NT	PTR7 PTR7 repetitive element;
7792	18948		8.09	2.0E-43	T03007.1	EST_HUMAN	Human ribosomal protein L23a mRNA, complete cds
1627	10840	20018	4.61	1.0E-43	AF154836.1	NT	FB1G5 Fetal brain, Stratagene Homo sapiens cDNA clone FB1G5.3 and similar to LINE-1
1627	10840	20017	4.61	1.0E-43	AF154836.1	NT	Homo sapiens Ras-like GTP-binding protein (RAB27A) gene, exons 1b and 2
1680	10882	20079	2.93	1.0E-43	AL163284.2	NT	Homo sapiens Ras-like GTP-binding protein (RAB27A) gene, exons 1b and 2
2683	11865	21077	3.71	1.0E-43	BF348283.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C084
5939	15155	24588	7.68	1.0E-43	4507168	NT	602022313F1 NCL CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4157688 5'
5939	15155	24587	7.68	1.0E-43	4507168	NT	Homo sapiens Sp4 transcription factor (SP4) mRNA
6071	14518	23580	1.78	1.0E-43	R18751.1	EST_HUMAN	Homo sapiens Sp4 transcription factor (SP4) mRNA
6486	15683		2.88	1.0E-43	AF198490.1	NT	y940e01.r1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:34732 5' similar to SP-BD38_MOUSE P28658 BRAIN PROTEIN DN38.
6730	15925	25384	39.18	1.0E-43	AW863878.1	EST_HUMAN	Homo sapiens 8q22.1 region and MTG8 (CBFA2T1) gene, partial cds
7535	16740	26231	7.71	1.0E-43	AI894881.1	EST_HUMAN	EST1375749 IMAGE sequences, MAGH Homo sapiens cDNA
7805	17120	26651	3.87	1.0E-43	11424378	NT	wr87h01.x1 NCL CGAP_Kd11 Homo sapiens cDNA clone IMAGE:2494705 3'
8379	17404		3.42	1.0E-43	AL137884.1	EST_HUMAN	Homo sapiens calcium channel, voltage-dependent, alpha 1E subunit (CACNA1E), mRNA
8685	17654	23880	2.23	1.0E-43	AI875416.1	EST_HUMAN	DKFZp781D1015_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp781D1015 5'
8914	17802	23927	3.14	9.0E-44	11418322	NT	w89804.x1 NCL CGAP_P728 Homo sapiens cDNA clone IMAGE:2313775 3'
900	10135	19287	7.58	8.0E-44	AI222885.1	EST_HUMAN	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA
900	10135	19288	7.56	8.0E-44	AI222885.1	EST_HUMAN	qh23g01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1845552 3'
7723	16922	26431	3.57	8.0E-44	Y10498.2	NT	qh23g01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1845552 3'
8185	17317	26881	2.01	8.0E-44	L29139.1	NT	Homo sapiens mRNA for thymidine kinase, partial
8638	17625	23974	3.72	8.0E-44	11527389	NT	Homo sapiens myosin mRNA, partial cds
8878	17680	23884	1.44	8.0E-44	11418088	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide F (POLR2F), mRNA
							Homo sapiens putative nuclear protein (HRIHFB2122), mRNA

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Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9048	18142	23749	2.3	8.0E-44	11418099	NT	Homo sapiens protein kinase C, alpha binding protein (PRKCABP), mRNA
866	9911		0.83	7.0E-44	R08035.1	EST_HUMAN	ye89e01.1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:124920 5'
2200	11397	20621	1.86	7.0E-44	6031888	NT	Homo sapiens LIM domain-containing preferred translocation partner in lipoma (LPP) mRNA
2621	12159	21283	1.71	7.0E-44	AF048729.1	NT	Homo sapiens minisatellite ms32 repeat region
2621	12159	21284	1.71	7.0E-44	AF048729.1	NT	Homo sapiens minisatellite ms32 repeat region
3844	13081	22175	2.85	7.0E-44	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4227	13430	22522	1.29	7.0E-44	AF231819.1	NT	Homo sapiens chromosome 21 unknown mRNA
4227	13430	22523	1.29	7.0E-44	AF231819.1	NT	Homo sapiens chromosome 21 unknown mRNA
6524	15720	25184	4.61	7.0E-44	AU168839.1	EST_HUMAN	AU158839 Y78AA1 Homo sapiens cDNA clone Y78AA1000498 3'
8246	17376	26909	3.42	8.0E-44	AW654050.1	EST_HUMAN	EST368120 MAGE resequences, MAGEC Homo sapiens cDNA
308	9581		2.5	5.0E-44	AJ288880.1	NT	Homo sapiens KIAA0851 gene (partial), X13 gene and LZTFL1 gene
337	9805		2.23	5.0E-44	AJ288880.1	NT	Homo sapiens KIAA0851 gene (partial), X13 gene and LZTFL1 gene
6424	15621	25085	4.3	5.0E-44	AI568523.1	EST_HUMAN	tr40d02.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2170083 3' similar to contains OFR.11
6872	16084		2.33	5.0E-44	AU124571.1	EST_HUMAN	OFR OFR repetitive element;
3392	12819	21750	2.73	4.0E-44	AL163303.2	NT	AU124571 NT2RM4 Homo sapiens cDNA clone NT2RM4000218 5'
5039	14223		1.73	4.0E-44	AI435225.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C103
7789	10883	28497	3.15	4.0E-44	U90878.1	NT	H11402.x1 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2130147 3'
1766	10887		1.21	3.0E-44	6812477	NT	Homo sapiens carboxyl terminal LIM domain protein (GLIM1) mRNA, complete cds
2497	11686	20805	3.27	3.0E-44	BE880628.1	EST_HUMAN	Homo sapiens karyopherin alpha 6 (Importin alpha 7) (KPNA6), mRNA
3063	12289	21423	6.4	3.0E-44	AA168851.1	EST_HUMAN	601491528F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3893839 5'
1056	10282	19432	2.91	2.0E-44	4826885	NT	zp18505.1 Stratagene fetal retina 837202 Homo sapiens cDNA clone IMAGE:609777 5'
1056	10282	19433	2.91	2.0E-44	4826885	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 1 (DDX1) mRNA
1216	10433	19589	5.8	2.0E-44	5803200	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 1 (DDX1) mRNA
1216	10433	19590	5.8	2.0E-44	5803200	NT	Homo sapiens transmembrane trafficking protein (TMP21), mRNA
1319	10534	19698	2.92	2.0E-44	AF133588.1	NT	Homo sapiens transmembrane trafficking protein (TMP21), mRNA
1376	10590	19756	1.34	2.0E-44	BE465325.1	EST_HUMAN	Homo sapiens RAB38 (RAB38) mRNA, complete cds
2120	11319	20537	1.8	2.0E-44	AF070851.1	NT	hw1406.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182838 3' similar to SW:OXYB_HUMAN
2571	11758		1.58	2.0E-44	5901933	NT	P22059 OXYSTEROL-BINDING PROTEIN.;
3447	12872	21807	1.06	2.0E-44	D87875.1	NT	Homo sapiens tissue-type bone marrow zinc finger protein 4 mRNA, complete cds
4567	13761	22857	1.87	2.0E-44	AW864378.1	EST_HUMAN	Homo sapiens adaptor-related protein complex 4, sigma 1 subunit (CLAPS4), mRNA
6256	15437	24876	4.1	2.0E-44	11419228	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
6256	15437	24877	4.1	2.0E-44	11419228	NT	PM4-SN0016-120500-003-404 SN0016 Homo sapiens cDNA
							Homo sapiens glutamate receptor, metabotropic 3 (GRM3), mRNA
							Homo sapiens glutamate receptor, metabotropic 3 (GRM3), mRNA

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8283	17388		1.56	2.0E-44	BE244902.1	EST_HUMAN	TCBAP1E2785 Padiatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TC8A Homo sapiens cDNA clone TCBAP2795
54	9351	18468	5.21	1.0E-44	7657334	NT	Homo sapiens MisshepanNIK-related kinase (MINK), mRNA
54	9351	18407	5.21	1.0E-44	7657334	NT	Homo sapiens MisshepanNIK-related kinase (MINK), mRNA
587	9835	18954	2.08	1.0E-44	AW853132.1	EST_HUMAN	RC1-CT0249-030300-028-h12 CT0249 Homo sapiens cDNA
1206	10424		1.61	1.0E-44	AW694803.1	EST_HUMAN	RC1-BN0039-110300-012-501 BN0039 Homo sapiens cDNA
1553	10767		8.02	1.0E-44	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2191	11388	20810	4.39	1.0E-44	AA434554.1	EST_HUMAN	z653d02.r1 Soares_total_fetus_Nb2HF8_6w Homo sapiens cDNA clone IMAGE:773763 5' similar to contains THR.13 THR repetitive element;
2191	11388	20811	4.39	1.0E-44	AA434554.1	EST_HUMAN	z653d02.r1 Soares_total_fetus_Nb2HF8_6w Homo sapiens cDNA clone IMAGE:773763 5' similar to contains THR.13 THR repetitive element;
2715	11884	21111	1.46	1.0E-44	AF198779.1	NT	Homo sapiens transcription factor IGHM enhancer 3, JM1.1 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel $\alpha 2$
3708	12928		4.68	1.0E-44	AA455869.1	EST_HUMAN	ae01c09.s1 Soares_NhiMPu_S1 Homo sapiens cDNA clone IMAGE:811894 3'
7684	16788		11.94	1.0E-44	AV714808.1	EST_HUMAN	AV714808 DCB Homo sapiens cDNA clone DCBBYE03 5'
8061	17188	26735	4.59	1.0E-44	10092884	NT	Homo sapiens Sushi domain (SCR repeat) containing (BK65A6.2), mRNA
8117	17251	26791	3.02	1.0E-44	AW846987.1	EST_HUMAN	RC1-CT0188-150989-011-C08 CT0188 Homo sapiens cDNA
8117	17251	26792	3.02	1.0E-44	AW846987.1	EST_HUMAN	RC1-CT0188-150989-011-C08 CT0188 Homo sapiens cDNA
4576	13770	22885	1.21	9.0E-45	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
4576	13770	22888	1.21	9.0E-45	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
2490	11880	20897	16.54	8.0E-45	5174718	NT	Homo sapiens TRK-fused gene (NOTE: non-standard symbol and name) (TFG) mRNA
5112	14282	23378	7.96	8.0E-45	5174718	NT	Homo sapiens TRK-fused gene (NOTE: non-standard symbol and name) (TFG) mRNA
2811	12148		1.44	7.0E-45	AL160131.1	NT	Novel human gene mapping to chromosome 22
3958	13171		7.02	6.0E-45	AW157670.1	EST_HUMAN	au83h07.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782809 3' similar to SW:R13A_HUMAN P40429 60S RIBOSOMAL PROTEIN L13A;
9008	16340		1.27	6.0E-45	11418213	NT	Homo sapiens ADP-ribosylation factor GTPase activating protein 1 (ARFGAP1), mRNA
902	10137		1.9	5.0E-45	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
1971	11175	20381	4.35	5.0E-45	BF333627.1	EST_HUMAN	CMA-CN0044-180200-515-01 CN0044 Homo sapiens cDNA
3176	12411	21547	2	5.0E-45	AI523768.1	EST_HUMAN	tg94f07.x1 NCJ CGAP CLL1 Homo sapiens cDNA clone IMAGE:2116453 3' similar to SW:PAX1_MOUSE P06084 PAIRED BOX PROTEIN PAX-1;
5445	14871	23829	8.89	5.0E-45	AA397781.1	EST_HUMAN	zt72d03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:727677 3' similar to contains element TAR1 repetitive element;
6778	15973	25430	2.31	5.0E-45	4759223	NT	Homo sapiens programmed cell death 6 (PDCD5), mRNA

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8192	17324	26867	2.63	5.0E-45	8923688	NT	Homo sapiens golgin-like protein (GLP), mRNA
1152	10374	18525	11.82	4.0E-45	X95826.1	NT	H. sapiens ART4 gene
2255	11450	20668	3.38	4.0E-45	BE265822.1	EST_HUMAN	601194440F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3538425 5'
8281	17388		1.88	4.0E-45	BE044076.1	EST_HUMAN	h038h04.x1 NCI_CGAP_UH Homo sapiens cDNA clone IMAGE:3039511 3' similar to contains MER28.b3 MER29 repetitive element;
8298	18285	23684	2.19	4.0E-45	11435947	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
8907	17788		2.18	4.0E-45	BF976077.1	EST_HUMAN	602084052F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4248253 5'
3305	12535		0.97	3.0E-45	T71480.1	EST_HUMAN	y035107.r1 Soares fetal liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:110245 5'
4063	12535		0.95	3.0E-45	T71480.1	EST_HUMAN	y035107.r1 Soares fetal liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:110245 5'
5244	14417		1.88	3.0E-45	AJ288473.1	NT	Homo sapiens mRNA for TRAF and TNF receptor associated protein (trap gene)
6713	15008	25367	2.67	3.0E-45	4758451	NT	Homo sapiens golgi autoantigen, golgin subfamily a, 2 (GOLGA2) mRNA
7168	18346	26824	16.25	3.0E-45	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
7168	18345	26825	16.25	3.0E-45	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
9127	18274		1.98	3.0E-45	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
2468	11657		1.59	2.0E-45	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
2898	12234	21384	0.98	2.0E-45	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
5886	15103	24514	5.4	2.0E-45	L01865.1	NT	Human eosinophil Charcot-Leyden crystal (CLC) protein (lysophospholipase) gene, promoter and exon 1
7381	18077	28084	21.38	2.0E-45	BE834360.1	EST_HUMAN	MRO-HT0923-180800-201-802 HT0923 Homo sapiens cDNA
7732	18229	28437	4.48	2.0E-45	AA458770.1	EST_HUMAN	aa87112.r1 Strabagene fetal retina 837202 Homo sapiens cDNA clone IMAGE:838319 5' similar to
8037	17173	28712	2.46	2.0E-45	AW270280.1	EST_HUMAN	TR.G11445589 G11445589 R-SLY1.;
8037	17173	28713	2.46	2.0E-45	AW270280.1	EST_HUMAN	xp72a03.x1 NCI_CGAP_Ov40 Homo sapiens cDNA clone IMAGE:2745888 3'
9169	17884		2.8	2.0E-45	11418157	NT	xp72a03.x1 NCI_CGAP_Ov40 Homo sapiens cDNA clone IMAGE:2745888 3'
122	9888		3.43	1.0E-45	BE388655.1	EST_HUMAN	Homo sapiens calcium channel, voltage-dependent, alpha 11 subunit (CACNA11), mRNA
416	8668		3.82	1.0E-45	BE388655.1	EST_HUMAN	Homo sapiens cDNA clone IMAGE:3606183 5'
479	9731	18865	0.98	1.0E-45	4506412	NT	601284360F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3606183 5'
1182	10403	19557	1.87	1.0E-45	7857280	NT	Homo sapiens RAP1A, member of RAS oncogene family (RAP1A), mRNA
3087	12303	21428	12.47	1.0E-45	U32188.1	NT	Homo sapiens Langerhans cell specific c-type lectin (LANGERIN), mRNA
3467	12682	21828	0.69	1.0E-45	8659558	NT	Human pro-a2 chain of collagen type XI (COL11A2) gene, complete cds
4473	13871	22782	8.02	1.0E-45	BE388633.1	EST_HUMAN	Homo sapiens chromosome 21 open reading frame 1 (C21orf4), mRNA
8814	16008	25472	4.31	1.0E-45	BE687843.1	EST_HUMAN	601289116F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3618803 5'
8502	17541	24029	4.45	1.0E-45	11418099	NT	601511228F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3612535 5'
8898	17884		7.85	1.0E-45	11528281	NT	Homo sapiens protein kinase C, alpha binding protein (PRKCABP), mRNA
							Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA

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Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8702	17687		8.94	1.0E-45	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
8133	17942	23881	2.76	1.0E-45	11418157	NT	Homo sapiens calcium channel, voltage-dependent, alpha 1I subunit (CACNA1I), mRNA
6864	16659		11.57	9.0E-48	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
7210	16387	25869	8.54	9.0E-48	AW246964.1	EST_HUMAN	2822449.5 prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822449 5'
2405	11597	20817	20.18	9.0E-48	AI433261.1	EST_HUMAN	132708.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2132189 3' similar to gb:J00314_ma2
2405	11597	20818	20.16	9.0E-48	AI433261.1	EST_HUMAN	TUBULIN BETA-1 CHAIN (HUMAN);
6482	15678		5.81	9.0E-48	BE187244.1	EST_HUMAN	132708.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2132189 3' similar to gb:J00314_ma2
8185	17287		3.37	9.0E-48	11418729	NT	TUBULIN BETA-1 CHAIN (HUMAN);
4578	13772		10.04	7.0E-48	BE386165.1	EST_HUMAN	RC5-HT0506-280200-012-C12 HT0506 Homo sapiens cDNA
4820	14009		1.25	7.0E-48	BE084388.1	EST_HUMAN	Homo sapiens ribosomal protein L44 (RPL44), mRNA
5692	14802	24285	3.93	7.0E-48	8822708	NT	601277282F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3818119 6'
8832	17743		1.33	7.0E-48	AL163249.2	NT	RC4-BT0310-110300-015-f10 BT0310 Homo sapiens cDNA
2711	11880	21107	6.12	9.0E-48	AI884381.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ10847 (FLJ10847), mRNA
2711	11890	21108	6.12	9.0E-48	AI884381.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C048
5724	14942	24338	9.61	9.0E-48	AI635448.1	EST_HUMAN	wm31108.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2437575 3' similar to contains MER19.12
7828	18404		2.87	9.0E-48	BE784971.1	EST_HUMAN	MER19 repetitive element ;
209	9489		8.85	5.0E-48	AL163210.2	NT	wm31108.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2437575 3' similar to contains MER19.12
3502	12726	21862	1.86	5.0E-48	BE677194.1	EST_HUMAN	MER19 repetitive element ;
3502	12726	21863	1.88	5.0E-48	BE677194.1	EST_HUMAN	ts58h10.x1 NCI_CGAP_Kid8 Homo sapiens cDNA clone IMAGE:2232835 3' similar to TR:O60363 O60363
5877	15191	24608	1.87	5.0E-48	BF590442.1	EST_HUMAN	SA GENE. ;
6059	15249	24671	4.32	5.0E-48	BF347226.1	EST_HUMAN	601478408F1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:3880985 6'
647	9893		2.39	4.0E-48	AA601143.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C010
1878	10891	20077	8.19	4.0E-48	AW770544.1	EST_HUMAN	7d81g01.x1 Lupeld_dorsal_root_ganglion Homo sapiens cDNA clone IMAGE:3279408 3'
							7d81g01.x1 Lupeld_dorsal_root_ganglion Homo sapiens cDNA clone IMAGE:3279408 3'
							naa3807.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3298757 3' similar to TR:O75202
							O75202 HOMOLOG OF RAT KIDNEY-SPECIFIC ;
							602021164F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4156870 5'
							na54608.s1 NCI_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1104520 3' similar to gb:X53741_ma1
							FIBULIN-1, ISOFORM A PRECURSOR (HUMAN);
							1186c03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3008936 3' similar to gb:X14008_ma1
							LYSOZYME C PRECURSOR (HUMAN); contains element MER37 repetitive element ;

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1679	10891	20078	8.19	4.0E-48	AW770544.1	EST_HUMAN	h186c03.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3008838 3' similar to gb:X14008_ma1 LYSOZYME C PRECURSOR (HUMAN); contains element MER37 repetitive element;
2696	11878	21080	18.7	4.0E-48	MT18048.1	NT	Human endogenous retrovirus RTVL-H2
5411	14639	23788	2.3	4.0E-48	M36852.1	NT	Human Ig germline gamma-3 heavy-chain gene V region, partial cds
5411	14639	23789	2.3	4.0E-48	M36852.1	NT	Human Ig germline gamma-3 heavy-chain gene V region, partial cds
6656	17828	23807	1.88	4.0E-48	AB002059.1	NT	Homo sapiens DNA for Human P2XM1, complete cds
2250	11445	20687	1.82	3.0E-48	7857203	NT	Homo sapiens addic 82 kDa protein mRNA (HSU16562), mRNA
2392	11585	20803	2.31	3.0E-48	AF160212.1	NT	Homo sapiens VAMP-associated 33 kDa protein mRNA, complete cds
6701	15998	25357	6.58	3.0E-48	AI831482.1	EST_HUMAN	wj49c04.x1 NCL_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2408150 3' similar to contains THR.b2 THR repetitive element;
8105	17239	26777	2.69	3.0E-48	D31765.1	NT	Human mRNA for KIAA0061 gene, partial cds
847	10084	18243	8.45	2.0E-48	AA48846.1	EST_HUMAN	ne06a09.s1 NCL_CGAP_Cc3 Homo sapiens cDNA clone IMAGE:880408 3' similar to contains THR.b2 THR repetitive element;
1544	10758		1.74	2.0E-48	AA678248.1	EST_HUMAN	Z27a11.s1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:431898 3'
1618	10831	20008	4.27	2.0E-48	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
4694	14181	23270	1.44	2.0E-48	AA398288.1	EST_HUMAN	z159a02.r1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:726850 5' similar to SW:RSP1_MOUSE Q01730 RSP-1 PROTEIN;
6285	15488	24907	7.31	2.0E-48	8910569	NT	Mus musculus sperm tail associated protein (Slap), mRNA
8488	15685		4.32	2.0E-48	BE889151.1	EST_HUMAN	601445137F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3848287 5'
7788	16991		1.77	2.0E-48	7857233	NT	Homo sapiens small acidic protein (IMAGE145052), mRNA
8422	18241		2	2.0E-48	BF028854.1	EST_HUMAN	601785225F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3987328 5'
8689	16135		1.33	2.0E-48	H48391.1	EST_HUMAN	y32d01.r1 Soares fetal liver spleen_1NFLS Homo sapiens cDNA clone IMAGE:208977 5'
8727	17878		1.27	2.0E-48	AA001788.1	EST_HUMAN	zh84f12.r1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:428015 5'
8931	18127	23812	6.9	2.0E-48	AW277214.1	EST_HUMAN	xq78h03.x1 NCL_CGAP_Lu34 Homo sapiens cDNA clone IMAGE:2756789 3'
1240	10456	18615	7.9	1.0E-48	4502694	NT	Homo sapiens cell division cycle 10 (homologous to CDC10 of S. cerevisiae) (CDC10) mRNA
2248	11441	20665	4.25	1.0E-48	AW978518.1	EST_HUMAN	EST380625 MAGE resequences, MAGP Homo sapiens cDNA
2384	11557	20779	3.53	1.0E-48	H97330.1	EST_HUMAN	EST48b095 WATM1 Homo sapiens cDNA clone 48b095
3216	12450	21582	4.7	1.0E-48	AA631812.1	EST_HUMAN	np78b02.s1 NCL_CGAP_P2 Homo sapiens cDNA clone IMAGE:1132385 similar to gb:X76717 H.sapiens MT-11 mRNA. (HUMAN);
4880	14078		2.9	1.0E-48	AB023197.1	NT	Homo sapiens mRNA for KIAA0980 protein, partial cds
5335	14769	24128	5.85	1.0E-48	BF194707.1	EST_HUMAN	7a2b01.x1 NCL_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3843705 3'
5643	18080	24250	5.13	1.0E-48	8923762	NT	Homo sapiens centaurin-alpha 2 protein (HSA272195), mRNA

Table 4

Single Exon Probes Expressed In HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5843	18060	24251	5.13	1.0E-46	8923762	NT	Homo sapiens centaurin-alpha 2 protein (HSA272195), mRNA
7439	14759	24126	4.91	1.0E-46	BF184707.1	EST_HUMAN	7692601.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3843705 3'
8451	17508	24017	1.5	1.0E-46	BF531102.1	EST_HUMAN	602072284F1 NCI_CGAP_Bim87 Homo sapiens cDNA clone IMAGE:4215398 5'
8451	17508	24018	1.5	1.0E-46	BF531102.1	EST_HUMAN	602072284F1 NCI_CGAP_Bim87 Homo sapiens cDNA clone IMAGE:4215398 5'
9244	18015		1.63	1.0E-46	AV715377.1	EST_HUMAN	AV715377 DCB Homo sapiens cDNA clone DCBAIE03 5'
775	10014		4.91	9.0E-47	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
4952	14139	23233	2.1	9.0E-47	AW770928.1	EST_HUMAN	h83604.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3009534 3' similar to TR:O75703 O75703
8978	18228	23699	1.93	9.0E-47	11417968	NT	HYPOPHYTHETICAL 12.4 KD PROTEIN. ;
1777	10887	20179	44.01	8.0E-47	Y18538.1	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
1777	10887	20180	44.01	8.0E-47	Y18538.1	NT	Homo sapiens HLA-C gene, exon 5, individual 19323
						NT	Homo sapiens HLA-C gene, exon 5, individual 19323
2678	11858	21073	1.3	8.0E-47	5453955	NT	Homo sapiens protein phosphatase 2, regulatory subunit B (B56), epsilon isoform (PPP2R5E) mRNA
2889	12228	21360	2.14	8.0E-47	AJ228043.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
2613	11702	20917	3.72	6.0E-47	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
6847	16036	25500	5.32	6.0E-47	A1895189.1	EST_HUMAN	ts28h02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2286859 3'
5918	15133	24542	5.84	5.0E-47	11423972	NT	Homo sapiens CDC37 (cell division cycle 37, S. cerevisiae, homolog) (CDC37), mRNA
7375	18591		8.37	5.0E-47	M78560.1	EST_HUMAN	EST00738 Fetal brain, Stratagene (cat#838208) Homo sapiens cDNA clone HFBCE07
1404	10817	18783	4.3	4.0E-47	4557556	NT	Homo sapiens E1A binding protein p300 (EP300) mRNA
8151	17283		6.74	4.0E-47	AW515509.1	EST_HUMAN	xs65607.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2848597 3' similar to SW:INT8_MOUSE
551	9802	18928	2.54	3.0E-47	BE907634.1	EST_HUMAN	Q64252 VIRAL INTEGRATION SITE PROTEIN INT-6. (1):
551	9802	18928	2.54	3.0E-47	BE907634.1	EST_HUMAN	601497639F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3889721 5'
828	10086	18219	7.18	3.0E-47	N57483.1	EST_HUMAN	601497639F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3889721 5'
953	10188	18342	10.82	3.0E-47	AL163284.2	NT	y54604.s1 Soares_multiple sclerosis_2NIB-MSP Homo sapiens cDNA clone IMAGE:277327 3'
3273	12506	21637	0.76	3.0E-47	4504116	NT	Homo sapiens chromosome 21 segment HS21C084
3943	13150		6.42	3.0E-47	U83181.1	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
4358	13558	22853	1.97	3.0E-47	M12959.1	NT	Homo sapiens nuclear dual-specificity phosphatase (SDF1) mRNA, partial cds
5882	14885	24273	4.5	3.0E-47	AW408800.1	EST_HUMAN	Human T-cell receptor active alpha-chain mRNA from JM cell line, complete cds
5882	14885	24274	4.5	3.0E-47	AW408800.1	EST_HUMAN	UI-HF-BM0-act-d-07-0-J1.1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3083205 5'
5907	15124		1.87	3.0E-47	AI222413.1	EST_HUMAN	UI-HF-BM0-act-d-07-0-J1.1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3083205 5'
150	9432	18568	1.51	2.0E-47	4505318	NT	qh04607.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843716 3'
976	10207	19361	2.74	2.0E-47	AL163209.2	NT	Homo sapiens myosin phosphatase, target subunit 2 (MYPT2), mRNA
976	10207	19362	2.74	2.0E-47	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009

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Table 4

Single Exon Probes Expressed In HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1573	10786	18981	1.75	2.0E-47	7662109	NT	Homo sapiens KIAA0428 gene product (KIAA0428), mRNA
1852	10668	20048	4.28	2.0E-47	AA524514.1	EST_HUMAN	ng43h12.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:8937807 3'
4340	13542	22833	2.14	2.0E-47	4504888	NT	Homo sapiens ring finger protein (C3HC4 type) 8 (RNF8), mRNA
4378	13580	22879	1.98	2.0E-47	AA569592.1	EST_HUMAN	nt23g07.s1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:914852
4378	13580	22880	1.98	2.0E-47	AA569592.1	EST_HUMAN	nt23g07.s1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:914852
4508	13704	22798	2.32	2.0E-47	5174848	NT	Homo sapiens RevRex activation domain binding protein-related (RAB-R) mRNA
4827	14018	23115	1.05	2.0E-47	AW985168.1	EST_HUMAN	EST377239 IMAGE resequences, MAGI Homo sapiens cDNA
5187	14348		0.78	2.0E-47	AID41128.1	EST_HUMAN	ov61h03.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1841845 3'
6447	15644	25111	3	2.0E-47	D87875.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
6447	15644	25112	3	2.0E-47	D87875.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
8488	18272	23879	2.83	2.0E-47	R42423.1	EST_HUMAN	yf82e08.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:29868 3' similar to contains OFR repetitive element
1408	10622	18786	6.74	1.0E-47	AI333428.1	EST_HUMAN	qp99h03.x1 Soares_fetal_lung_NH19W Homo sapiens cDNA clone IMAGE:1931189 3'
3812	13030	22139	0.92	1.0E-47	BE280477.1	EST_HUMAN	601155321F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138893 5'
3812	13030	22140	0.92	1.0E-47	BE280477.1	EST_HUMAN	601155321F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138893 5'
5108	14288	23371	2.65	1.0E-47	AW813906.1	EST_HUMAN	RC3-ST0197-130400-017-h02 ST0197 Homo sapiens cDNA
6102	15198	24614	8.41	1.0E-47	A1880886.1	EST_HUMAN	at19e06.x1 Barabedorta HPLRB8 Homo sapiens cDNA clone IMAGE:2355586 3' similar to gb:M22905
6738	15833		6.84	1.0E-47	AW884848.1	EST_HUMAN	RAS-RELATED PROTEIN RAP-1A (HUMAN); h184a11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2878972 3' similar to gb:M26328 KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN); Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
1691	10804	19879	4.07	9.0E-48	AF223391.1	NT	CX42-MT0100-310700-290-f05 MT0100 Homo sapiens cDNA
3531	12754	21887	0.75	9.0E-48	BF359947.1	EST_HUMAN	601310479F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3832083 5'
7877	16878	26381	3.33	9.0E-48	BE393813.1	EST_HUMAN	Homo sapiens aminocyclase 1 (ACY1), mRNA
1257	10473		2.18	8.0E-48	4501800	NT	Homo sapiens aminocyclase 1 (ACY1), mRNA
1258	10473		1.89	8.0E-48	4501900	NT	Homo sapiens aminocyclase 1 (ACY1), mRNA
3100	12338	21463	3.19	8.0E-48	AW768477.1	EST_HUMAN	h181b03.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:3001133 3' similar to gb:X84707 BREAST BASIC CONSERVED PROTEIN 1 (HUMAN);
3100	12338	21464	3.19	8.0E-48	AW768477.1	EST_HUMAN	h181b03.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:3001133 3' similar to gb:X84707 BREAST BASIC CONSERVED PROTEIN 1 (HUMAN);
487	9750		1.35	7.0E-48	AB033035.1	NT	Homo sapiens mRNA for KIAA1209 protein, partial cds
488	9750		17.38	7.0E-48	AB033035.1	NT	Homo sapiens mRNA for KIAA1209 protein, partial cds
1488	10701	19875	1.1	7.0E-48	6912719	NT	Homo sapiens toubled-like kinase 1 (TLK1), mRNA
1614	10827	20002	4.69	7.0E-48	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA

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5903	15120	24531	24.65	7.0E-48	11418831	NT	Homo sapiens histidyl-tRNA synthetase (HARS), mRNA
3576	12789	21925	0.7	8.0E-48	A1781111.1	EST_HUMAN	wf68h03.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2389613 3'
6832	16125	25581	2.22	8.0E-48	11427428	NT	Homo sapiens hypothetical protein FLJ11008 (FLJ11008), mRNA
6888	16168	25638	3.11	8.0E-48	AA189080.1	EST_HUMAN	zq45b08.s1 Stratiene hNT neuron (#837233) Homo sapiens cDNA clone IMAGE:632627 3' similar to contains Alu repetitive element
3280	14466	21642	1.58	5.0E-48	4828891	NT	Homo sapiens phosphodiesterase 1A, calmodulin-dependent (PDE1A), mRNA
7529	18734	26224	4.02	4.0E-48	A1820420.1	EST_HUMAN	b47a02.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2254154 3'
1391	10605	19769	1.14	3.0E-48	AV680884.1	EST_HUMAN	AV680884 GKC Homo sapiens cDNA clone GKORE12 5'
1945	11149	20350	24.98	3.0E-48	4885170	NT	Homo sapiens chromosome X open reading frame 8 (CXORF8), mRNA
1945	11149	20351	24.98	3.0E-48	4885170	NT	Homo sapiens chromosome X open reading frame 8 (CXORF8), mRNA
3308	12623	21754	1	3.0E-48	AF172453.1	NT	Homo sapiens op10 growth factor receptor mRNA, complete cds
3609	12830	21851	0.78	3.0E-48	AW684531.1	EST_HUMAN	h1412.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2972255 3' similar to SW:DCRB_HUMAN
4233	13436		0.69	3.0E-48	AA009541.1	EST_HUMAN	P58555 DOWN SYNDROME CRITICAL REGION PROTEIN B.;
5611	14835	24210	2.35	3.0E-48	BE084571.1	EST_HUMAN	z04g03.r1 Soares fetal liver spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:428844 5'
7451	16859	26148	10.07	3.0E-48	BF514170.1	EST_HUMAN	MR4-BT0657-060400-201-e10 BT0657 Homo sapiens cDNA
47	9344	18454	1.14	2.0E-48	AA631940.1	EST_HUMAN	UIH-BW1-anti-a-10-Q-JL.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3082267 3'
4529	13725	22822	1.18	2.0E-48	BE248085.1	EST_HUMAN	fmc7 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR17-28
6298	15479	24822	4.24	2.0E-48	AB040934.1	NT	TCBAP1D3842 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project-TCBA Homo sapiens cDNA clone TCBAP3842
6304	15485	24829	3.75	2.0E-48	11486238	NT	Homo sapiens mRNA for KIAA1501 protein, partial cds
8448	14481	23532	2.71	2.0E-48	AA485007.1	EST_HUMAN	Homo sapiens mRNA for KIAA1501 protein, partial cds
8769	18191	23760	1.52	2.0E-48	BE737154.1	EST_HUMAN	Homo sapiens v-rel avian reticuloendotheliosis viral oncogene homolog A (nuclear factor of kappa light polypeptide gene enhancer in B-cells 3 (p85)) (RELA), mRNA
58	9354	18471	3.21	1.0E-48	7706534	NT	z60cd03.r1 Soares ovary tumor NihOT Homo sapiens cDNA clone IMAGE:810052 5'
883	10119	19281	12.45	1.0E-48	4502168	NT	601305064F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3639782 5'
1063	10308	19459	2.62	1.0E-48	7657430	NT	Homo sapiens cisplatin resistance-associated overexpressed protein (LOC51747), mRNA
1083	10308	19460	2.62	1.0E-48	7657430	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
1303	10519	19678	3.47	1.0E-48	5032032	NT	Homo sapiens EBNA-2 co-activator (100KD) (p100), mRNA
1894	11091	20282	16.8	1.0E-48	AL163302.2	NT	Homo sapiens EBNA-2 co-activator (100KD) (p100), mRNA
3463	12688	21824	1.05	1.0E-48	AL163248.2	NT	Homo sapiens RNA binding motif protein 8 (RBM8) mRNA
5183	14342	23431	1.34	1.0E-48	M10976.1	NT	Homo sapiens chromosome 21 segment HS21C102
							Homo sapiens chromosome 21 segment HS21C048
							Human endogenous retroviral DNA (4-1), complete retroviral segment

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6189	16371	24812	2.4	1.0E-48	4755137	NT	Homo sapiens huntingtin (Huntington disease) (HD) mRNA
6843	18032	25497	6.77	1.0E-48	AB033071.1	NT	Homo sapiens mRNA for KIAA1245 protein, partial cds
8411	18218		1.41	1.0E-48	W20785.1	EST_HUMAN	15d6 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
1878	11179	20387	1.78	8.0E-49	AB028497.1	NT	Mus musculus MysPDZ mRNA for myosin containing PDZ domain, complete cds
5690	14910	24303	3.04	8.0E-49	10048417	NT	Mus musculus T-box 20 (Tbx20), mRNA
5690	14910	24304	3.04	8.0E-49	10048417	NT	Mus musculus T-box 20 (Tbx20), mRNA
8568	16754	26217	5.17	8.0E-49	U23850.1	NT	Human Inositol 1,4,5 triphosphate receptor type 1 mRNA, partial cds
7433	18642	26134	1.89	8.0E-49	AI823722.1	EST_HUMAN	ts38d12.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2230871 3' similar to contains Alu repetitive element; contains element PTR5 repetitive element;
136	9853	18788	2.75	7.0E-49	5729990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMCA4) mRNA
136	9853	18789	2.75	7.0E-49	5729990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMCA4) mRNA
398	9853	18788	2.43	7.0E-49	5729990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMCA4) mRNA
398	9853	18789	2.43	7.0E-49	5729990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMCA4) mRNA
399	9853	18788	3.58	7.0E-49	5729990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMCA4) mRNA
399	9853	18789	3.58	7.0E-49	5729990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMCA4) mRNA
1228	10448	19802	3.33	7.0E-49	AL163284.2	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMCA4) mRNA
5424	14651	23787	1.65	7.0E-49	AI807191.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C084
							Wf25h04.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2356683 3' similar to TR:054923
							O54923 RSEC15.;
202	9482	18615					ba55g05.x1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2800504 3' similar to gb:X17208 40S RIBOSOMAL PROTEIN S4 (HUMAN); gb:M20632 Mouse LLRep3 protein mRNA from a repetitive element, complete (MOUSE);
4093	13301	22401	52.05	8.0E-49	AW731740.1	EST_HUMAN	DKFZp761A138_s1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761A138 3'
7828	17020	26535	0.65	8.0E-49	AL162091.1	EST_HUMAN	UIH-B13-alo-a-09-Q-U1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068048 3'
8166	17288	26840	2.57	8.0E-49	AW452218.1	EST_HUMAN	EST77525 Pancreas tumor III Homo sapiens cDNA 5' end
8166	17288	26841	3.61	8.0E-49	AA388558.1	EST_HUMAN	EST77525 Pancreas tumor III Homo sapiens cDNA 5' end
8795	18104		4.03	8.0E-49	AA707597.1	EST_HUMAN	428c08.s1 Scores_fetal_liver_epiblen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:451894 3'
719	9861	19088	13.78	5.0E-49	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
719	9861	19089	13.78	5.0E-49	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1763	10974	20182	7.07	5.0E-49	AA172121.1	EST_HUMAN	zp28c07.r1 Stratiene neuroepithelium (8337231) Homo sapiens cDNA clone IMAGE:810880 5' similar to TR:G233226 G233228 RTVL-H PROTEIN; contains LTR7 LTR7 repetitive element;
2707	11888	21103	11.9	5.0E-49	U17714.1	NT	Homo sapiens putative tumor suppressor ST13 (ST13) mRNA, complete cds
3240	12474	21605	12.59	5.0E-49	11438355	NT	Homo sapiens similar to ribosomal protein S27 (metalloprotein 1) (H. sapiens) (LOC833362), mRNA

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531	9782	18904	35.35	4.0E-49	AW189533.1	EST_HUMAN	x08b01.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2875593 3' similar to WP:B0350.2B
8652	18333		3.3	4.0E-49	AA210788.1	EST_HUMAN	CE08703; x09005.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:982977 5'
8742	17687		3.88	4.0E-49	AF240788.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
567	9817	18939	1.66	3.0E-49	X88988.1	NT	H. sapiens mRNA for acetyl-CoA carboxylase
2810	11794		2.65	3.0E-49	AA016131.1	EST_HUMAN	z631c05.r1 Soares refina N2b4HR Homo sapiens cDNA clone IMAGE:380584 5' similar to contains L1.13 L1 repetitive element;
5004	14101	23281	2.37	3.0E-49	U46999.1	NT	Human type IV collagen (COL4A8) gene, exon 40
6259	15440	24879	10.15	3.0E-49	H39479.1	EST_HUMAN	EST125612 WATM1 Homo sapiens cDNA clone Z5e12
7849	17040	26557	2.43	3.0E-49	AA337561.1	EST_HUMAN	EST42572 Endometrial tumor Homo sapiens cDNA 5' end
667	9913		2.08	2.0E-49	BE165880.1	EST_HUMAN	MR3-HT0487-150200-113-p01 HT0487 Homo sapiens cDNA
3189	12423	21658	1.34	2.0E-49	N26448.1	EST_HUMAN	yx23d06.r1 Soares melanocyte 2Nblm Homo sapiens cDNA clone IMAGE:282571 5'
4823	14012	23111	0.61	2.0E-49	BF511946.1	EST_HUMAN	UHLB14-eps-4-02-0-U1.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3088538 3'
8494	16891		2.82	2.0E-49	M88033.1	EST_HUMAN	EST02858 Fetal brain, Strabagene (catf838206) Homo sapiens cDNA clone HFBCY60
909	10144		5.03	1.0E-49	BF035327.1	EST_HUMAN	601458531F1 NIH_MGC 68 Homo sapiens cDNA clone IMAGE:3862088 5'
1538	10751	19924	47.43	1.0E-49	4557987	NT	Homo sapiens keratin 18 (KRT18) mRNA
1770	10980	20170	4.77	1.0E-49	BE255218.1	EST_HUMAN	601115789F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3358273 5'
5283	14454		1.02	1.0E-49	7708703	NT	Homo sapiens putative G-protein coupled receptor (SH120), mRNA
5372	14801	23711	4.6	1.0E-49	BF131007.1	EST_HUMAN	601820053F1 NIH_MGC 58 Homo sapiens cDNA clone IMAGE:4052062 5'
6175	16367	24798	3.23	1.0E-49	BE398110.1	EST_HUMAN	601290330F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3620863 5'
6175	16357	24787	3.23	1.0E-49	BE398110.1	EST_HUMAN	601290330F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3620863 5'
6207	15388	24831	2.52	1.0E-49	N25884.1	EST_HUMAN	yw78g12.s1 Soares placenta_8tbd9weeks_2NblmP8tbd9W Homo sapiens cDNA clone IMAGE:258406 3' similar to gb:X65873 KINESIN HEAVY CHAIN (HUMAN);
6207	15388	24832	2.52	1.0E-49	N25884.1	EST_HUMAN	yw78g12.s1 Soares placenta_8tbd9weeks_2NblmP8tbd9W Homo sapiens cDNA clone IMAGE:258406 3' similar to gb:X65873 KINESIN HEAVY CHAIN (HUMAN);
7617	16820	26315	1.92	1.0E-49	AV751477.1	EST_HUMAN	AV751477 NPD Homo sapiens cDNA clone NPDAWE04 5'
7859	17048	26567	4	1.0E-49	11427368	NT	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 1 (BIG1), mRNA
8280	17387		1.68	1.0E-49	BE159343.1	EST_HUMAN	MRO-HT0407-010200-008-02 HT0407 Homo sapiens cDNA
8844	17629		2.64	1.0E-49	11418322	NT	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA
9187	18115		1.42	1.0E-49	11418123	NT	Homo sapiens KIAA0063 gene product (KIAA0063), mRNA
5018	14205		1.18	9.0E-50	AF101475.1	NT	Homo sapiens glycine N-methyltransferase (GNMT) gene, complete cds
173	9454	18585	2.7	8.0E-50	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
728	9968	19108	2	8.0E-50	X95097.2	NT	Homo sapiens mRNA for VIP receptor 2

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726	8868	19107	2	8.0E-50	XG5097.2	NT	Homo sapiens mRNA for VIP receptor 2
1734	10948	20128	3.93	8.0E-50	4501890	NT	Homo sapiens actinin, alpha 1 (ACTN1) mRNA
2444	11635	20855	1.38	8.0E-50	7706394	NT	Homo sapiens p47 (LOC51874), mRNA
2444	11635	20856	1.38	8.0E-50	7706394	NT	Homo sapiens p47 (LOC51874), mRNA
2680	11841	21055	2.33	8.0E-50	4828858	NT	Homo sapiens capping protein (actin filament) muscle Z-line, beta (CAPZB), mRNA
7947	17087	28816	1.88	8.0E-50	AA633487.1	EST_HUMAN	np82d08.s1 NCL_CGAP_B2 Homo sapiens cDNA clone IMAGE:1130891 3' similar to gb:J05459
825	8870	18982	0.7	7.0E-50	BE088581.1	EST_HUMAN	GLUTATHIONE S-TRANSFERASE TESTIS/BRAIN (HUMAN);
7341	18587	26045	21.23	7.0E-50	AI872137.1	EST_HUMAN	QV0-BT0703-280400-211-608 BT0703 Homo sapiens cDNA
4338	13537		0.72	6.0E-50	BE784381.1	EST_HUMAN	wms5g11.x1 NCL_CGAP_U12 Homo sapiens cDNA clone IMAGE:2439908 3'
6533	15728		4.02	6.0E-50	BE044078.1	EST_HUMAN	601688585F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943577 5'
7392	16808	26095	5.98	6.0E-50	AA312078.1	EST_HUMAN	h03b04.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:3038511 3' similar to contains MER28.b3
7392	16808	26098	5.98	6.0E-50	AA312078.1	EST_HUMAN	MER28 repetitive element;
1762	10973	20160	0.98	5.0E-50	BF332838.1	EST_HUMAN	EST182775 Jurkat T-cells V1 Homo sapiens cDNA 5' end
1762	10973	20161	0.98	5.0E-50	BF332838.1	EST_HUMAN	EST182775 Jurkat T-cells V1 Homo sapiens cDNA 5' end
8258	17383	26916	2.05	5.0E-50	AA403053.1	EST_HUMAN	CM0-BT0782-300500-398-605 BT0782 Homo sapiens cDNA
927	10161		3.35	4.0E-50	AA601143.1	EST_HUMAN	CM0-BT0792-300500-398-605 BT0792 Homo sapiens cDNA
3425	12650	21780	1.59	4.0E-50	AL163248.2	NT	z62b01.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728889 5' similar to TR:G1335769
1907	11113		6.69	3.0E-50	M18048.1	NT	G1335769 GAG-POL POLYPROTEIN;
2484	11874	20881	3.11	3.0E-50	BE259198.1	EST_HUMAN	nc54609.s1 NCL_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1104520 3' similar to gb:X63741_ma1
3288	12501	21632	1.29	3.0E-50	AA748142.1	EST_HUMAN	FIBULIN-1, ISOFORM A PRECURSOR (HUMAN);
3733	12953	22070	1.01	3.0E-50	AW755254.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C048
5259	14432	23507	0.72	3.0E-50	AW593886.1	EST_HUMAN	Human endogenous retrovirus RTVL-H2
6354	15534	24987	4.84	3.0E-50	AF233436.2	NT	601109717F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3350309 5'
6354	15534	24988	4.84	3.0E-50	AF233436.2	NT	cb03f06.s1 NCL_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1322827 3'
7687	16868	26367	1.83	3.0E-50	11436955	NT	CMYA5 Human cardiac muscle expression library Homo sapiens cDNA clone 4151835 similar to CMYA5
							Cardiomyopathy associated gene 5
							h026d01.x1 NCL_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2848744 3' similar to SW:C1TC_HUMAN
							P11598 C-1-TETRAHYDROFOLATE SYNTHASE, CYTOPLASMIC; contains Alu repetitive element;
							Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1a mRNA, complete cds
							Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1a mRNA, complete cds
							Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8000	18435	25922	5.9	3.0E-50	AJ245621.1	NT	Homo sapiens CTL2 gene
787	10028		5.18	2.0E-50	AF055068.1	NT	Homo sapiens MHC class 1 region
1087	10311	19404	5.21	2.0E-50	4557752	NT	Homo sapiens midline 1 (Oplz/BBB syndrome) (MID1) mRNA
3255	12488	21619	0.7	2.0E-50	AF111188.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds, and unknown genes
4898	14088	23179	1.7	2.0E-50	AW889159.1	EST_HUMAN	MR3-SN0066-040500-008-R01 SN0068 Homo sapiens cDNA
4898	14088	23180	1.7	2.0E-50	AW889159.1	EST_HUMAN	MR3-SN0066-040500-008-R01 SN0068 Homo sapiens cDNA
6816	15812	25289	10.73	2.0E-50	X068956.1	NT	Human HALPHA44 gene for alpha-tubulin, exons 1-3
6816	15812	25270	10.73	2.0E-50	X068956.1	NT	Human HALPHA44 gene for alpha-tubulin, exons 1-3
8164	17286		2.75	2.0E-50	AF023881.1	NT	Macaca mulatta cyclophilin A mRNA, complete cds
488	9721	18852	2.18	1.0E-50	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
2333	11528		11.32	1.0E-50	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
9224	18126		1.7	9.0E-51	D25217.2	NT	Homo sapiens mRNA for KIAA0027 protein, partial cds
4696	13769	22858	18.84	8.0E-51	AA610842.1	EST_HUMAN	np88a09.s1 NCL CGAP Lu1 Homo sapiens cDNA clone IMAGE:1142440 3' similar to gb:X12671_ma1
6358	15538	24892	1.97	8.0E-51	11439587	NT	HETEROGENEOUS PDZ-73 nuclear (PDZ-73/NY-CO-38), mRNA
2980	12217	21352	0.7	7.0E-51	AW274720.1	EST_HUMAN	xn34e03.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2895564 3' similar to TR:Q8Z340
3250	12483	21815	1.43	7.0E-51	AW889219.1	EST_HUMAN	Q8Z340 ATYPICAL PKC SPECIFIC BINDING PROTEIN. ;
3338	12567	21705	0.77	7.0E-51	AW274720.1	EST_HUMAN	QV4-NT0028-200400-180-d05 NT0028 Homo sapiens cDNA
4149	13355	22457	1.28	7.0E-51	AL079828.1	EST_HUMAN	xn34e03.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2895564 3' similar to TR:Q8Z340
4149	13355	22458	1.26	7.0E-51	AL079828.1	EST_HUMAN	Q8Z340 ATYPICAL PKC SPECIFIC BINDING PROTEIN. ;
4344	13548	22837	2.74	7.0E-51	AW285003.1	EST_HUMAN	DKFZp434B2228_r1 434 (synonym: hbs3) Homo sapiens cDNA clone DKFZp434B2228 5'
8183	17315	26858	2	7.0E-51	AF181449.1	NT	DKFZp434B2228_r1 434 (synonym: hbs3) Homo sapiens cDNA clone DKFZp434B2228 5'
1513	10727	19898	1.08	6.0E-51	6878763	NT	UI-HBW0-ep-b-05-0-UI.s1 NCL CGAP_Sub8 Homo sapiens cDNA clone IMAGE:2728817 3'
1948	11162	20354	8.26	6.0E-51	7657268	NT	Homo sapiens HSPC331 mRNA, partial cds
3450	12675	21810	15.12	6.0E-51	7657268	NT	Homo sapiens putative DNA binding protein (M86), mRNA
4288	13497	22582	0.85	6.0E-51	9810553	NT	Homo sapiens KIAA0928 protein Msc2 interacting nuclear target (MINT) homolog (KIAA0928), mRNA
4288	13497	22583	0.85	6.0E-51	9810553	NT	Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 9 (SLC2A9), mRNA
5653	14876	24203	6.45	6.0E-51	AF070083.1	NT	Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 9 (SLC2A9), mRNA
5653	14876	24204	6.45	6.0E-51	AF070083.1	NT	Homo sapiens mitogen-activated protein kinase kinase 1 (MKK4) gene, exon 4
6070	14517	23558	2.48	8.0E-51	11428685	NT	Homo sapiens mitogen-activated protein kinase kinase 1 (MKK4) gene, exon 4

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7808	17001	28513	2.12	8.0E-51	11528289	NT	Homo sapiens interleukin 17 receptor (IL17R), mRNA
8060	17185	28733	1.75	8.0E-51	5453949	NT	Homo sapiens protein phosphatase 2, regulatory subunit B (B56), alpha isoform (PPP2R5A) mRNA
8060	17195	28734	1.75	8.0E-51	5453949	NT	Homo sapiens protein phosphatase 2, regulatory subunit B (B56), alpha isoform (PPP2R5A) mRNA
801	10040	19181	10.27	5.0E-51	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
813	10051	18205	1.85	5.0E-51	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
888	11883	18384	0.97	5.0E-51	AL133204.1	NT	Novel human gene mapping to chromosome X
1587	10800	18876	1.72	5.0E-51	6031880	NT	Homo sapiens 26S proteasome-associated pad1 homolog (POH1) mRNA
2553	11741	20857	8.89	5.0E-51	AJ007558.1	NT	Homo sapiens mRNA for nucleoporin 155
3820	13138	22253	2.4	5.0E-51	M30838.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
3820	13138	22254	2.4	5.0E-51	M30838.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
5104	14284	23368	2.25	5.0E-51	AB037832.1	NT	Homo sapiens mRNA for KIAA1411 protein, partial cds
7820	17021	26536	4.88	5.0E-51	5903136	NT	Homo sapiens RNA binding motif protein 3 (RBM3), mRNA
132	9415	18550	20.31	3.0E-51	AI587348.1	EST_HUMAN	trb1c09.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2224720 3' similar to gb:M28328
1184	10405	19559	34.42	3.0E-51	AI587348.1	EST_HUMAN	KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
4318	13519	22814	2.02	3.0E-51	AL158142.1	NT	trb1c09.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2224720 3' similar to gb:M28328
8972	17842		1.46	3.0E-51	AF003528.1	NT	KERATIN, TYPE I CYTOSKELETAL 19 (HUMAN);
371	9637	18770	1.81	2.0E-51	4507788	NT	Novel human gene mapping to chromosome 22
695	9838	19088	0.84	2.0E-51	BE391063.1	EST_HUMAN	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
695	9838	19089	0.84	2.0E-51	BE391063.1	EST_HUMAN	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A) mRNA
1683	10878	20061	10.84	2.0E-51	AA233352.1	EST_HUMAN	601285694F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607463 5'
3713	12833	22051	3.07	2.0E-51	AI492415.1	EST_HUMAN	601285694F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607463 5'
4483	13691	22784	0.82	2.0E-51	AW137828.1	EST_HUMAN	z30a05.r1 Stragene NT2 neuronal precursor 837230 Homo sapiens cDNA clone IMAGE:604880 5' similar to TR:G233228 G233228 RTVL-H PROTEIN, contains LTR7.13 LTR7 repetitive element;
5684	14886	24276	3.73	2.0E-51	BE782015.1	EST_HUMAN	trb1c09.x1 NCI_CGAP_Ki411 Homo sapiens cDNA clone IMAGE:2131732 3'
6917	10110	25576	2.88	2.0E-51	AI917078.1	EST_HUMAN	UI-H-B11-adj-d-02-Q-U1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2718851 3'
6984	18142	25811	8.5	2.0E-51	BE165980.1	EST_HUMAN	601470446F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3873563 5'
							ts74a07.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2236980 3' similar to SW:TRKC_HUMAN
							Q16288 NT-3 GROWTH FACTOR RECEPTOR PRECURSOR;
							MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA

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Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7871	14640	23770	9	2.0E-51	A1732851.1	EST_HUMAN	0634f09.x5 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1325609 3' similar to SW:NME1_MOUSE P35438 GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 1 PRECURSOR;
7871	14640	23771	9	2.0E-51	A1732851.1	EST_HUMAN	0634f09.x5 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1325609 3' similar to SW:NME1_MOUSE P35438 GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 1 PRECURSOR;
8087	17837	23911	1.62	2.0E-51		NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (MLL T4), mRNA
114	8402	18531	19.07	1.0E-51	11419159	NT	Homo sapiens eukaryotic translation initiation factor 4A, isoform 1 (EIF4A1) mRNA
1485	10888		45.14	1.0E-51	4503528	NT	AV742248 CB Homo sapiens cDNA clone CBFBC12 5'
5048	14230	23314	0.83	1.0E-51	BE770039.1	EST_HUMAN	601464995F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3888248 5'
5391	14820	23734	3.38	1.0E-51	T18882.1	EST_HUMAN	b120581 Testis 1 Homo sapiens cDNA clone IMAGE:3888248 5'
8248	18392		3.62	1.0E-51	AV760590.1	EST_HUMAN	AV760590 MDS Homo sapiens cDNA clone MDSB02 5'
7280	18489	25991	1.97	9.0E-52	R91638.1	EST_HUMAN	yq10h04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:186567 5' similar to SP:YGAF_ECOLI_P37339 HYPOTHETICAL PROTEIN IN GABP 3 REGION;
7280	18489	25992	1.97	9.0E-52	R91638.1	EST_HUMAN	yq10h04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:186567 5' similar to SP:YGAF_ECOLI_P37339 HYPOTHETICAL PROTEIN IN GABP 3 REGION;
8737	17883		4.59	9.0E-52	AA777821.1	EST_HUMAN	z85a07.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:186567 5' similar to contains THR.t3 THR repetitive element;
155	9437	18571	6.6	8.0E-52	AA720574.1	EST_HUMAN	mw21g02.s1 NCI_CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR.t3 THR repetitive element;
1487	10700	18974	1.22	8.0E-52	X84900.1	NT	H. sapiens mRNA for laminin-5, alpha3b chain
1630	10843	20020	2.78	8.0E-52	11968028	NT	Homo sapiens hypothetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA
1630	10843	20021	2.78	8.0E-52	11968028	NT	Homo sapiens hypothetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA
3971	10843	20020	8.23	8.0E-52	11968028	NT	Homo sapiens hypothetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA
3971	10843	20021	8.23	8.0E-52	11968028	NT	Homo sapiens hypothetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA
1185	10415		2.09	6.0E-52	BE072409.1	EST_HUMAN	QV3-BT0537-271209-049-d07 BT0537 Homo sapiens cDNA
1689	10882	20068	7.15	6.0E-52	AF109807.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
7781	16957	28488	2.04	6.0E-52	BE048172.1	EST_HUMAN	tz46h04.y1 NCI_CGAP_Brm52 Homo sapiens cDNA clone IMAGE:2281671 5' similar to SW:PGBM_MOUSE_Q05783 BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN PRECURSOR;

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4433	13633	22729	1.94	5.0E-52	Z78898.1	NT	H. sapiens flow-sorted chromosome 6 HindIII fragment, SC6pa18H7
1637	10851	20029	1.58	4.0E-52	AF257318.1	NT	Homo sapiens SH3-containing protein SH3GLB1 mRNA, complete cds
1758	10869	20154	1.94	4.0E-52	4758843	NT	Homo sapiens nucleoporin 155kD (NUP155) mRNA
3901	13117	22234	0.8	4.0E-52	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
4850	13844	22835	0.97	4.0E-52	5174560	NT	Homo sapiens 5,10-methylenetetrahydrofolate dehydrogenase, 5,10-methylenetetrahydrofolate
6832	15828	25280	4.42	4.0E-52	11417035	NT	cyclohydrolase, 10-formyltetrahydrofolate synthetase (MTHFD) mRNA
8584	17584		5.5	4.0E-52	11418177	NT	Homo sapiens hydroxylase 4 (HSD17B4), mRNA
8083	17805		8.29	4.0E-52	AB002059.1	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
4088	13278		14.34	3.0E-52	11437042	NT	Homo sapiens DNA for Human P2XM, complete cds
568	9819	18940	2.3	2.0E-52	M10976.1	NT	Homo sapiens hypothetical protein FLJ10875 (FLJ10875), mRNA
568	9819	18941	2.3	2.0E-52	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
2463	11654	20876	15.22	2.0E-52	BE207575.1	EST_HUMAN	Human endogenous retroviral DNA (4-1), complete retroviral segment
2683	11873		26.07	2.0E-52	BF677892.1	EST_HUMAN	bb68b07.y1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3030421 5' similar to gb:X184693 M.musculus.
4997	14184	23272	4.01	2.0E-52	AL137188.3	NT	mRNA for Zfp-1 zinc finger protein (MOUSE).
5038	14222	23306	1.36	2.0E-52	A1141802.1	EST_HUMAN	602084710F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4248891 5'
5038	14222	23307	1.36	2.0E-52	A1141802.1	EST_HUMAN	Novel human gene mapping to chromosome 20, similar to membrane transporters
5537	14761	24128	3.39	2.0E-52	AW848041.1	EST_HUMAN	qs58a05.s1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1690784 3'
5819	15036	24437	1.65	2.0E-52	11141868	NT	qs58a05.s1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1690784 3'
6869	16864		10.62	2.0E-52	AF147880.1	NT	IL3-CT0214-231289-053-E12 CT0214 Homo sapiens cDNA
7118	16283	26774	5.48	2.0E-52	5730038	NT	Homo sapiens interleukin 21 receptor (IL21R), mRNA
7118	16283	25775	5.48	2.0E-52	5730038	NT	Macaca mulatta beta-tubulin mRNA, complete cds
7756	16852	28458	8.11	2.0E-52	A1831462.1	EST_HUMAN	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
7756	16852	28459	8.11	2.0E-52	A1831462.1	EST_HUMAN	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
7769	16865	28478	3.72	2.0E-52	AV715377.1	EST_HUMAN	wj49c04.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2408150 3' similar to contains THR.b2
7892	17108		2.13	2.0E-52	W70260.1	EST_HUMAN	THR repetitive element;
8140	17272		3.68	2.0E-52	11417890	NT	wj49c04.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2408150 3' similar to contains THR.b2
8365	18375	23591	12.95	2.0E-52	AW236297.1	EST_HUMAN	THR repetitive element;
8783	17712		4.63	2.0E-52	A1808895.1	EST_HUMAN	wj49c04.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone DCBAIE03 5'
							AV715377 DGB Homo sapiens cDNA clone DCBAIE03 5'
							z648g12.r1 Soares_fetal_NH19W Homo sapiens cDNA clone IMAGE:344038 5'
							Homo sapiens LIM domain kinase 2 (LIMK2), mRNA
							xn72a07.x1 NCI_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2700036 3' similar to contains Alu
							repetitive element; contains element LTR2 repetitive element;
							wf67405.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2360849 3' similar to TR:Q16859
							Q16859 CARBOXYESTERASE;

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Table 4
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
539	9790	18914	1.76	1.0E-52	AA634445.1	EST_HUMAN	zu75h12.s1 Soares_bacile_NHT Homo sapiens cDNA clone IMAGE:743878 3'
1378	10593	18759	3.28	1.0E-52	4504028	NT	Homo sapiens glutamate-aminonitrate ligase (glutamine synthase) (GLUL) mRNA
3024	12680	21388	1.82	1.0E-52	S81070.1	NT	pol-epsilon reverse transcriptase homolog (retroviral element) [human, endogenous retroviral element RTVL-Hp1, Genomic, 680 nt]
6355	14585	23661	3.88	1.0E-52	M29428.1	NT	Human P-glycoprotein (MDR1) gene, exon 4
5827	15044	24448	2.75	1.0E-52	U38864.1	NT	Human PMS2 related (hPMSR2) gene, complete cds
6284	15445	24884	2.67	1.0E-52	X07292.1	NT	Human aldolase C gene for fructose-1,6-bisphosphate aldolase
7350	16668	26058	15.62	1.0E-52	U48296.1	NT	Homo sapiens protein tyrosine phosphatase PTPCAAX1 (hPTPCAAX1) mRNA, complete cds
7413	16825		2.67	1.0E-52	11428321	NT	Homo sapiens proteasome (prosome, macropain) subunit, beta type, 2 (PSMB2), mRNA
3773	12891	22108	0.85	9.0E-53	4506084	NT	Homo sapiens protein kinase, cAMP-dependent, regulatory, type II, beta (PRKAR2B) mRNA
8614	17811		3.78	7.0E-53	BF238465.1	EST_HUMAN	601904771F1 NIH_MGC_64 Homo sapiens cDNA clone IMAGE:4132783 5'
8057	18245		6.71	7.0E-53	AI421782.1	EST_HUMAN	64407.x1 NCI_CGAP_Bim23 Homo sapiens cDNA clone IMAGE:2068077 3' similar to contains THR.11 THR repetitive element;
4076	13286	22384	6.55	5.0E-53	4758543	NT	Homo sapiens heterogeneous nuclear ribonucleoprotein C (C1/G2) (HNRPC) mRNA
8668	17642		1.81	5.0E-53	AW813563.1	EST_HUMAN	RC3-ST0197-151089-011-g10 ST0197 Homo sapiens cDNA
51	9348	18461	2.26	4.0E-53	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
51	9348	18462	2.25	4.0E-53	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
7768	16862	26473	3.53	4.0E-53	BF128701.1	EST_HUMAN	601810889F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4053977 5'
7768	16862	26474	3.53	4.0E-53	BF128701.1	EST_HUMAN	601810889F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4053977 5'
2622	11806	21023	1.8	3.0E-53	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
3712	12832	22050	1.7	3.0E-53	AW050838.1	EST_HUMAN	wz22c07.x1 Soares_Dickgrasfe_cdon_NHCD Homo sapiens cDNA clone IMAGE:2558786 3'
4588	13782	22874	0.81	3.0E-53	AW803563.1	EST_HUMAN	IL2-JM0081-240300-055-003 UM0081 Homo sapiens cDNA
6562	15768	25221	5.16	3.0E-53	S72043.1	NT	GIF=growth inhibitory factor [human, brain, Genomic, 2015 nt]
6788	15983		8.94	3.0E-53	5601953	NT	Homo sapiens FGFR1 oncogene partner (FOP), mRNA
8493	17838		1.41	3.0E-53	11428423	NT	Homo sapiens acetyl-Coenzyme A carboxylase alpha (ACACA), mRNA
484	9717		5.34	2.0E-53	AA366556.1	EST_HUMAN	EST17525 Pancreas tumor III Homo sapiens cDNA 5' end
2286	11491	20711	43.89	2.0E-53	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
2501	11890		11.89	2.0E-53	4502316	NT	Homo sapiens ATPase, H+ transporting, lysosomal (vacuolar proton pump) 31kD; Vacuolar proton-ATPase, subunit E; V-ATPase, subunit E (ATP6E), mRNA
3212	12448	21579	0.8	2.0E-53	AF083822.1	NT	Homo sapiens dihydropyridine receptor alpha 2 subunit (CACNA2D1) gene, exon 6
4036	13248	22349	2.27	2.0E-53	M61873.1	NT	Human Krueppel-related DNA-binding protein (TF34) gene, partial cds
5406	14634	23746	2.32	2.0E-53	BF334740.1	EST_HUMAN	PM1-CT0386-170800-001-g03 CT0386 Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5408	14834	23747	2.32	2.0E-53	BF334740.1	EST_HUMAN	PM1-CT03098-170800-001-g03 CT0398 Homo sapiens cDNA
6880	18071		6.07	2.0E-53	AW245678.1	EST_HUMAN	2822865 5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822865 5'
1447	10880	18835	1.18	1.0E-53	AJ271738.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
3387	12614	21747	1.42	1.0E-53	AB028898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
4884	14171	23281	1.03	1.0E-53	BE286388.1	EST_HUMAN	601178725F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531819 5'
6801	15908	25454	12.97	1.0E-53	X78536.1	NT	H. sapiens mRNA for hnRNPcore protein A1
8359	17451	26581	1.49	1.0E-53	AW245422.1	EST_HUMAN	2822843 3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822843 3'
3218	12452	21585	0.62	9.0E-54	4504118	NT	Homo sapiens IQ motif containing GTPase activating protein 1 (IQGAP1) mRNA
5330	18050	23634	5.28	9.0E-54	4508788	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
212	9492	18624	5.45	8.0E-54	BE388785.1	EST_HUMAN	601272863F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3814031 5'
1803	11012	20205	2.01	8.0E-54	4504610	NT	Homo sapiens insulin-like growth factor 2 receptor (IGF2R) mRNA
4747	13838	23041	0.71	8.0E-54	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
4747	13838	23042	0.71	8.0E-54	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
5128	13838	23041	0.72	8.0E-54	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
5128	13838	23042	0.72	8.0E-54	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
5831	14855	24238	22.45	8.0E-54	6005700	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA
369	9683	18820	1.42	7.0E-54	AA812637.1	EST_HUMAN	el78c12.s1 Soares_testis_NHT Homo sapiens cDNA clone 1377046 3' similar to contains MER30.13 MER30 repetitive element;
1798	11007	20200	1.3	7.0E-54	Y18845.1	NT	Homo sapiens mRNA for monocyte chemotactic protein-2
2171	11388	20589	8.45	7.0E-54	N27177.1	EST_HUMAN	yw68d12.s1 Soares_placenta_8to8weeks_2NBHP8a9W Homo sapiens cDNA clone IMAGE:257389 3'
7688	18867	26368	2.02	7.0E-54	8923698	NT	similar to contains LTR7.b3 LTR7 repetitive element;
7688	18867	26368	2.02	7.0E-54	8923698	NT	Homo sapiens golgin-like protein (GLP), mRNA
7839	17031		6.68	7.0E-54	AI180189.1	EST_HUMAN	Homo sapiens golgin-like protein (GLP), mRNA
24	9320	18424	4.02	6.0E-54	AB003618.1	NT	qb07g03.x1 Soares_fetal_heart_NBH19W Homo sapiens cDNA clone IMAGE:1705204 3' similar to contains OFR.t1 OFR repetitive element;
390	9884	18821	1.74	8.0E-54	8922148	NT	Homo sapiens DNA for MICB, exon 4, 5 and partial cds
390	9884	18822	1.74	8.0E-54	8922148	NT	Homo sapiens hypothetical protein DKFZp434M035 (DKFZp434M035), mRNA
3251	12484	21618	1.3	6.0E-54	8922148	NT	Homo sapiens hypothetical protein DKFZp434M035 (DKFZp434M035), mRNA
3981	13165	22303	1.18	8.0E-54	8922148	NT	Homo sapiens hypothetical protein DKFZp434M035 (DKFZp434M035), mRNA
4437	13655	22749	0.75	8.0E-54	4502872	NT	Homo sapiens chloride channel 6 (CLCN6) mRNA
4891	14079		1.7	6.0E-54	AV754748.1	EST_HUMAN	AV754748 TP Homo sapiens cDNA clone TPGAAC10 5'
5024	14079		2.37	6.0E-54	Y09846.1	NT	H. sapiens shc pseudogene, p86 isoform
						NT	H. sapiens shc pseudogene, p86 isoform

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7890	18425	25912	4.04	6.0E-54	AW813597.1	EST_HUMAN	RC3-ST0197-161089-011-008 ST0197 Homo sapiens cDNA
2119	11318	20538	3.92	5.0E-54	P51523	SWISSPROT	ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2)
187	9496		74.6	4.0E-54	AF110103.1	NT	Tupaisa belangeri beta-actin mRNA, partial cds
993	10198	19351	100.21	4.0E-54	AA308764.1	EST_HUMAN	EST177608 Jurkat T-cells VI Homo sapiens cDNA 5' end similar to glyceraldehyde-3-phosphate dehydrogenase
1774	10984	20175	3.48	4.0E-54	D38521.1	NT	Human mRNA for KIAA0077 gene, partial cds
1774	10984	20176	3.48	4.0E-54	D38521.1	NT	Human mRNA for KIAA0077 gene, partial cds
3198	12403		1.94	4.0E-54	AI815088.1	EST_HUMAN	wd28411.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2329269 3' similar to TR:O02711
83	9386	18515	11.44	3.0E-54	AA313487.1	EST_HUMAN	O02711 PRO-POL-DUTPASE POLYPROTEIN ;
2587	11773		1.32	3.0E-54	AI808757.1	EST_HUMAN	EST185371 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
7652	18852	26350	4.71	3.0E-54	BF345600.1	EST_HUMAN	IL-BT189-190398-007 BT189 Homo sapiens cDNA
7908	17123	26854	3.14	3.0E-54	AA39382.1	EST_HUMAN	602019408F1 NCJ_CGAP_Bim67 Homo sapiens cDNA clone IMAGE:4155121 5'
8484	17519	24022	2.89	3.0E-54	AW954559.1	EST_HUMAN	z170f12.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:727727 5' similar to TR:G181315
8512	18337		2.75	3.0E-54	AW748965.1	EST_HUMAN	G181315 ANDROGEN-DEPENDENT EXPRESSED PROTEIN ;
648	9894	19018	8.02	2.0E-54	5031800	NT	EST366829 MAGI2 resequenced, MAGC Homo sapiens cDNA
1373	10587	18763	1.05	2.0E-54	4507184	NT	RC1-BT0313-131188-011-009 BT0313 Homo sapiens cDNA
							Homo sapiens killer cell lectin-like receptor subfamily G, member 1 (KLRG1), mRNA
							Homo sapiens nuclear antigen Sp100 (SP100) mRNA
2604	11692	20912	2.47	2.0E-54	AW163175.1	EST_HUMAN	eu82g03.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783784 5' similar to
2560	11746	20968	2.11	2.0E-54	AL163210.2	NT	SW:CUL1_HUMAN Q13616 CULLIN HOMOLOG 1 ;
							Homo sapiens chromosome 21 segment HS21C010
2647	12086	21215	1.44	2.0E-54	AW057524.1	EST_HUMAN	wy60b12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2552927 3' similar to
							TR:Q82084 Q82084 PHOSPHOLIPASE C NEIGHBORING ;
3523	12747		6.73	2.0E-54	AA52925.1	EST_HUMAN	n145g09.s1 NCJ_CGAP_P18 Homo sapiens cDNA clone IMAGE:865488 similar to gb:X53777 60S
4187	13391		3.92	2.0E-54	4502842	NT	RIBOSOMAL PROTEIN L23 (HUMAN);
4434	13634		1.21	2.0E-54	AF208161.1	NT	Homo sapiens chaperonin containing T-complex subunit 8 (CCT8) mRNA
4438	13638		1.27	2.0E-54	AL163201.2	NT	Homo sapiens syncytin precursor, mRNA, complete cds
5168	14345	23434	0.8	2.0E-54	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
5558	14780	24148	4.58	2.0E-54	11428657	NT	Homo sapiens chromosome 21 segment HS21C001
5586	14819	24195	12.42	2.0E-54	AB046811.1	NT	Homo sapiens KIAA0100 gene product (KIAA0100), mRNA
5595	14819	24186	12.42	2.0E-54	AB046811.1	NT	Homo sapiens mRNA for KIAA1591 protein, partial cds
							Homo sapiens mRNA for KIAA1591 protein, partial cds
6128	16312	24748	7.59	2.0E-54	11428544	NT	Homo sapiens neurofibromin 1 (neurofibromatosis, von Recklinghausen disease, Watson disease) (NF1), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6973	16181	25622	4.05	2.0E-64	AB001026.1	NT	Homo sapiens mRNA for brain ryanodine receptor, complete cds
8217	17348		4.24	2.0E-54	7657454	NT	Homo sapiens pescadillo (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA
8981	17863	23887	1.6	2.0E-54	8567387	NT	Homo sapiens period (Drosophila) homolog 3 (PER3), mRNA
4461	13659		1.8	1.0E-64	BF316418.1	EST_HUMAN	601899230F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4128535 5'
9168	17963		3.74	1.0E-54	AU077341.1	EST_HUMAN	AU077341 Sugeno cDNA library Homo sapiens cDNA clone Zv6C880 similar to 5'-end region of Human gamma-glutamyl transpeptidase mRNA, 5 end
1322	10537		0.87	8.0E-55	Y07829.2	NT	Homo sapiens RFB30 gene for RING finger protein
1325	10540		2.14	8.0E-55	Y07829.2	NT	Homo sapiens RFB30 gene for RING finger protein
7750	18948		2.48	8.0E-55	AW409714.1	EST_HUMAN	fh02a02.x1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2860807 5'
1089	10313	19467	1.07	7.0E-55	R08348.1	EST_HUMAN	Y26a04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:127988 5' similar to SP-C561_BOVIN P10897 CYTOCHROME:
7762	18958	28467	15.98	7.0E-55	A1581058.1	EST_HUMAN	tq29f09.x1 NCI_CGAP_U1 Homo sapiens cDNA clone IMAGE:2210249 3'
7762	18958	28468	15.68	7.0E-55	A1581058.1	EST_HUMAN	tq29f09.x1 NCI_CGAP_U1 Homo sapiens cDNA clone IMAGE:2210249 3'
8987	17851		1.49	7.0E-55	H23398.1	EST_HUMAN	ym57g07.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:52444 5'
9136	18263		5.18	7.0E-55	H23398.1	EST_HUMAN	ym57g07.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:52444 5'
8048	17182	28722	2.17	6.0E-55	AB040934.1	NT	Homo sapiens mRNA for KIAA1501 protein, partial cds
1740	10952	20134	1.32	5.0E-55	AA704871.1	EST_HUMAN	z95b09.s1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:482817 3'
1740	10952	20135	1.32	5.0E-55	AA704871.1	EST_HUMAN	z95b09.s1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:482817 3'
4782	13971	23074	1.49	5.0E-55	AW208021.1	EST_HUMAN	UI-H-B11-afy-g-09-0-U1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2723638 3'
5888	15115	24528	1.68	5.0E-55	4502240	NT	Homo sapiens arylsulfatase E (chondrodysplasia punctata 1) (ARSE), mRNA
5888	15115	24527	1.68	5.0E-55	4502240	NT	Homo sapiens arylsulfatase E (chondrodysplasia punctata 1) (ARSE), mRNA
6781	15978	25434	2.25	5.0E-55	4506302	NT	Homo sapiens protein tyrosine phosphatase, receptor type, alpha polypeptide (PTPRA) mRNA
8555	17577		3.35	5.0E-55	11417972	NT	Homo sapiens pescadillo (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA
57	11968	18470	3.39	4.0E-55	AW957894.1	EST_HUMAN	EST1370084 MAGE resequences, MAGE Homo sapiens cDNA
678	9922	18053	48.87	4.0E-55	4828973	NT	Homo sapiens RNA binding motif protein, Y chromosome, family 1, member A1 (RBMV1A1) mRNA
1442	10656	18830	1.18	4.0E-55	7881713	NT	Homo sapiens predicted osteoblast protein (GS3788), mRNA
1442	10656	18831	1.18	4.0E-55	7881713	NT	Homo sapiens predicted osteoblast protein (GS3788), mRNA
1503	10716		1.45	4.0E-55	BF061411.1	EST_HUMAN	7J52b10.x1 Soares NSF_F8_QW_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3390043 3' similar to contains L1.13 L1 repetitive element:
1894	11167	20406	2.71	4.0E-55	4508180	NT	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 2 (PSMA2) mRNA
1904	11167	20407	2.71	4.0E-55	4508180	NT	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 2 (PSMA2) mRNA
2055	11266	20469	8.48	4.0E-55	4503314	NT	Homo sapiens diacylglycerol kinase, gamma (90kD) (DGKG) mRNA
2055	11266	20470	8.48	4.0E-55	4503314	NT	Homo sapiens diacylglycerol kinase, gamma (90kD) (DGKG) mRNA
2278	11471	20683	7.25	4.0E-55	4507784	NT	Homo sapiens ubiquitin-conjugating enzyme E2 variant 1 (UBE2V1) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2550	11738		0.98	4.0E-55	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
3247	12480	21812	0.94	4.0E-55	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
6578	15774		5.57	4.0E-55	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
7781	16976		5.6	4.0E-55	W28189.1	EST_HUMAN	43c5 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
8465	17520		7.9	4.0E-55	BF303941.1	EST_HUMAN	60188575F2 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4120338 5'
8402	17480		3.27	3.0E-55	BE178519.1	EST_HUMAN	PM1-HT0803-080300-001-g08 HT0803 Homo sapiens cDNA
9181	17973		1.68	3.0E-55	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
382	9848	18781	2.24	2.0E-55	XG7147.1	NT	Human endogenous retrovirus pHE.1 (ERV9)
558	9808		1.09	2.0E-55	MT0976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
655	9801	19027	3.38	2.0E-55	4607288	NT	Homo sapiens syntaxin-binding protein 1 (STXB1) mRNA, and translated products
2813	12151	21288	0.82	2.0E-55		NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A) mRNA
4785	13974	23077	2.73	2.0E-55	BE17888.1	EST_HUMAN	CM1-HT0876-150800-357-g03 HT0876 Homo sapiens cDNA
6819	16013		2.85	2.0E-55	AI002838.1	EST_HUMAN	sm88H05.s1 Strategene schizo brain S11 Homo sapiens cDNA clone IMAGE:1684185 3' similar to contains
7523	18728	28219	2.48	2.0E-55	AU119344.1	EST_HUMAN	THR.b2 THR repetitive element
98	9389	18518	1.2	1.0E-55	4505080	NT	AU118344 HEMBA1 Homo sapiens cDNA clone HEMBA1005583 5'
						NT	Homo sapiens mannose-6-phosphate receptor (cation dependent) (M6PR) mRNA
194	9474	18605	60.19	1.0E-55	U09823.1	NT	Oryctolagus cuniculus New Zealand white elongation factor 1 alpha (Rabefia2) mRNA, complete cds
591	9830	18948	0.67	1.0E-55	AI028718.1	EST_HUMAN	ov65g08.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1844160 3'
1158	10380	18532	5.24	1.0E-55	AB020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
1821	11125	20320	2.45	1.0E-55	BE277881.1	EST_HUMAN	601120116F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2887027 5'
1821	11125	20321	2.45	1.0E-55	BE277881.1	EST_HUMAN	601120116F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2887027 5'
2203	11488		8.1	1.0E-55	5803174	NT	Homo sapiens SMA3 (SMA3), mRNA
2483	11673	20890	79.35	1.0E-55	X13111.1	NT	Human mRNA for HLA-A11E, a MHC class I molecule (major histocompatibility complex)
2520	11708	20923	5.19	1.0E-55	AB007888.2	NT	Homo sapiens mRNA for KIAA0408 protein, partial cds
2520	11708	20924	5.19	1.0E-55	AB007888.2	NT	Homo sapiens mRNA for KIAA0408 protein, partial cds
2573	11758	20978	8.98	1.0E-55	LS4057.1	NT	Homo sapiens CLP mRNA, partial cds
3867	13182	22281	3.78	1.0E-55	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C087
4282	13485	22584	1.09	1.0E-55	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
4742	13833		1.08	1.0E-55	N77281.1	EST_HUMAN	y44g03.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:245820 5'
4845	14034	23128	1.85	1.0E-55	AB037163.1	NT	Homo sapiens DSCR5b mRNA, complete cds
4845	14034	23127	1.85	1.0E-55	AB037163.1	NT	Homo sapiens DSCR5b mRNA, complete cds
5182	14341	23430	0.97	1.0E-55	8923125	NT	Homo sapiens hypothetical protein FLJ20126 (FLJ20126), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5778	14993	24397	8.65	1.0E-55	11433048	NT	Homo sapiens hect domain and RLD 2 (HERC2), mRNA
5778	14998	24398	8.65	1.0E-55	11433048	NT	Homo sapiens hect domain and RLD 2 (HERC2), mRNA
7488	16883	26178	5.26	1.0E-55	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
7488	16883	26177	5.26	1.0E-55	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
7884	16419	26908	2.62	1.0E-55	U50950.1	NT	Human Infant brain unknown product mRNA, complete cds
8003	16438	25925	2.12	1.0E-55	T10045.1	EST_HUMAN	seq1575 b4HB3MA Cdx8-HAP-F1 Homo sapiens cDNA clone b4HB3MA-COT8-HAP-F161 5' similar to similar
8241	15422	24983	1.68	9.0E-58	BE378074.1	EST_HUMAN	to Chinese Hamster DHFR-coamplified protein mRNA
2690	11871	21085	5.74	7.0E-58	H19834.1	EST_HUMAN	Yn62g03.r1 Scores adult brain N2b5HB55Y Homo sapiens cDNA clone IMAGE:173044 5' similar to contains
6353	15533	24985	2.12	7.0E-58	AW361213.1	EST_HUMAN	THR repetitive element:
6353	15533	24986	2.12	7.0E-58	AW361213.1	EST_HUMAN	RC1-CT0252-231089-013-507 CT0252 Homo sapiens cDNA
1687	10880	20084	1.85	5.0E-58	AW997712.1	EST_HUMAN	RC1-CT0252-231089-013-507 CT0252 Homo sapiens cDNA
8651	18324	23689	2.18	5.0E-58	H55099.1	EST_HUMAN	RC3-BN0059-170200-011-001 BN0053 Homo sapiens cDNA
29	8325	18428	18.75	4.0E-58	AF141349.1	NT	CHR220038 Chromosome 22 exon Homo sapiens cDNA clone C22_55 5'
29	8325	18429	18.75	4.0E-58	AF141349.1	NT	Homo sapiens beta-tubulin mRNA, complete cds
2689	11850	21085	3.18	4.0E-58	4507728	NT	Homo sapiens beta-tubulin mRNA, complete cds
2689	11850	21088	3.18	4.0E-58	4507728	NT	Homo sapiens tubulin, beta polypeptide (TUBB) mRNA
2784	9783	18808	3.7	4.0E-58	AF003528.1	NT	Homo sapiens tubulin, beta polypeptide (TUBB) mRNA
2785	11781	20881	1.3	4.0E-58	AI632488.1	EST_HUMAN	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
2785	11781	20882	1.3	4.0E-58	AI632488.1	EST_HUMAN	wb08008.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2305181 3' similar to SW:DCOR_MUSPA
5773	14981	24391	5.54	4.0E-58	AF217508.1	NT	P27119 ORNITHINE DECARBOXYLASE:
5773	14981	24392	5.54	4.0E-58	AF217508.1	NT	wb08009.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2305181 3' similar to SW:DCOR_MUSPA
7497	18704	26188	11.09	4.0E-58	AI498098.1	EST_HUMAN	P27119 ORNITHINE DECARBOXYLASE:
7497	18704	26189	11.09	4.0E-58	AI498098.1	EST_HUMAN	Homo sapiens uncharacterized bone marrow protein BM031 mRNA, complete cds
1348	10584	19728	4.55	3.0E-58	88924029	NT	Homo sapiens uncharacterized bone marrow protein BM031 mRNA, complete cds
1735	10947	20130	1.43	3.0E-58	6912743	NT	bm65g12.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2163048 3'
2118	11317	20535	1.09	3.0E-58	6912697	NT	bm65g12.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2163048 3'
3089	12325	21447	1.88	3.0E-58	AA325826.1	EST_HUMAN	tm65g12.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2163048 3'
3089	12325	21448	1.88	3.0E-58	AA325826.1	EST_HUMAN	tm65g12.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2163048 3'
3824	13042		2.27	3.0E-58	AF055086.1	NT	Homo sapiens hypothetical protein PRO1304 (PRO1304), mRNA
							Homo sapiens 5'-3' exoribonuclease 2 (XRN2), mRNA
							Homo sapiens oncogene TC21 (TC21), mRNA
							EST28889 Cerebellum II Homo sapiens cDNA 5' end
							EST28889 Cerebellum II Homo sapiens cDNA 5' end
							Homo sapiens MHC class I region

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3895	13111	22229	0.98	3.0E-58	BE389512.1	EST_HUMAN	601310203F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3631848 5'
4382	13583	22685	0.8	3.0E-58	7657042	NT	Homo sapiens Down syndrome candidate region 1 (DSCR1), mRNA
4416	13618	22712	5.14	3.0E-58	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
4570	13764	22860	2.83	3.0E-58	5802085	NT	Homo sapiens superkiller viralicidic activity 2 (S. cerevisiae homolog)-like (SKIV2L), mRNA
4817	14008		1.75	3.0E-58	BE889572.1	EST_HUMAN	601438154F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3923100 5'
5142	14321	23413	0.78	3.0E-58	6812593	NT	Homo sapiens phosphatidylinositol transfer protein, beta (PITPNB), mRNA
5528	14752	24118	1.73	3.0E-58	4759183	NT	Homo sapiens sparc/osteonectin, cncv and kazal-like domains proteoglycan (testican) (SPOCK) mRNA
5528	14752	24119	1.73	3.0E-58	4759183	NT	Homo sapiens sparc/osteonectin, cncv and kazal-like domains proteoglycan (testican) (SPOCK) mRNA
6030	15238	24681	5.37	3.0E-58	11421124	NT	Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), mRNA
6723	15818	25377	8	3.0E-58	11418704	NT	Homo sapiens bone morphogenetic protein 5 (BMP5), mRNA
7211	16388	25870	2.39	3.0E-58	11434958	NT	Homo sapiens KIAA0317 gene product (KIAA0317), mRNA
7891	17051	26571	5.15	3.0E-58	5902013	NT	Homo sapiens nuclear pore complex interacting protein (NP1P), mRNA
7891	17051	26572	5.15	3.0E-58	5902013	NT	Homo sapiens nuclear pore complex interacting protein (NP1P), mRNA
8510	17548	23884	1.24	3.0E-58	11434876	NT	Homo sapiens caveolin 3 (CAV3), mRNA
8510	17548	23885	1.24	3.0E-58	11434876	NT	Homo sapiens caveolin 3 (CAV3), mRNA
530	9781		2.09	2.0E-58	AA198818.1	EST_HUMAN	zq52a08.e1 Stratigene neuroepithelium (#837231) Homo sapiens cDNA clone IMAGE:645208 3'
740	11976	19122	1.19	2.0E-58	BE084386.1	EST_HUMAN	RC4-BT0310-110300-015-110 BT0310 Homo sapiens cDNA
740	11976	19123	1.19	2.0E-58	BE084388.1	EST_HUMAN	RC4-BT0310-110300-015-110 BT0310 Homo sapiens cDNA
2945	12183	21316	1.53	2.0E-58	AB037835.1	NT	Homo sapiens mRNA for KIAA1414 protein, partial cds
3288	12519		0.92	2.0E-58	AB008681.1	NT	Homo sapiens gene for activin receptor type IIB, complete cds
3507	12731	21889	1.14	2.0E-58	AV703184.1	EST_HUMAN	AV703184 ADB Homo sapiens cDNA clone ADBCFG10 5'
6121	15305	24738	1.71	2.0E-58	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
987	10218		24.65	1.0E-58	AF190630.1	NT	Macaca fascicularis protein tyrosine phosphatase (PRL-1) mRNA, complete cds
3655	12876	21894	1.84	1.0E-58	AW588633.1	EST_HUMAN	hg23c11.x1 NCI CGAP_GC8 Homo sapiens cDNA clone IMAGE:2946452 3'
3655	12876	21905	1.84	1.0E-58	AW588633.1	EST_HUMAN	hg23c11.x1 NCI CGAP_GC8 Homo sapiens cDNA clone IMAGE:2946452 3'
631	8878		2.23	9.0E-57	AW588633.1	EST_HUMAN	QV0-OT0033-070300-152-h03 OT0033 Homo sapiens cDNA
7773	16968	26481	2.07	9.0E-57	AF228497.1	NT	Homo sapiens serine protease 17 (KLK4) gene, complete cds
7773	16968	26482	2.07	9.0E-57	AF228497.1	NT	Homo sapiens serine protease 17 (KLK4) gene, complete cds
8053	17189	26729	1.8	9.0E-57	AB020861.1	NT	Homo sapiens mRNA for cyclin B2, complete cds
13	8309	18411	0.69	8.0E-57	8923349	NT	Homo sapiens hypothetical protein FLJ20371 (FLJ20371), mRNA
302	9575	18708	2.41	8.0E-57	AW816405.1	EST_HUMAN	QV4-ST0234-181199-037-05 ST0234 Homo sapiens cDNA

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
894	10129	19281	4.82	8.0E-57	AW284599.1	EST_HUMAN	x05d10.x1 NCI_CGAP_Bm53 Homo sapiens cDNA clone IMAGE:2769261 3' similar to gb:U05876
1785	10895	20181	1.75	8.0E-57	AA498109.1	EST_HUMAN	INTERFERON-GAMMA RECEPTOR BETA CHAIN PRECURSOR (HUMAN);
5080	14240	23328	0.9	8.0E-57	BE288916.1	EST_HUMAN	z051b12.l1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:767151 5'
5287	18235	23703	2.72	8.0E-57	11418185	NT	800844440.F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2860884 5'
5853	15071	24481	13.17	8.0E-57	AB023177.1	NT	Homo sapiens acotinase 2, mitochondrial (ACO2), mRNA
5853	15071	24482	13.17	8.0E-57	AB023177.1	NT	Homo sapiens mRNA for KIAA0980 protein, partial cds
6398	15577	26034	2.28	8.0E-57	AB020844.1	NT	Homo sapiens mRNA for KIAA0837 protein, partial cds
6398	15577	25035	2.28	8.0E-57	AB020844.1	NT	Homo sapiens mRNA for KIAA0837 protein, partial cds
8013	9309	18411	3.51	8.0E-57	8823349	NT	Homo sapiens hypothetical protein FLJ20371 (FLJ20371), mRNA
8751	17894	23925	1.48	8.0E-57	7019528	NT	Homo sapiens monocarboxylate transporter 3 (SLC16A8), mRNA
8802	17786	23925	2.02	8.0E-57	11545732	NT	Homo sapiens SH3-domain binding protein 1 (SH3BP1), mRNA
2587	11782	21001	1.89	7.0E-57	7657592	NT	Homo sapiens smg GDS-ASSOCIATED PROTEIN (SMAP), mRNA
2587	11782	21002	1.89	7.0E-57	7657592	NT	Homo sapiens smg GDS-ASSOCIATED PROTEIN (SMAP), mRNA
3238	12472	21804	0.78	7.0E-57	6005978	NT	Homo sapiens Kruppel-like factor 8 (KLF8), mRNA
3859	13075	22180	2.26	7.0E-57	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
3859	13075	22181	2.25	7.0E-57	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
9253	18270		4.12	5.0E-57	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
3738	12856	22072	2.71	4.0E-57	AB026888.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
814	10052	19206	1.2	3.0E-57	4507798	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E8-associated protein, Angelman syndrome) (UBE3A) mRNA
1339	10553		55.7	3.0E-57	AA230278.1	EST_HUMAN	nc13107.a1 NCI_CGAP_Prl Homo sapiens cDNA clone IMAGE:1008037 similar to SW:RS10_HUMAN
2354	11547	20768	1.08	3.0E-57	AA348335.1	EST_HUMAN	P48783 40S RIBOSOMAL PROTEIN S10. ;
2684	11845	21059	1.09	3.0E-57	BE878822.1	EST_HUMAN	EST54770 Hippocampus II Homo sapiens cDNA 5' and
2684	11845	21060	1.09	3.0E-57	BE878822.1	EST_HUMAN	733b10.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3288443 3' similar to WP:Y47H9C.2
3536	12759	21880	2.57	3.0E-57	AF232708.1	NT	CE20283 ;
3875	12898		43.08	3.0E-57	AW853984.1	EST_HUMAN	733b10.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3288443 3' similar to WP:Y47H9C.2
5719	14937	24333	3.4	3.0E-57	BE786337.1	EST_HUMAN	CE20283 ;
6507	15703	25169	3.32	3.0E-57	W28130.1	EST_HUMAN	Homo sapiens cell-line tsA201a chloride ion current inducer protein I(Cln) gene, complete cds
6515	15711	25175	2.34	3.0E-57	11545798	NT	RC3-C10254-110300-027-410 CT0254 Homo sapiens cDNA
							601588898.F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944302 5'
							4216 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
							Homo sapiens hypothetical protein FLJ11656 (FLJ11656), mRNA

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6516	15711	25176	2.34	3.0E-57	11545788	NT	Homo sapiens hypothetical protein FLJ11658 (FLJ11658), mRNA
6734	15929	25388	5.84	3.0E-57	AU117659.1	EST_HUMAN	AU117659 HEMBAT Homo sapiens cDNA clone HEMBA1001910 5'
7482	16890	28172	3.42	3.0E-57	AW248374.1	EST_HUMAN	2820473.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820473 5'
8517	18343	23605	6.01	3.0E-57	W23871.1	EST_HUMAN	2845411.1 Scores fetal_lung_NbHL18W Homo sapiens cDNA clone IMAGE:308549 5'
8903	18240		1.57	3.0E-57	AW179575.1	EST_HUMAN	RC0-HT0112-080899-001-C06 HT0112 Homo sapiens cDNA
1492	10706	19878	1.63	2.0E-57	AF246219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
1492	10705	19878	1.63	2.0E-57	AF246219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
2365	11556	20760	0.98	2.0E-57	BE172526.1	EST_HUMAN	MIR0-HT0559-010400-009-h10 HT0559 Homo sapiens cDNA
2698	11869	21083	2.54	2.0E-57	AA845419.1	EST_HUMAN	sk02b02.s1 Scores parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1404747 3' similar to contains Alu repetitive element; contains element MER22 repetitive element;
3417	12642		2.73	2.0E-57	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
3905	13121	22239	0.65	2.0E-57	BE073284.1	EST_HUMAN	MIR0-BT0551-060300-103-b03 BT0551 Homo sapiens cDNA
4169	13373	22472	2.44	2.0E-57	AA018299.1	EST_HUMAN	ze40c08.r1 Scores retina N2b4HR Homo sapiens cDNA clone IMAGE:361450 5'
4169	13373	22473	2.44	2.0E-57	AA018299.1	EST_HUMAN	ze40c08.r1 Scores retina N2b4HR Homo sapiens cDNA clone IMAGE:361450 5'
4511	13707	22800	8.55	2.0E-57	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C003
5522	14747		1.89	2.0E-57	AA016131.1	EST_HUMAN	ze31c05.r1 Scores retina N2b4HR Homo sapiens cDNA clone IMAGE:360584 5' similar to contains L1.13 L1 repetitive element;
5674	14894		31.59	2.0E-57	BF116268.1	EST_HUMAN	7n80f04.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3570866 3' similar to contains TAR1.H
7819	17012	26525	2.46	2.0E-57	11424084	NT	MER22 repetitive element;
7819	17012	26526	2.46	2.0E-57	11424084	NT	Homo sapiens hypothetical protein FLJ20041 (FLJ20041), mRNA
7890	17050	26569	1.78	2.0E-57	AJ245503.1	NT	Homo sapiens hypothetical protein FLJ20041 (FLJ20041), mRNA
7890	17050	26570	1.78	2.0E-57	AJ245503.1	NT	Homo sapiens partial mRNA for PEX5 related protein
2168	11395	26817	2.63	1.0E-57	AW503208.1	EST_HUMAN	Homo sapiens partial mRNA for PEX5 related protein
6878	15873		3.15	1.0E-57	BE043031.1	EST_HUMAN	UHFH-BNO-ekd-g-07-0-UJ.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078348 5'
8680	17650		5.48	1.0E-57	AW470791.1	EST_HUMAN	hs32a08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3030082 3' similar to TR:O00246 O00246
8680	17832	23309	1.56	9.0E-58	BE395061.1	EST_HUMAN	HYPOTHETICAL 9.3 KD PROTEIN;
596	8943		2.21	8.0E-58	BE668715.1	EST_HUMAN	hs33a08.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2875489 3' similar to contains THR.b3
690	8906	19033	9.69	8.0E-58	A1798376.1	EST_HUMAN	THR repetitive element;
690	8906	19034	9.69	8.0E-58	A1798376.1	EST_HUMAN	THR repetitive element;
							601308486F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3631000 5'
							601445948F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3850211 5'
							634607.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2220181 3' similar to TR:O15475 O15475
							UNNAMED HERV-H PROTEIN;
							tr34b07.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2220181 3' similar to TR:O15475 O15475
							UNNAMED HERV-H PROTEIN;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1824	11032	20228	2.33	8.0E-58	11434921	NT	Homo sapiens putative protein O-mannosyltransferase (POMT2), mRNA
1824	11032	20227	2.33	8.0E-58	11434921	NT	Homo sapiens putative protein O-mannosyltransferase (POMT2), mRNA
2828	12167		2.9	8.0E-58	7706132	NT	Homo sapiens DHHC1 protein (LOC51304), mRNA
4940	14127	23223	6.17	7.0E-58	BE206903.1	EST_HUMAN	ba05g04.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823510 5' similar to TR:Q61488 Q61489 DHM1 PROTEIN.
7432	16841		7.04	7.0E-58	5174542	NT	Homo sapiens MADS box transcription enhancer factor 2, polypeptide B (myocyte enhancer factor 2B) (MEF2B) mRNA
7503	16710	26197	3.9	7.0E-58	AW504109.1	EST_HUMAN	UI-HF-BNO-all-g-10-Q-UJ1.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078867 5'
7503	16710	26198	3.9	7.0E-58	AW504109.1	EST_HUMAN	UI-HF-BNO-all-g-10-Q-UJ1.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078867 5'
2218	11415	20840	1.85	6.0E-58	BE395081.1	EST_HUMAN	601309465F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3631000 5'
2343	11638	20760	12.89	6.0E-58	AU130689	EST_HUMAN	AU130689 NT2RP3 Homo sapiens cDNA clone NT2RP3001283 5'
2853	12091	21220	1.15	6.0E-58	BE242150.1	EST_HUMAN	TCAAP1E1219 Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project=TCAA Homo sapiens cDNA clone TCAAP1219
2853	12091	21221	1.15	6.0E-58	BE242150.1	EST_HUMAN	TCAAP1E1219 Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project=TCAA Homo sapiens cDNA clone TCAAP1219
8778	17709		1.8	6.0E-58	11526391	NT	Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA
305	9578	18710	4.63	5.0E-58	4507334	NT	Homo sapiens synaptotagmin 1 (SYNJ1), mRNA
717	9859	19097	4.77	5.0E-58	BE763984.1	EST_HUMAN	RC4-NT0057-160600-016-b05 NT0057 Homo sapiens cDNA
1202	10422	19576	3.01	5.0E-58	AW787948.1	EST_HUMAN	CN3-UM0043-240300-127-e07 UM0043 Homo sapiens cDNA
1202	10422	19577	3.01	5.0E-58	AW787948.1	EST_HUMAN	CN3-UM0043-240300-127-e07 UM0043 Homo sapiens cDNA
1203	10422	19576	2.7	5.0E-58	AW787948.1	EST_HUMAN	CN3-UM0043-240300-127-e07 UM0043 Homo sapiens cDNA
1203	10422	19577	2.7	5.0E-58	AW787948.1	EST_HUMAN	CN3-UM0043-240300-127-e07 UM0043 Homo sapiens cDNA
3295	12626	21657	4.5	5.0E-58	AA988183.1	EST_HUMAN	cr68e07.s1 NCI_CGAP_Lu6 Homo sapiens cDNA clone IMAGE:1603908 3'
4245	13448	22539	0.92	5.0E-58	AK36745.1	EST_HUMAN	ts88e07.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2238468 3' similar to SW:PRO2_ACACA P19884 PROFILIN II.
5504	14726		2.2	5.0E-58	11498282	NT	Homo sapiens placenta-specific 1 (PLAC1), mRNA
5743	14962	24362	6	5.0E-58	H23072.1	EST_HUMAN	ym51h07.1 Scores Infant brain INIB Homo sapiens cDNA clone IMAGE:52071 5'
6451	15848	25116	11.24	5.0E-58	8922693	NT	Homo sapiens hypothetical protein FLJ10828 (FLJ10828), mRNA
8463	18265		2.43	5.0E-58	11526293	NT	Homo sapiens cat eye syndrome chromosome region, candidate 1 (CECR1), mRNA
8163	17680		3.41	5.0E-58	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
378	9844	18778	4.45	4.0E-58	4502302	NT	Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit (oligomycin sensitivity conferring protein) (ATP5O) mRNA
808	10046	19198	1.31	4.0E-58	4504634	NT	Homo sapiens Interleukin 10 receptor, beta (IL10RB), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1494	10677	18850	1.04	4.0E-58	4503648	NT	Homo sapiens coagulation factor IX (plasma thromboplastic component, Christmas disease, hemophilia B) (F9) mRNA
2541	11729	20947	1.09	4.0E-58	AF285555.1	NT	Homo sapiens ubiquitin-conjugating BIR-domain enzyme APOLLON mRNA, complete cds
2595	11781	20999	1.73	4.0E-58	U38251.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 3
3297	12528	21659	1.07	4.0E-58	D18470.1	NT	Human mRNA, Xq terminal portion
3721	12841	22058	1.23	4.0E-58	5031660	NT	Homo sapiens EGF-like repeats and discoidin-like domains 3 (EDIL3), mRNA
7883	17071	28599	10.39	4.0E-58	11424059	NT	Homo sapiens E1B-55kDa-associated protein 5 (E1B-AP5), mRNA
340	9808		1.87	3.0E-58	R17878.1	EST_HUMAN	yg10e02.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:31693 5'
1393	10607	19771	1.82	3.0E-58	4758981	NT	Homo sapiens peptide YY (PYY) mRNA
2990	12227		0.78	3.0E-58	R17878.1	EST_HUMAN	yg10e02.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:31693 5'
3143	12378	21508	3.37	3.0E-58	BF569848.1	EST_HUMAN	602185789F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4308843 5'
3143	12378	21509	3.37	3.0E-58	BF569848.1	EST_HUMAN	602185789F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4308843 5'
948	10181	19337	12.44	2.0E-58	AF088624.1	NT	Homo sapiens 5-aminolevulinic synthase 2 (ALAS2) gene, complete cds
							bs08b07.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823733 5' similar to gb:X68381 60S RIBOSOMAL PROTEIN L6 (HUMAN); gb:X81887 M.musculus mRNA for TAX responsive element binding protein (MOUSE);
1297	10512		47.14	2.0E-58	BE208532.1	EST_HUMAN	
5371	18052	23878	3.36	2.0E-58	BE907186.1	EST_HUMAN	601498861F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3901811 5'
5371	18052	23710	3.36	2.0E-58	BE907186.1	EST_HUMAN	601498861F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3901811 5'
							am57e02.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1538874 3' similar to WP:ZK328.1 CE05065 UBIQUITIN CONJUGATING ENZYME; RECOVERIN SUBFAMILY OF EF-HAND CALCIUM BINDING PROTEIN;
5717	14935	24331	1.81	2.0E-58	A1124874.1	EST_HUMAN	
6145	15329	24764	3.16	2.0E-58	AF134838.1	NT	Homo sapiens endocytic receptor Endo180 (ENDO180) mRNA, complete cds
6145	15329	24765	3.16	2.0E-58	AF134838.1	NT	Homo sapiens endocytic receptor Endo180 (ENDO180) mRNA, complete cds
7327	16543	26032	12.17	2.0E-58	BF307745.1	EST_HUMAN	601890812F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131891 5'
7538	18741	28232	1.94	2.0E-58	AW872841.1	EST_HUMAN	hm25f08.x1 NCI_CGAP_Thy4 Homo sapiens cDNA clone IMAGE:3013671 3'
729	9971	19109	0.78	1.0E-58	M85134.1	NT	Human complement component C5 mRNA, 3' end
1075	10300	19450	3.15	1.0E-58		NT	Homo sapiens NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9 (22kD, B22) (NDUFB9), mRNA
1335	10550	19714	0.84	1.0E-58	AW957182.1	EST_HUMAN	EST389252 MAGE resequences, MAGD Homo sapiens cDNA
1335	10550	19715	0.84	1.0E-58	AW957182.1	EST_HUMAN	EST389252 MAGE resequences, MAGD Homo sapiens cDNA
1400	10814	19778	1.13	1.0E-58	AJ238083.1	NT	Homo sapiens partial AF-4 gene, exons 2 to 7 and Alu repeat elements
1639	10853	20033	1.77	1.0E-58	BE468132.1	EST_HUMAN	hy10f08.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:3198835 3'
2615	11789	21015	1.71	1.0E-58	AF217514.1	NT	Homo sapiens uncharacterized bone marrow protein BM038 mRNA, complete cds
2754	11833	21149	2.78	1.0E-58	4759169	NT	Homo sapiens steroid regulatory element binding transcription factor 2 (SREBF2) mRNA

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2783	11181	20389	1.27	1.0E-58	5174444	NT	Homo sapiens G protein-coupled receptor 68A (GPR69A) mRNA
3511	12735	21874	0.63	1.0E-58	4758081	NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
3511	12735	21875	0.63	1.0E-58	4758081	NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
4890	14177	23288	5.91	1.0E-58	A1141083.1	EST_HUMAN	oz43h01.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1678128 3'
8245	17374		3.08	1.0E-58	X63392.1	NT	H. sapiens immunoglobulin kappa light chain variable region L14
2196	11393	20615	45.34	8.0E-59	4507378	NT	Homo sapiens TATA box binding protein (TBP) mRNA
6521	15717	25182	2.25	8.0E-59	A1761963.1	EST_HUMAN	wh50d08.x1 NCI_OGAP_K1411 Homo sapiens cDNA clone IMAGE:2384171 3'
182	11981		2.44	6.0E-59	BF035327.1	EST_HUMAN	601458531F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3862088 5'
4890	14167	23257	1.07	6.0E-59	AW868159.1	EST_HUMAN	MR3-SN0088-040500-008-101 SN0088 Homo sapiens cDNA
3091	12327	21450	7.79	5.0E-59	A1807484.1	EST_HUMAN	Wf48c11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2358836 3'
4601	13855	22853	7.37	5.0E-59	X83497.1	NT	H. sapiens DNA for ZNF80-linked ERV9 long terminal repeat
6084	14530	23555	8.55	5.0E-59	AW162304.1	EST_HUMAN	au68c07.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781228 3' similar to contains element TAR1 repetitive element;
7481	16889	26171	3.22	5.0E-59	11434908	NT	Homo sapiens hypothetical protein (LOC57143), mRNA
803	10042	19194	4.8	4.0E-59	D80008.1	NT	Human mRNA for KIAA0164 gene, partial cds
4803	13882	23100	0.98	4.0E-59	4508758	NT	Homo sapiens ryanodine receptor 3 (RYR3) mRNA
4803	13882	23101	0.98	4.0E-59	4508758	NT	Homo sapiens ryanodine receptor 3 (RYR3) mRNA
8832	18197		2.83	4.0E-59	AF057720.1	NT	Homo sapiens 17-beta-hydroxysteroid dehydrogenase IV (HSD17B4) gene, promoter region and exon 1
8	8305		4.61	3.0E-59	AW965524.1	EST_HUMAN	EST377582 MAGE resequences, MAGI Homo sapiens cDNA
231	8508	18637	5.08	3.0E-59	7682247	NT	Homo sapiens KIAA00880 gene product (KIAA00880), mRNA
1685	10897	20084	11.45	3.0E-59	4505860	NT	Homo sapiens plasminogen activator, tissue (PLATa) mRNA
1685	10897	20085	11.45	3.0E-59	4505860	NT	Homo sapiens plasminogen activator, tissue (PLATa) mRNA
2099	11289	20512	8.64	3.0E-59	AB029035.1	NT	Homo sapiens mRNA for KIAA1112 protein, partial cds
2099	11289	20513	8.64	3.0E-59	AB029035.1	NT	Homo sapiens mRNA for KIAA1112 protein, partial cds
3093	12328	21454	3.99	3.0E-59	4502014	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
3093	12328	21455	3.99	3.0E-59	4502014	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
3815	13033	22144	1.19	3.0E-59	4508044	NT	Homo sapiens zona pellucida glycoprotein 2 (sperm receptor) (ZP2) mRNA
4692	13883	22885	2.22	3.0E-59	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4859	14047	23142	1.63	3.0E-59	7427522	NT	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), mRNA
5780	14079	24377	2.17	3.0E-59	8924074	NT	Homo sapiens hypothetical protein PRO1741 (PRO1741), mRNA
8235	16416	24857	1.83	3.0E-59	5454137	NT	Homo sapiens nuclear receptor co-repressor 1 (NCOR1), mRNA
8780	17701		5.3	3.0E-59	11417868	NT	Homo sapiens gamma-glutamyltransferase-like activity 1 (GGTLA1), mRNA
8975	16153		8.01	2.0E-59	AA309774.1	EST_HUMAN	EST180633 Jurkat T-cells V Homo sapiens cDNA 5' end

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7407	16618	28110	2.31	2.0E-59	AW410688.1	EST_HUMAN	fr07h04.x1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2861854 5'
7407	16619	28111	2.31	2.0E-69	AW410688.1	EST_HUMAN	fr07h04.x1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2861854 5'
8508	17644	24030	13.36	2.0E-59	A1831809.1	EST_HUMAN	wa36c12.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2300182 3' similar to TR:Q86542
8061	18220	23883	4.11	2.0E-59	L11645.1	NT	Q86542 RTVL-H PROTEIN, contains LTR7.b1 LTR7 repetitive element;
168	8448		12.28	1.0E-59	BE288411.1	EST_HUMAN	Homo sapiens alpha-tubulin mRNA, complete cds
2580	11768		3.15	1.0E-59	AA748468.1	EST_HUMAN	601176757F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531927 5'
7431	15488	24943	9.26	1.0E-59	AJ130894.1	NT	oe56h11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1309028 3' similar to TR:Q13537
772	10012	19160	1.38	8.0E-60	AW977845.1	EST_HUMAN	Q13537 MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE.;
1487	10680	18853	5.94	8.0E-60	4759159	NT	Homo sapiens mRNA for transcription factor
2138	11336	20554	4.87	8.0E-60	5174858	NT	EST388948 IMAGE resequences, MAGO Homo sapiens cDNA
2138	11336	20555	4.87	8.0E-60	5174858	NT	Homo sapiens small nuclear ribonucleoprotein D3 polypeptide (18kD) (SNRPD3) mRNA
6448	15645	25113	4.12	8.0E-60	X17033.1	NT	Homo sapiens differentiation-related gene 1 (nickel-specific induction protein) (RTP) mRNA
6764	15648	25408	3.64	8.0E-60	11428949	NT	Homo sapiens differentiation-related gene 1 (nickel-specific induction protein) (RTP) mRNA
7409	18621	26113	5.82	8.0E-60	AL163204.2	NT	Human mRNA for integrin alpha-2 subunit
7409	18621	26114	5.82	8.0E-60	AL163204.2	NT	Homo sapiens S-antigen, retina and pineal gland (arrestin) (SAG), mRNA
762	10003	19151	24.23	7.0E-60	AF055066.1	NT	Homo sapiens chromosome 21 segment HS21C004
763	10003	19151	103.89	7.0E-60	AF055066.1	NT	Homo sapiens chromosome 21 segment HS21C004
825	10063	19215	1.61	7.0E-60	4504634	NT	Homo sapiens MHC class 1 region
2088	11286	20511	4.34	7.0E-60	AF077188.1	NT	Homo sapiens Interleukin 10 receptor, beta (IL10RB), mRNA
4160	13384	22484	3.55	7.0E-60	4505488	NT	Homo sapiens cullin 4A (CUL4A) mRNA, complete cds
4573	13787	22882	0.92	7.0E-60	AF284750.1	NT	Homo sapiens ornithine decarboxylase 1 (ODC1) mRNA
6878	16070	25540	3.61	7.0E-60	H58041.1	EST_HUMAN	Homo sapiens ALR-like protein mRNA, partial cds
7804	17118	28650	1.95	7.0E-60	H58041.1	EST_HUMAN	Y1204.11 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:205087 5' similar to contains LTR5 repetitive element;
2145	11343	20561	2.1	6.0E-60	BE964974.2	EST_HUMAN	Y1204.11 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:205087 5' similar to contains LTR5 repetitive element;
6811	15807		10.84	6.0E-60	H52456.1	EST_HUMAN	601658751R1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886089 3'
83	8378	18505	0.9	5.0E-60	A1807917.1	EST_HUMAN	Y1204.11 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:201953 5' similar to contains OFR repetitive element;
83	8378	18508	0.9	5.0E-60	A1807917.1	EST_HUMAN	wf52c07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2359212 3'
2201	11398	20622	2.69	4.0E-60	AW503208.1	EST_HUMAN	wf52c07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2359212 3'
2201	11398	20623	2.69	4.0E-60	AW503208.1	EST_HUMAN	UI-HF-BNO-akt-g-07-0-UJ.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078348 5'
							UI-HF-BNO-akt-g-07-0-UJ.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078348 5'

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Table 4
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2927	12165		1.39	4.0E-60	AA290037.1	EST_HUMAN	EST11498 Uterus Homo sapiens cDNA 5' end similar to similar to retrovirus-related pol
1827	11035	20230	4.76	3.0E-60	BE562611.1	EST_HUMAN	601336448F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3690395 5'
1827	11035	20231	4.76	3.0E-60	BE562611.1	EST_HUMAN	601336448F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3690395 5'
1835	11043		4.97	3.0E-60	6031180	NT	Homo sapiens prohibitin (PHB) mRNA
4451	13850	22745	1.87	3.0E-60	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
6508	14731	24093	2.37	3.0E-60	AW836106.1	EST_HUMAN	RC3-LT0023-200100-012-601 L.T0023 Homo sapiens cDNA
6601	15767	25253	6.71	3.0E-60	5174844	NT	Homo sapiens proline dehydrogenase (proline addase) (PRODH) mRNA
6601	15797	25254	6.71	3.0E-60	5174844	NT	Homo sapiens proline dehydrogenase (proline addase) (PRODH) mRNA
6697	15892	25353	7.68	3.0E-60	5174844	NT	Homo sapiens proline dehydrogenase (proline addase) (PRODH) mRNA
8140	18257		1.6	3.0E-60	AA485286.1	EST_HUMAN	ab0704.r1 Stragene lung (#837210) Homo sapiens cDNA clone IMAGE:840151 5' similar to contains LTR10.H LTR10 repetitive element;
32	8328	18433	1.51	2.0E-60	AY008285.1	NT	Homo sapiens solute carrier (SLC25A18) mRNA, complete cds; nuclear gene for mitochondrial product
1428	10841	18812	5.12	2.0E-60	Z11694.1	NT	H.sapiens 41kDa protein kinase related to rat ERK2
1688	10808	20093	1.43	2.0E-60	M24903.1	NT	Human bcr protein mRNA, 5' end
2447	11638	20859	1.02	2.0E-60	AW380450.1	EST_HUMAN	RC1-HT0268-031289-012-02 HT0268 Homo sapiens cDNA
3554	12777	21808	0.7	2.0E-60	4767887	NT	Homo sapiens v-ref murine sarcoma viral oncogene homolog B1 (BRAF) mRNA
3982	13108	22228	0.86	2.0E-60	AF231818.1	NT	Homo sapiens chromosome 21 unknown mRNA
6018	14608	23577	2.21	2.0E-60	4503044	NT	Homo sapiens corticotropin releasing hormone receptor 2 (CRHR2) mRNA
6018	14608	23578	2.21	2.0E-60	4503044	NT	Homo sapiens corticotropin releasing hormone receptor 2 (CRHR2) mRNA
6128	15310	24743	4.04	2.0E-60	AA311159.1	EST_HUMAN	EST181949 Jurkat T-cells V Homo sapiens cDNA 5' end similar to similar to prothymosin, alpha
6128	15310	24744	4.04	2.0E-60	AA311159.1	EST_HUMAN	EST181949 Jurkat T-cells V Homo sapiens cDNA 5' end similar to similar to prothymosin, alpha
6737	15932	25362	5.05	2.0E-60	L36033.1	NT	Human pre-B cell stimulating factor homologue (SDF1b) mRNA, complete cds
7065	16242	25717	4.11	2.0E-60	11891859	NT	Homo sapiens sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 8A (SEMA8A), mRNA
7065	16242	25718	4.11	2.0E-60	11891859	NT	Homo sapiens sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 8A (SEMA8A), mRNA
7981	17140	26871	1.64	2.0E-60	4507368	NT	Homo sapiens threonyl-RNA synthetase (TARS), mRNA
7961	17140	26872	1.64	2.0E-60	4507368	NT	Homo sapiens threonyl-RNA synthetase (TARS), mRNA
8787	17723		8	2.0E-60	11418192	NT	Homo sapiens non-histone chromosome protein 2 (S. cerevisiae)-like 1 (NHP2L1), mRNA
8938	18188		1.56	2.0E-60	AF068757.1	NT	Homo sapiens somatostatin receptor subtype 3 (SSTR3) gene, 5' flanking region and partial cds
8940	17818		1.23	2.0E-60	11418088	NT	Homo sapiens similar to HSPC022 protein (H. sapiens) (LOC63504), mRNA
8954	17828		1.25	2.0E-60	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
528	9778	18902	1.68	1.0E-60	BE178596.1	EST_HUMAN	PM3-HT0605-270200-001-608 HT0605 Homo sapiens cDNA

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Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3880	13098	22213	1.78	1.0E-60	AU143389.1	EST_HUMAN	AU143389 Y78AA1 Homo sapiens cDNA clone Y78AA1001854 5'
4976	14163	23254	1.83	1.0E-60	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
6704	15888		3.72	1.0E-60	AA244041.1	EST_HUMAN	nc04e12.r1 NCI_CGAP_P11 Homo sapiens cDNA clone IMAGE:1007182 similar to contains L1.L1 L1 repetitive element;
1107	10331	18481	4.23	9.0E-61	AU118344.1	EST_HUMAN	AU118344 HEMBA1 Homo sapiens cDNA clone HEMBA1005583 5'
2630	11813	21031	1.13	8.0E-61	AW008478.1	EST_HUMAN	w05b10.x1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2508555 3'
2630	11813	21032	1.13	8.0E-61	AW008478.1	EST_HUMAN	w05b10.x1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2508555 3'
2803	12141		2.68	8.0E-61	X57147.1	NT	Human endogenous retrovirus pHE.1 (ERV9)
270	9545	18674	2.65	6.0E-61	BE409310.1	EST_HUMAN	601300838F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635480 5'
821	10059	19212	1.54	6.0E-61	BE409310.1	EST_HUMAN	601300838F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635480 5'
1328	10544	19707	12.57	6.0E-61	AF118860.1	NT	Homo sapiens PRO2014 mRNA, complete cds
1807	10820	19998	0.91	6.0E-61	BE257400.1	EST_HUMAN	601109238F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3350145 5'
1825	10838	20015	3.27	6.0E-61	AA596033.1	EST_HUMAN	nm08109.s1 NCI_CGAP_Lar1 Homo sapiens cDNA clone IMAGE:1088887 3'
3277	12510	21840	11.97	6.0E-61	AU130688.1	EST_HUMAN	AU130688 NT2RP3 Homo sapiens cDNA clone NT2RP3001263 5'
5673	14893	24286	3.18	6.0E-61	S79249.1	NT	lg-beta/B29=CD70b (alternatively spliced) [human, B cells, mRNA Partial, 375 nt]
6227	15408	24850	1.8	6.0E-61	U24498.1	NT	Human autosomal dominant polycystic kidney disease protein 1 (PKD1) gene
6342	15623	24971	1.88	6.0E-61	AF035737.1	NT	Homo sapiens general transcription factor 2.1 (GTF2I) mRNA, complete cds
8888	10059	19212	1.82	6.0E-61	BE409310.1	EST_HUMAN	601300838F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635480 5'
1653	10887	20049	2.83	6.0E-61	4508008	NT	Homo sapiens protein phosphatase 1, regulatory subunit 10 (PPP1R10) mRNA
3001	12237	21387	2.23	6.0E-61	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C078
3118	12351	21479	1	6.0E-61	AB020632.1	NT	Homo sapiens mRNA for KIAA0825 protein, partial cds
3182	12397	21532	1.6	6.0E-61		NT	Homo sapiens amyloid beta (A4) precursor protein (protease resdn-ii, Alzheimer disease) (APP), mRNA
3959	13174		1.78	6.0E-61	AJ228041.1	NT	Homo sapiens 950 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
5026	8831	18783	0.7	6.0E-61	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
5275	14447	23519	1.08	6.0E-61	AF001445.1	NT	Homo sapiens core binding factor alpha1 subunit (CBFA1) gene, exon 2
5275	14447	23520	1.08	6.0E-61	AF001445.1	NT	Homo sapiens core binding factor alpha1 subunit (CBFA1) gene, exon 2
8480	17829		4.52	4.0E-61	AV731140.1	EST_HUMAN	AV731140 HTF Homo sapiens cDNA clone HTFARB01 5'
505	9757	18884	1.65	2.0E-61	8822829	NT	Homo sapiens hypothetical protein FLJ11026 (FLJ11026), mRNA
1220	10438	19594	1.84	2.0E-61	BE168410.1	EST_HUMAN	QV3-HT0513-060400-147-401 HT0513 Homo sapiens cDNA
1220	10438	19595	1.84	2.0E-61	BE168410.1	EST_HUMAN	QV3-HT0513-060400-147-401 HT0513 Homo sapiens cDNA
1841	10855	20036	1.84	2.0E-61	N53039.1	EST_HUMAN	W53d11.s1 Soares fetal liver spleen 1NFS Homo sapiens cDNA clone IMAGE:248453 3' similar to gb:25444 60S RIBOSOMAL PROTEIN L35A (HUMAN);
7045	19222	25698	2.74	2.0E-61	AW500258.1	EST_HUMAN	U1HF-BN0-akd-f-12-0-U1.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3076774 5'

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Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7162	16329	25812	3.6	2.0E-61	11421778	NT	Homo sapiens polymerase (RNA) III (DNA directed) (39kD) (RPC39), mRNA
7491	16889		22.39	2.0E-61	11419729	NT	Homo sapiens ribosomal protein L44 (RPL44), mRNA
441	9895		0.8	1.0E-61	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
782	10021	19171	1.88	1.0E-61	5453829	NT	Homo sapiens origin recognition complex, subunit 2 (yeast homolog)-like (ORC2L) mRNA
1828	11034	20229	4.25	1.0E-61	6005983	NT	Homo sapiens zona pellucida glycoprotein 3A (sperm receptor) (ZP3A), mRNA
2163	11361	20579	1.74	1.0E-61	AW927281.1	EST_HUMAN	XM11508.Y1 NCL_CGAP_L15 Homo sapiens cDNA clone IMAGE:2683389 5' similar to contains element
2788	12028	21155	1.09	1.0E-61	BE386383.1	EST_HUMAN	MSR1 repetitive element
3354	12582	21722	0.78	1.0E-61	7662319	NT	601273513F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3814687 5'
4432	13632	22727	0.74	1.0E-61	4759249	NT	Homo sapiens KIAA0808 gene product (KIAA0808), mRNA
4432	13632	22728	0.74	1.0E-61	4759249	NT	Homo sapiens TRAF family member-associated NFKB activator (TANK) mRNA
4873	14061	23155	9.51	1.0E-61	AW288181.1	EST_HUMAN	Homo sapiens TRAF family member-associated NFKB activator (TANK) mRNA
4873	14061	23156	9.51	1.0E-61	AW288181.1	EST_HUMAN	UIH-BW0-ajl-b-08-0-J1.s1 NCL_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2732871 3'
4878	14186	23268	0.79	1.0E-61	AL163210.2	NT	UIH-BW0-ajl-b-08-0-J1.s1 NCL_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2732871 3'
6041	15208	24628	10.68	1.0E-61	M30135.1	NT	Homo sapiens chromosome 21 segment HS21C010
6504	15701	25167	4.48	1.0E-61	11034840	NT	Human P40 T-cell and mast cell growth factor (P40) gene, complete cds
6564	15760	25222	3.39	1.0E-61	AF224689.1	NT	Homo sapiens growth hormone releasing hormone (GHRH), mRNA
6850	16039		2.62	1.0E-61	AW999726.1	EST_HUMAN	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
7084	16261	25738	12.12	1.0E-61	1142892	NT	MRO-BN0070-040400-010-101 BN0070 Homo sapiens cDNA
7228	16450	25839	3.5	1.0E-61	11425578	NT	Homo sapiens KIAA0871 protein (KIAA0871), mRNA
8414	18231	23700	3.11	1.0E-61	11430460	NT	Homo sapiens actinin, alpha 4 (ACTN4), mRNA
8414	18231	23701	3.11	1.0E-61	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
9115	17833	23977	7.99	1.0E-61	11418127	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
9280	18097	23805	1.55	1.0E-61	11430460	NT	Homo sapiens GTP binding protein 1 (GTPBP1), mRNA
4548	13743	22844	1.6	8.0E-62	AA830420.1	EST_HUMAN	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
1115	10339	19489	1.36	7.0E-62	AV714334.1	EST_HUMAN	cc88h11.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1354725 3' similar to SW:POL_MLVRK
3480	12704	21840	0.65	7.0E-62	P17480	SW/ISSPROT	P31795 POL POLYPROTEIN ; AV714334 DCB Homo sapiens cDNA clone DCBAMA08 5'
7890	17106	26036	4.29	7.0E-62	AI208681.1	EST_HUMAN	NUCLEAR TRANSCRIPTION FACTOR 1 (UPSTREAM BINDING FACTOR 1) (UBF-1) (AUTOANTIGEN NOR-90)
2858	12194		1.27	8.0E-62	U09410.1	NT	qp58a04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1839150 3' similar to TR:O15103
3362	12590		5.35	8.0E-62	11418255	NT	O15103 HYPOTHETICAL 27.3 KD PROTEIN ; Human zinc finger protein ZNF131 mRNA, partial cds
							Homo sapiens CGI-58 protein (CGI-58), mRNA

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6346	15527	24875	3.81	6.0E-02	AI762801.1	EST_HUMAN	wf04d02.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2389251 3'
6346	15527	24876	3.81	6.0E-02	AI762801.1	EST_HUMAN	wf04d02.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2389251 3'
6896	16056	25523	2.47	6.0E-02	AW814393.1	EST_HUMAN	MR3-ST0203-130100-025-a09 ST0203 Homo sapiens cDNA
422	9875	18815	2.46	5.0E-02	AI950528.1	EST_HUMAN	wf51d07.x1 NCI_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2547204 3' similar to SW:GG95_HUMAN
2370	11563	20784	4.37	5.0E-02	AJ271735.1	NT	Q08378 GOLGIN-95, contains element MER22 repetitive element;
2370	11563	20785	4.37	5.0E-02	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
3397	12824	21765	2.42	5.0E-02	4508758	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
4319	13520	22815	1.97	5.0E-02	AA431093.1	EST_HUMAN	zw78d09.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:782344 3' similar to SW:NRDC_RAT
4566	13761		1.27	5.0E-02	AW905887.1	EST_HUMAN	P47246 NARDILYSIN;
6821	16114	25590	4.64	5.0E-02	AW410887.1	EST_HUMAN	RC5-NN1089-100500-021-H03 NN1089 Homo sapiens cDNA
7815	17008	26520	2.31	5.0E-02	11425574	NT	fn07g09.x1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2861816 5'
7815	17008	26521	2.31	5.0E-02	11425574	NT	Homo sapiens muscle specific gene (M8), mRNA
850	10087	18246	3.3	4.0E-02	AW181479.1	EST_HUMAN	Homo sapiens muscle specific gene (M9), mRNA
850	10087	18247	3.3	4.0E-02	AW181479.1	EST_HUMAN	au71d03.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781701 5' similar to gb:M37104
851	10087	18248	3.33	4.0E-02	AW181479.1	EST_HUMAN	ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
851	10087	18247	3.33	4.0E-02	AW181479.1	EST_HUMAN	ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
851	10087	18247	3.33	4.0E-02	AW181479.1	EST_HUMAN	ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
2421	11612	20834	27.87	4.0E-02	AI827800.1	EST_HUMAN	ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
2421	11612	20835	27.87	4.0E-02	AI827800.1	EST_HUMAN	ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
3377	12605		9.57	4.0E-02	4557887	NT	ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
6041	14226		0.86	4.0E-02	AJ243213.1	NT	ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
6250	14423	23500	0.81	4.0E-02	4758323	NT	ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
5826	14850	24232	1.84	4.0E-02	4508878	NT	ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
5786	16003	24407	2.71	4.0E-02	11420654	NT	wf12b08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2350359 3' similar to
6151	15335	24772	1.76	4.0E-02	11421041	NT	gb:X57138_ma1 HISTONE H2B.2 (HUMAN);
							wf12b08.x1 Soares_NFL_T_GBC_S1 HISTONE H2B.2 (HUMAN);
							gb:X57138_ma1 HISTONE H2B.2 (HUMAN);
							Homo sapiens keratin 18 (KRT18) mRNA
							Homo sapiens partial 5HT4 receptor gene, exons 2 to 5
							Homo sapiens enhancer of zeste (Drosophila) homolog 2 (EZH2) mRNA
							Homo sapiens solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 2 (SLC13A2) mRNA
							Homo sapiens ubiquitin specific protease 9, X chromosome (Drosophila fat facets related) (USP9X), mRNA
							Homo sapiens phosphoribosyl pyrophosphate synthetase 2 (PRPS2), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6348	15528	24977	2.14	4.0E-62	7657057	NT	Homo sapiens eukaryotic translation initiation factor 2B, subunit 2 (beta, 39kD) (EIF2B2), mRNA
6348	15528	24978	2.14	4.0E-62	7657057	NT	Homo sapiens eukaryotic translation initiation factor 2B, subunit 2 (beta, 39kD) (EIF2B2), mRNA
6731	15828	25385	10.64	4.0E-62	AB033089.1	NT	Homo sapiens mRNA for KIAA1263 protein, partial cds
7582	18787	26281	2.72	4.0E-62	Z78768.1	NT	H.sapiens flow-sorted chromosome 8 HindIII fragment, SC8pA16D3
7582	18787	26282	2.72	4.0E-62	Z78768.1	NT	H.sapiens flow-sorted chromosome 8 HindIII fragment, SC8pA16D3
7779	16974	26487	22.33	4.0E-62	S70594.1	NT	thyroid-stimulating hormone alpha subunit (human, Genomic, 288 nt, segment 3 of 4)
8309	17477	26593	2.09	4.0E-62	11418088	NT	Homo sapiens putative nuclear protein (HRIHFB2122), mRNA
8831	18190		2.62	4.0E-62	11418182	NT	Homo sapiens non-histone chromosome protein 2 (S. cerevisiae)-like 1 (NHP2L1), mRNA
9047	17920	23873	1.7	4.0E-62	11418322	NT	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA
9069	17915	23870	7.8	4.0E-62	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
9069	17915	23871	7.8	4.0E-62	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
9148	17952	23883	2.58	4.0E-62	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
74	9368	18496	1.85	3.0E-62	4557784	NT	Homo sapiens neurofibromin 2 (bilateral acoustic neuroma) (NF2) mRNA
3011	12247	21376	0.74	3.0E-62	AB040809.1	NT	Homo sapiens mRNA for KIAA1476 protein, partial cds
3011	12247	21377	0.74	3.0E-62	AB040809.1	NT	Homo sapiens mRNA for KIAA1476 protein, partial cds
3676	12897	22017	15.04	3.0E-62	X52858.1	NT	Human cyclophilin-related processed pseudogene
6635	15630	25292	6.49	3.0E-62	AI632733.1	EST_HUMAN	wa33f04.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2289903 3' similar to contains THR.12 THR repetitive element:
1238	10455	19814	2.67	2.0E-62	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
7128	18303		5.65	2.0E-62	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
8188	17318		28.63	2.0E-62	BF330876.1	EST_HUMAN	QV4-BT0257-081199-017-603 BT0257 Homo sapiens cDNA
1051	10277	19430	2	1.0E-62	AF248540.1	NT	Homo sapiens interectin 2 (SH3D1B) mRNA, complete cds
1530	10744	19917	17.89	1.0E-62	L78810.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
1788	10978	20167	1.58	1.0E-62	AA625207.1	EST_HUMAN	af70e11.1 Soares_NH-MPU_S1 Homo sapiens cDNA clone IMAGE:1047404 5' similar to WP-K01H12.1 CE03453:
2865	12103	21234	0.94	1.0E-62	AL039044.1	EST_HUMAN	DKFZp568F104_r1 568 (synonym: hnf42) Homo sapiens cDNA clone DKFZp568F104 5'
3402	12628		2.08	1.0E-62	AB040911.1	NT	Homo sapiens mRNA for KIAA1478 protein, partial cds
4526	13722	22818	1.26	1.0E-62	8923201	NT	Homo sapiens hypothetical protein FLJ20212 (FLJ20212), mRNA
6138	15320	24754	2.5	1.0E-62	AA722878.1	EST_HUMAN	zg89f10.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:408771 3'
6136	15320	24755	2.5	1.0E-62	AA722878.1	EST_HUMAN	zg89f10.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:408771 3'
6806	16001	25460	2.36	1.0E-62	X15533.1	NT	H.sapiens lysosomal acid phosphatase gene (EC 3.1.3.2) Exon 9
6806	16001	25461	2.36	1.0E-62	X15533.1	NT	H.sapiens lysosomal acid phosphatase gene (EC 3.1.3.2) Exon 9
6940	16084	25552	3.51	1.0E-62	AA465170.1	EST_HUMAN	aa33d08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:815055 3'

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7908	17121	26862	2.84	1.0E-02	Z78688.1	NT	H. sapiens flow-sorted chromosome 8 HindIII fragment, SC9pA14D8
8917	17804		2.3	1.0E-02	11418322	NT	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA
9129	17940	23880	3.35	1.0E-02	11430480	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
343	9811	18738	2.08	9.0E-03	AW818405.1	EST_HUMAN	QV4-ST0234-181199-037-05 ST0234 Homo sapiens cDNA
2314	11508		1.26	9.0E-03	C18159.1	EST_HUMAN	C18159 Human placenta cDNA (TFijwara) Homo sapiens cDNA clone GEN-558C10 5'
4018	13230	22332	7.81	9.0E-03	AB002348.2	NT	Homo sapiens mRNA for KIAA0350 protein, partial cds
4018	13230	22333	7.81	9.0E-03	AB002348.2	NT	Homo sapiens mRNA for KIAA0350 protein, partial cds
5300	14487	26928	2.91	9.0E-03	11418185	NT	Homo sapiens aconitase 2, mitochondrial (ACO2), mRNA
6157	15340	24777	3.67	9.0E-03	11426883	NT	Homo sapiens nucleoporin 89kD (NUP89), mRNA
7610	16813	26309	2	9.0E-03	BF203408.1	EST_HUMAN	60186582BF1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4088487 5'
2312	11508	20727	1	8.0E-03	4557734	NT	Homo sapiens monoamine oxidase A (MAOA), nuclear gene encoding mitochondrial protein, mRNA
2341	11534	20757	4.33	8.0E-03	5031810	NT	Homo sapiens IL2-inducible T-cell kinase (ITK), mRNA
3438	12683	21765	4.09	8.0E-03	AF198349.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
3438	12683	21766	4.09	8.0E-03	AF198349.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
4262	13455	22547	3.98	8.0E-03	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
937	10170		1.24	7.0E-03	AB72137.1	EST_HUMAN	wm55g11.1 NCI_CGAP_U2 Homo sapiens cDNA clone IMAGE:2439908 3'
5358	14588		21.03	6.0E-03	AA420803.1	EST_HUMAN	nc63f02.1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:745947 similar to gb:Y00361 60S
3293	12524	21658	0.98	4.0E-03	AL163278.2	NT	RIBOSOMAL PROTEIN (HUMAN);
3798	13014	22128	1.48	4.0E-03	AB014607.1	NT	Homo sapiens chromosome 21 segment HS21C078
3788	13014	22127	1.48	4.0E-03	AB014607.1	NT	Homo sapiens mRNA for KIAA0707 protein, partial cds
5848	15063	24471	2.59	4.0E-03	AW750372.1	EST_HUMAN	Homo sapiens mRNA for KIAA0707 protein, partial cds
5848	15063	24472	2.59	4.0E-03	AW750372.1	EST_HUMAN	CM3-BT0595-180100-072-g09 BT0595 Homo sapiens cDNA
7692	16891	26399	2.35	4.0E-03	AW134709.1	EST_HUMAN	CM3-BT0595-180100-072-g09 BT0595 Homo sapiens cDNA
7692	16891	26400	2.35	4.0E-03	AW134709.1	EST_HUMAN	UI-H-B11-abq-a-02-Q-J1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2712482 3'
1804	11110	20304	2.09	3.0E-03	AB018260.1	NT	UI-H-B11-abq-a-02-Q-J1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2712482 3'
2734	11813	21129	0.97	3.0E-03	J00310.1	NT	Homo sapiens mRNA for KIAA0717 protein, partial cds
2773	10482	19823	11.76	3.0E-03	6005963	NT	Human Met-RNA-1 gene 1
5859	15077	24490	31.49	3.0E-03	11545810	NT	Homo sapiens zinc finger protein 144 (Met-18) (ZNF144), mRNA
196	9476	19608	1.26	2.0E-03	U07804.1	NT	Homo sapiens hepatocellular carcinoma antigen gene 520 (LOC83928), mRNA
203	9483	18616	1.81	2.0E-03	4885226	NT	Human DNA topoisomerase I mRNA, partial cds
504	9756		1.42	2.0E-03	4557624	NT	Homo sapiens eyes absent (Drosophila) homolog 2 (EYA2), mRNA
							Homo sapiens glutamate-cysteine ligase (gamma-glutamylcysteine synthetase), catalytic (72.8kD) (GLCLC) mRNA

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838	10074	18231	2.04	2.0E-03	7857042	NT	Homo sapiens Down syndrome candidate region 1 (DSCR1), mRNA
1548	10782	18938	1.88	2.0E-03	AB030388.1	NT	Homo sapiens RHCE mRNA for Rh blood CE group antigen polypeptide, complete cds
1548	10782	18937	1.88	2.0E-03	AB030388.1	NT	Homo sapiens RHCE mRNA for Rh blood CE group antigen polypeptide, complete cds
1737	10849	20132	2.19	2.0E-03	BE410739.1	EST_HUMAN	601301627F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638103 5'
3120	12355	21484	1.16	2.0E-03	4502188	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
3253	12488	21618	2.53	2.0E-03	AF109718.1	NT	Homo sapiens chromosome 3 subtelomeric region
3883	13089	22218	2.35	2.0E-03	L39891.1	NT	Homo sapiens polycystic kidney disease-associated protein (PKD1) gene, complete cds
4882	14070	23187	1.1	2.0E-03	AF111187.2	NT	Homo sapiens Jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
5213	14388	23473	0.87	2.0E-03	6912817	NT	Homo sapiens glutamyl-peptide cyclotransferase (glutamyl cyclase) (QPCT), mRNA
5308	18049	23542	1.88	2.0E-03	11418429	NT	Homo sapiens similar to ectorucleotide pyrophosphatase/phosphodiesterase 3 (H. sapiens) (LOC63214), mRNA
5608	14830	24208	2.73	2.0E-03	BF373541.1	EST_HUMAN	QV1-FT0170-040700-285-c05 FTO170 Homo sapiens cDNA
5608	14830	24207	2.73	2.0E-03	BF373541.1	EST_HUMAN	QV1-FT0170-040700-285-c05 FTO170 Homo sapiens cDNA
7332	18548	28038	27.58	2.0E-03	N78945.1	EST_HUMAN	zb18b05.s1 Soares_fetal_jung_NbHL18W Homo sapiens cDNA clone IMAGE:302385 3' similar to gb:X17208.40S RIBOSOMAL PROTEIN S4 (HUMAN);
7355	18571	28082	2.88	2.0E-03	AF088810.1	NT	Homo sapiens neurodin III-alpha gene, partial cds
7355	18571	28083	2.88	2.0E-03	AF088810.1	NT	Homo sapiens neurodin III-alpha gene, partial cds
8513	18133	23748	5.24	2.0E-03	11418185	NT	Homo sapiens aconitase 2, mitochondrial (ACO2), mRNA
4335	13538	22827	2.88	1.0E-03	F08485.1	EST_HUMAN	HSCZVD111 normalized infant brain cDNA Homo sapiens cDNA clone c-zvd11
4335	13538	22828	2.88	1.0E-03	F08485.1	EST_HUMAN	HSCZVD111 normalized infant brain cDNA Homo sapiens cDNA clone c-zvd11
8819	15815		2.88	1.0E-03	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
9197	18248		7.48	1.0E-03	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
6416	15613	25077	8.1	9.0E-04	AI478180.1	EST_HUMAN	hm50b07.x1 NCL_OGAP_Kid11 Homo sapiens cDNA clone IMAGE:2181525 3'
1053	10279		18.75	8.0E-04	BE280798.1	EST_HUMAN	601155232F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138038 5'
5730	14949	24348	3.59	8.0E-04	BE885755.1	EST_HUMAN	601508988F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3910336 5'
8320	17423		4.21	8.0E-04	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
8374	17480		2.3	8.0E-04	T80851.1	EST_HUMAN	y888502.r1 Stratiogene lung (#837210) Homo sapiens cDNA clone IMAGE:78178 5'
3503	12727		0.98	7.0E-04	BE394321.1	EST_HUMAN	601311455F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3833204 5'
4743	13834	23037	2.89	7.0E-04	4507490	NT	Homo sapiens thimet oligopeptidase 1 (THOP1) mRNA
4743	13834	23038	2.89	7.0E-04	4507490	NT	Homo sapiens thimet oligopeptidase 1 (THOP1) mRNA
7088	18283	25741	4.75	7.0E-04	Y07848.1	NT	Homo sapiens EWS, gar22, rrp22 and bam22 genes

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Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1697	10909	20084	3.93	6.0E-64	AI651992.1	EST_HUMAN	w651e07.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2309220 3' similar to gb:M15182 BETA-GLUCURONIDASE PRECURSOR (HUMAN);
1697	10909	20085	3.63	6.0E-64	AI651992.1	EST_HUMAN	w651e07.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2309220 3' similar to gb:M15182 BETA-GLUCURONIDASE PRECURSOR (HUMAN);
3086	12322	21443	4.98	6.0E-64	AW026445.1	EST_HUMAN	wv13e03.x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2529436 3'
3086	12322	21444	4.98	6.0E-64	AW026445.1	EST_HUMAN	wv13e03.x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2529436 3'
5501	14727	24087	2.09	6.0E-64	Y18933.1	NT	Homo sapiens MCP-1 gene and enhancer region
5501	14727	24088	2.09	6.0E-64	Y18933.1	NT	Homo sapiens MCP-1 gene and enhancer region
5507	14732	24084	6.03	6.0E-64	M13975.1	NT	Homo sapiens protein kinase C beta-II type (PRKCB1) mRNA, complete cds
6179	16361	24700	2.45	6.0E-64	11525878	NT	Homo sapiens mesenchyme homeo box 1 (MEOX1), mRNA
6179	16361	24800	2.45	6.0E-64	11525878	NT	Homo sapiens mesenchyme homeo box 1 (MEOX1), mRNA
6861	16051	25518	8.49	6.0E-64	11420355	NT	Homo sapiens acetyl-CoA synthetase (LOC55902), mRNA
6908	16176	25647	2.76	6.0E-64	S78475.1	NT	tkc [human, brain, mRNA, 2715 nt]
7353	16569	26059	9.75	6.0E-64	11420197	NT	Homo sapiens stromal antigen 3 (STAG3), mRNA
7353	16569	26060	9.75	6.0E-64	11420197	NT	Homo sapiens stromal antigen 3 (STAG3), mRNA
7687	12322	21443	2.09	6.0E-64	AW026445.1	EST_HUMAN	wv13e03.x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2529436 3'
7687	12322	21444	2.09	6.0E-64	AW026445.1	EST_HUMAN	wv13e03.x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2529436 3'
8532	17558	23980	4.22	6.0E-64	11526188	NT	Homo sapiens interleukin 10 receptor, beta (IL10RB), mRNA
830	10088	19222	2.38	5.0E-64	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
830	10088	19223	2.38	5.0E-64	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
1346	10561	19726	1.1	5.0E-64	AB020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
1426	10639	19809	1.34	5.0E-64	L40933.1	NT	Homo sapiens phosphoglucomutase-related protein (PGMRP) gene, complete cds
1426	10639	19810	1.34	5.0E-64	L40933.1	NT	Homo sapiens phosphoglucomutase-related protein (PGMRP) gene, complete cds
1686	10688	20086	1.67	5.0E-64	U98358.1	NT	Human (3) yinib protein homolog mRNA, complete cds
2778	10687	19862	5.41	5.0E-64	7682205	NT	Homo sapiens KIAA0618 gene product (KIAA0618), mRNA
2778	10687	19863	5.41	5.0E-64	7682205	NT	Homo sapiens KIAA0618 gene product (KIAA0618), mRNA
3935	13151	22267	6.01	5.0E-64	AF017433.1	NT	Homo sapiens putative transcription factor CR53 (CR53) mRNA, partial cds
4083	13292	22381	0.68	5.0E-64	AB020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
7390	16904	26063	4.15	4.0E-64	AW813783.1	EST_HUMAN	RC3-ST0197-120200-015-ae03 ST0197 Homo sapiens cDNA
7390	16904	26094	4.15	4.0E-64	AW813783.1	EST_HUMAN	RC3-ST0197-120200-015-ae03 ST0197 Homo sapiens cDNA
2164	11362	20580	12.04	3.0E-64	C18895.1	EST_HUMAN	C18895 Homo placenta cDNA (TFujitara) Homo sapiens cDNA clone GEN-569E02 5'
3221	12455	21588	0.7	3.0E-64	BE794381.1	EST_HUMAN	801589565F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943577 5'
3420	12645	21774	1.42	3.0E-64	AV711714.1	EST_HUMAN	AV711714 DCA Homo sapiens cDNA clone DCAAMC01 5'
3420	12645	21775	1.42	3.0E-64	AV711714.1	EST_HUMAN	AV711714 DCA Homo sapiens cDNA clone DCAAMC01 5'

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5872	15080	24503	2.5	3.0E-04	BF370000.1	EST_HUMAN	RC8-FN0019-280800-011-G11 FN0019 Homo sapiens cDNA
6618	15814	25273	2.49	3.0E-04	AF248853.1	NT	Homo sapiens gdl matrix protein GM130 (GOLGA2) mRNA, complete cds
6618	15814	25274	2.49	3.0E-04	AF248853.1	NT	Homo sapiens gdl matrix protein GM130 (GOLGA2) mRNA, complete cds
6823	15819	25277	2.28	3.0E-04	BE208521.1	EST_HUMAN	bb72h12.y1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3047875 5' similar to gb:U08068 DNAJ PROTEIN HOMOLOG 2 (HUMAN);
6823	15819	25278	2.26	3.0E-04	BE208521.1	EST_HUMAN	bb72h12.y1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3047875 5' similar to gb:U08068 DNAJ PROTEIN HOMOLOG 2 (HUMAN);
7760	16884	26498	2.06	3.0E-04	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C048
7760	16884	26499	2.06	3.0E-04	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C048
8188	17320	26863	5.53	3.0E-04	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
1098	10320	19472	2.11	2.0E-04	AA608940.1	EST_HUMAN	af09408.s1 Soares, testis_NHT Homo sapiens cDNA clone IMAGE:1031151 3'
1401	10816	19779	3.29	2.0E-04	4757701	NT	Homo sapiens eIF4E-like cap-binding protein (4EHP) mRNA
2491	11681		2.83	2.0E-04	AI027030.1	EST_HUMAN	wo87b01.x1 NCI_CGAP_Kd11 Homo sapiens cDNA clone IMAGE:2482281 3' similar to contains element L1 repetitive element;
2496	11685	20903	8.65	2.0E-04	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C048
2498	11685	20904	8.65	2.0E-04	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C048
3105	12340	21488	2.07	2.0E-04	4504088	NT	Homo sapiens glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2) (GOT2), nuclear gene encoding mitochondrial protein, mRNA
5656	14879	24269	2.65	2.0E-04	AU124387.1	EST_HUMAN	AU124387 NT2RM2 Homo sapiens cDNA clone NT2RM2002113 5'
5668	15086	24500	4.15	2.0E-04	BF688537.1	EST_HUMAN	602123474F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4280395 5'
5630	15146	24557	2.05	2.0E-04	AI078387.1	EST_HUMAN	oz20603.x1 Soares, testis_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1676717 3'
5684	15179	24598	4.1	2.0E-04	M77185.1	NT	H. sapiens dpanline receptor D5 pseudogene 1, partial cds
7347	16563	26052	2.91	2.0E-04	BF528114.1	EST_HUMAN	602042882F1 NCI_CGAP_Bim67 Homo sapiens cDNA clone IMAGE:4180556 5'
7619	16822	26317	5.7	2.0E-04	AI922911.1	EST_HUMAN	wn81b08.x1 NCI_CGAP_UH Homo sapiens cDNA clone IMAGE:2452211 3'
7619	16822	26318	5.7	2.0E-04	AI922911.1	EST_HUMAN	wn81b08.x1 NCI_CGAP_UH Homo sapiens cDNA clone IMAGE:2452211 3'
7785	16880	26493	2.13	2.0E-04	AW864773.1	EST_HUMAN	PM2-SN0018-220300-002-e12 SN0018 Homo sapiens cDNA
8448	17607	24016	1.36	2.0E-04	8567397	NT	Homo sapiens period (Drosophila) homolog 3 (PER3), mRNA
8913	17801		2.65	2.0E-04	H55162.1	EST_HUMAN	CHR220101 Chromosome 22 exon Homo sapiens cDNA clone C22_132 5'
282	8538	18667	2.22	1.0E-04	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
1749	10861	20143	27.24	1.0E-04	AI928419.1	EST_HUMAN	af060c01.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2519136 3' similar to gb:L21606_cds1 PROTHYMOSIN ALPHA (HUMAN); contains element MSR1 repetitive element;
2873	12210	21348	0.82	1.0E-04	4507334	NT	Homo sapiens synapjanin 1 (SYNJ1), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3485	12709	21848	5.93	1.0E-04	AF190779.1	NT	Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel α
3561	12784	21913	1.41	1.0E-04	AF228527.1	NT	Homo sapiens TRIAD3 mRNA, partial cds
3561	12784	21914	1.41	1.0E-04	AF228527.1	NT	Homo sapiens TRIAD3 mRNA, partial cds
3878	13094	22211	0.78	1.0E-04	8822829	NT	Homo sapiens hypothetical protein FLJ11028 (FLJ11028), mRNA
8419	17491		2.5	1.0E-04	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
2241	11438	20860	1.5	9.0E-05	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
2241	11438	20881	1.5	9.0E-05	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
8088	17203		35.12	9.0E-05	BF330876.1	EST_HUMAN	QV4-BT0257-Q81198-Q17-e03 BT0257 Homo sapiens cDNA
8042	17178	28717	11.84	8.0E-05	AI829244.1	EST_HUMAN	aw58H07.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2619005 3' similar to
1063	10289	19440	2.01	6.0E-05	AV721898.1	EST_HUMAN	SV-RL21_HUMAN HTB 608 RIBOSOMAL PROTEIN L21.;
1890	11097		20.4	6.0E-05	AA550929.1	EST_HUMAN	ni86d10.s1 NCI CGAP_P11 Homo sapiens cDNA clone IMAGE:090379 similar to gb:K03002 60S RIBOSOMAL PROTEIN L32 (HUMAN);
6700	15895	25356	3.18	6.0E-05	AW083252.1	EST_HUMAN	xc07b09.x1 NCI CGAP_Co21 Homo sapiens cDNA clone IMAGE:2583545 3' similar to TR:Q63308 Q63308
6768	15963	25420	4.99	6.0E-05	AA427878.1	EST_HUMAN	LONG INTERSPERSED REPETITIVE DNA CONTAINING 7 ORFS; contains L1.b2 L1 repetitive element;
6768	15963	25421	4.99	6.0E-05	AA427878.1	EST_HUMAN	zw53b08.s1 Soares_tet1_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:773747 3'
7450	16859	26147	4.89	6.0E-05	BE567816.1	EST_HUMAN	zw53b08.s1 Soares_tet1_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:773747 3'
8030	17167	26705	4.81	6.0E-05	AL163210.2	NT	601340485F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3882877 5'
637	9882	19006	0.72	5.0E-05	AF064604.1	NT	Homo sapiens chromosome 21 segment HS21C010
1361	10578	19741	1.71	5.0E-05	7881951	NT	Homo sapiens KE03 protein mRNA, partial cds
1361	10578	19742	1.71	5.0E-05	7881951	NT	Homo sapiens KIAA0156 gene product (KIAA0156), mRNA
2123	11322	20340	1.56	5.0E-05	AB033768.1	NT	Homo sapiens KIAA0156 gene product (KIAA0156), mRNA
3222	12456	21589	2.37	5.0E-05	4507848	NT	Homo sapiens hPAD-coctony10 mRNA for peptidylarginine deaminase type I, complete cds
3222	12456	21590	2.37	5.0E-05	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
188	9478	18611	2.79	4.0E-05	AL120419.1	EST_HUMAN	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
753	9904	19138	1.27	4.0E-05	AI280468.1	EST_HUMAN	DKFZp761G108_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761G108 5'
753	9904	19139	1.27	4.0E-05	AI280468.1	EST_HUMAN	qin46e01.x1 Soares_placenta_8to9weeks_2NHP8b09W Homo sapiens cDNA clone IMAGE:1891800 3'
1086	10310	19483	1.28	4.0E-05	4828735	NT	qin46e01.x1 Soares_placenta_8to9weeks_2NHP8b09W Homo sapiens cDNA clone IMAGE:1891800 3'

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Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1479	10892	19887	28.34	4.0E-65	4506838	NT	Homo sapiens ribosomal protein L34 (RPL34) mRNA
2305	11489	20719	3.54	4.0E-65	BE221489.1	EST_HUMAN	h226e04.x1 NCI_CGAP_Mel15 Homo sapiens cDNA clone IMAGE:3171102 3'
2305	11489	20720	3.54	4.0E-65	BE221489.1	EST_HUMAN	h226e04.x1 NCI_CGAP_Mel15 Homo sapiens cDNA clone IMAGE:3171102 3'
3920	13142	22259	0.96	4.0E-65	AW983185.1	EST_HUMAN	RC2-BN0033-160200-013-a03 BN0033 Homo sapiens cDNA
5735	14954	24352	4.42	4.0E-65	AB033093.1	NT	Homo sapiens mRNA for KIAA1267 protein, partial cds
6736	14954	24353	4.42	4.0E-65	AB033093.1	NT	Homo sapiens hypothetical protein FLJ22087 (FLJ22087), mRNA
6173	15355	24793	2.45	4.0E-65	11545780	NT	Homo sapiens PRO1474 mRNA, complete cds
7863	16863	28365	2.72	4.0E-65	AF119846.1	NT	Homo sapiens fragile X mental retardation, autosomal homolog 1 (FXR1), mRNA
8764	10310	19463	1.88	4.0E-65	4828735	NT	Homo sapiens gene for AF-6, complete cds
8901	17784		5.17	4.0E-65	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
8268	9478	18811	1.88	4.0E-65	AL120419.1	EST_HUMAN	DKFZp761G108.1 761 (synonym: hemy2) Homo sapiens cDNA clone DKFZp761G108 5'
97	9391	18521	1.28	3.0E-65	5031978	NT	Homo sapiens pre-B-cell colony-enhancing factor (PBEF) mRNA
88	8391	18621	1.04	3.0E-65	5031978	NT	Homo sapiens HZF9 mRNA for zinc finger protein
1239	11846		4.66	3.0E-65	X78832.1	NT	H. sapiens HZF9 mRNA for zinc finger protein
1543	10758	18630	0.92	3.0E-65	4504838	NT	Homo sapiens immunoglobulin superfamily, member 3 (IGSF3) mRNA, and translated products
							ov23f03.81 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1638173 3' similar to contains element
							MSR1 repetitive element;
1791	11001	20197	1.13	3.0E-65	A1000692.1	EST_HUMAN	Homo sapiens mRNA for KIAA0235 protein, partial cds
2847	12185	21317	0.99	3.0E-65	D87078.2	NT	Homo sapiens laminin, beta 1 (LAMB1), mRNA
3244	12477	21610	1.5	3.0E-65	4504850	NT	ov23f03.81 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1638173 3' similar to contains element
							MSR1 repetitive element;
3701	12921	22039	1.22	3.0E-65	A1000692.1	EST_HUMAN	Homo sapiens rab8 GTPase activating protein (GAP and centrosome-associated) (GAPCENA), mRNA
4651	13845	22638	1.58	3.0E-65	6912385	NT	zw85e06.1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:781042 5'
7927	16403	25988	15.68	3.0E-65	AA430006.1	EST_HUMAN	602155082F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4285868 5'
3382	12609	21743	7.64	2.0E-65	BF680204.1	EST_HUMAN	601190883F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3334741 5'
5985	15112		5.18	2.0E-65	BE263373.1	EST_HUMAN	602134359F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4286295 5'
6133	15317	24750	27.19	2.0E-65	BF576922.1	EST_HUMAN	Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 3 (SMARCD3), mRNA
7249	16489	25981	1.71	2.0E-65	11419247	NT	EST178755 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end similar to endogenous retrovirus
8373	17459		11.09	2.0E-65	AA307804.1	EST_HUMAN	601854033F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4073789 5'
8868	18111		3.24	2.0E-65	BF246080.1	EST_HUMAN	601783488F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4026501 5'
90	9383		0.99	1.0E-65	BF125544.1	EST_HUMAN	Homo sapiens putative Rab5 GDP/GTP exchange factor homologue (RABEX5), mRNA
545	9768	18920	1.2	1.0E-65	7657495	NT	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2007	11210	20420	1.4	1.0E-65	AB040946.1	NT	Homo sapiens mRNA for KIAA1513 protein, partial cds
3351	12578	21719	0.88	1.0E-65	BE466881.1	EST_HUMAN	h224609.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:3208888 3'
3875	13189	22287	1.9	1.0E-65	4504082	NT	Homo sapiens glypican 4 (GPC4) mRNA
3975	13189	22288	1.9	1.0E-65	4504082	NT	Homo sapiens glypican 4 (GPC4) mRNA
4189	13393	22491	4.44	1.0E-65	AW028340.1	EST_HUMAN	wx08c09.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2543152 3'
4189	13393	22492	4.44	1.0E-65	AW028340.1	EST_HUMAN	wx08c09.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2543152 3'
4230	13442		1.11	1.0E-65	AW062813.1	EST_HUMAN	EST374888 IMAGE resequencing, MAGG Homo sapiens cDNA
5065	14237	23325	1.09	1.0E-65	AW238282.1	EST_HUMAN	XP20c01.x1 NCI_CGAP_HN10 Homo sapiens cDNA clone IMAGE:2740898 3'
5055	14237	23326	1.09	1.0E-65	AW238282.1	EST_HUMAN	XP20c01.x1 NCI_CGAP_HN10 Homo sapiens cDNA clone IMAGE:2740898 3'
6770	15985	25423	2.68	1.0E-65	AU129040.1	EST_HUMAN	AU129040 NT2RP2 Homo sapiens cDNA clone NT2RP2004714 5'
6770	15985	25424	2.68	1.0E-65	AU129040.1	EST_HUMAN	AU129040 NT2RP2 Homo sapiens cDNA clone NT2RP2004714 5'
6774	15989		4.14	1.0E-65	11431984	NT	Homo sapiens inositol 1,4,5-trisphosphate receptor, type 1 (IPR1), mRNA
6906	16063	25529	7.42	1.0E-65	AI191716.1	EST_HUMAN	qc58a02.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1733450 3' similar to gb:M29581 ZINC FINGER PROTEIN 8 (HUMAN); contains MER19.11 MER19 repetitive element;
7243	16463	25953	2.12	1.0E-65	M26167.1	NT	Human platelet factor 4 variation 1 (PF4var1) gene, complete cds
7358	16574	26068	25.94	1.0E-65	4506060	NT	Homo sapiens ribosomal protein L7a (RPL7A) mRNA
7690	16888	26396	2.8	1.0E-65	BF698707.1	EST_HUMAN	602126238F1 NIH_MGC 58 Homo sapiens cDNA clone IMAGE:4283313 5'
7763	16959	26469	2.63	1.0E-65	AI621017.1	EST_HUMAN	is76a08.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2237170 3' similar to gb:L16633_ma1
8420	17492		2.48	1.0E-65	11418041	NT	PANCREATITIS ASSOCIATED PROTEIN 1 PRECURSOR (HUMAN);
8524	17554	23987	5.48	1.0E-65	11418322	NT	Homo sapiens TNF-inducible protein CG12-1 (CG12-1), mRNA
8963	17834		1.47	1.0E-65	11418248	NT	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA
71	9368	18492	0.93	9.0E-68	AL160311.1	NT	Homo sapiens sulfotransferase-related protein (SULTX3), mRNA
71	9368	18493	0.93	9.0E-68	AL160311.1	NT	Novel human gene mapping to chromosome 22
1362	10577	19743	2.59	9.0E-68	5031980	NT	Novel human gene mapping to chromosome 22
1362	10577	19744	2.59	9.0E-68	5031980	NT	Homo sapiens 26S proteasome-associated pad1 homolog (POH1) mRNA
1477	10690		4.32	9.0E-68	M87299.1	NT	Homo sapiens 26S proteasome-associated pad1 homolog (POH1) mRNA
3877	13063	22209	0.73	9.0E-68	M72393.1	NT	Human transposon-like element, partial
3877	13063	22210	0.73	9.0E-68	M72393.1	NT	Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds
4699	13860	22890	0.82	9.0E-68	AL137163.1	NT	Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds
7987	17103		1.9	7.0E-68	BE064410.1	EST_HUMAN	Novel human gene mapping to chromosome X
4359	13581	22855	1.14	8.0E-68	AI924653.1	EST_HUMAN	RC4-BT0311-141199-011-h08 BT0311 Homo sapiens cDNA
							wf57h07.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2449597 3' similar to WP:F15G9.4A
							CE18595;

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4359	13561	22859	1.14	6.0E-08	AB24853.1	EST_HUMAN	wnt57h07.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2449597 3' similar to WP:F15G9.4A CE18595;
4359	13561	22857	1.14	6.0E-08	AB24853.1	EST_HUMAN	wnt57h07.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2449597 3' similar to WP:F15G9.4A CE18595;
7719	18918	28428	9.19	6.0E-08	X89181.1	NT	H. sapiens mRNA for ribosomal protein L31
1376	10589	18755	2	5.0E-08	BE064410.1	EST_HUMAN	RC4-BT0311-141189-011-H08 BT0311 Homo sapiens cDNA
5140	14319	23410	0.97	5.0E-08	BE898644.1	EST_HUMAN	601681592F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3951781 5'
5140	14319	23411	0.97	5.0E-08	BE898644.1	EST_HUMAN	601681592F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3951781 5'
6852	18041	25505	6.48	5.0E-08	11420557	NT	Homo sapiens thyroid hormone receptor binding protein (AIB3), mRNA
800	10030	19190	1.09	4.0E-08	6870818	NT	Mus musculus fragile X mental retardation syndrome 1 homolog (Fmr1), mRNA
2245	11440	20684	4.3	4.0E-08	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
2437	11628		7.08	4.0E-08	AJ23384.1	NT	Homo sapiens germ-line DNA upstream of Jkappa locus
4783	13982		10.15	4.0E-08	8835487	NT	Human endogenous retrovirus, complete genome
5468	14692	24045	4.68	4.0E-08	11428643	NT	Homo sapiens methylene tetrahydrofolate dehydrogenase (NAD+ dependent), methenyltetrahydrofolate cyclohydrolase (MTHFD2), mRNA
6020	14510	23568	4.04	4.0E-08	AW965473.1	EST_HUMAN	EST377548 IMAGE resequences, MAGI Homo sapiens cDNA
6132	15316	24749	6.3	4.0E-08	U78168.1	NT	Homo sapiens cAMP-regulated guanine nucleotide exchange factor I (cAMP-GEFI) mRNA, complete cds
6347	14692	24045	2.08	4.0E-08	11428643	NT	Homo sapiens methylene tetrahydrofolate dehydrogenase (NAD+ dependent), methenyltetrahydrofolate cyclohydrolase (MTHFD2), mRNA
6481	15688	25154	10.1	4.0E-08	11421638	NT	Homo sapiens hypothetical protein FLJ20116 (FLJ20116), mRNA
1430	10843	19814	37.87	3.0E-08	4502098	NT	Homo sapiens solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 5 (SLC25A5), nuclear gene encoding mitochondrial protein, mRNA
1430	10843	19815	37.87	3.0E-08	4502098	NT	Homo sapiens solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 5 (SLC25A5), nuclear gene encoding mitochondrial protein, mRNA
1951	11155	20357	0.92	3.0E-08	N55323.1	EST_HUMAN	yz27g12.r1 Soares multiple sclerosis 2NBH-MSP Homo sapiens cDNA clone IMAGE:284326 5' similar to SW:H2B1_TIGCA P35088 HISTONE H2B.1/H2B.2 [2] PIR:B56812;
1951	11155	20358	0.92	3.0E-08	N55323.1	EST_HUMAN	yz27g12.r1 Soares multiple sclerosis 2NBH-MSP Homo sapiens cDNA clone IMAGE:284326 5' similar to SW:H2B1_TIGCA P35088 HISTONE H2B.1/H2B.2 [2] PIR:B56812;
1951	11155	20359	0.92	3.0E-08	N55323.1	EST_HUMAN	yz27g12.r1 Soares multiple sclerosis 2NBH-MSP Homo sapiens cDNA clone IMAGE:284326 5' similar to SW:H2B1_TIGCA P35088 HISTONE H2B.1/H2B.2 [2] PIR:B56812;
2668	11849	21064	3.9	3.0E-08	11141880	NT	Homo sapiens TGF(beta)-induced transcription factor 2 (TGIF2), mRNA
3081	12317	21439	7.06	3.0E-08	7692223	NT	Homo sapiens KIAA0849 gene product (KIAA0849), mRNA
5562	14785	24155	2.1	3.0E-08	11417948	NT	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5682	14785	24158	2.1	3.0E-68	11417046	NT	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA
8043	17179	26718	7.87	3.0E-68	5453949	NT	Homo sapiens protein phosphatase 2, regulatory subunit B (B56), alpha isoform (PPP2R5A) mRNA
63	9360	18484	1.32	2.0E-68	7657334	NT	Homo sapiens Minkapen/NIK-related kinase (MINK), mRNA
63	9350	18485	1.32	2.0E-68	7657334	NT	Homo sapiens Minkapen/NIK-related kinase (MINK), mRNA
428	9283	18385	1.17	2.0E-68	4505524	NT	Homo sapiens origin recognition complex, subunit 5 (yeast homolog)-like (ORCSL) mRNA, and translated products
428	9283	18386	1.17	2.0E-68	4505524	NT	Homo sapiens origin recognition complex, subunit 5 (yeast homolog)-like (ORCSL) mRNA, and translated products
1794	11003	20108	4.01	2.0E-68	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
3747	12867	22081	0.75	2.0E-68	AL117233.1	NT	Novel human gene mapping to chromosome 1
4041	13251	22352	0.82	2.0E-68	AF108388.1	NT	Homo sapiens sodium/calcium exchanger isoform NaCa3 (NCX1) mRNA, complete cds
4247	13450	22541	1.08	2.0E-68	8823788	NT	Homo sapiens histone deacetylase 8 (HDAC8 gene) (HSA277724), mRNA
4658	13852	22848	30.43	2.0E-68	AJ133287.2	NT	Homo sapiens HLA-B gene for human leukocyte antigen B
4658	13852	22848	30.43	2.0E-68	AJ133287.2	NT	Homo sapiens HLA-B gene for human leukocyte antigen B
8702	18338		2.82	2.0E-68	11418318	NT	Homo sapiens G-2 and S-phase expressed 1 (GTSE1), mRNA
1858	10871		8.34	1.0E-68	BE887173.1	EST_HUMAN	601508376F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3909831 5'
2846	12085	21213	1.61	1.0E-68	AV717817	EST_HUMAN	AV717817 DCB Homo sapiens cDNA clone DCBADC07 5'
2846	12085	21214	1.61	1.0E-68	AV717817.1	EST_HUMAN	AV717817 DCB Homo sapiens cDNA clone DCBADC07 5'
4379	12085	21213	3.84	1.0E-68	AV717817.1	EST_HUMAN	AV717817 DCB Homo sapiens cDNA clone DCBADC07 5'
4379	12085	21214	3.84	1.0E-68	AV717817.1	EST_HUMAN	AV717817 DCB Homo sapiens cDNA clone DCBADC07 5'
5387	14616	23728	5.7	1.0E-68	BF673088.1	EST_HUMAN	602152888F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4284151 5'
7516	16721	28211	2.06	1.0E-68	AF111187.2	NT	Homo sapiens Jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
8114	17832		1.35	1.0E-68	BE894192.1	EST_HUMAN	601437130F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3922303 5'
8530	17556		2.6	8.0E-67	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
385	9879	18816	2.26	7.0E-67	AW162232.1	EST_HUMAN	au75402.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782083 3' similar to gb:M37104
							ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
1389	10603	19768	1.83	7.0E-67	AA383416.1	EST_HUMAN	EST88812 Testis 1 Homo sapiens cDNA 5' end similar to C. elegans hypothetical protein, cosmid ZK353
1539	10752	19925	1.18	7.0E-67	W85947.1	EST_HUMAN	zh56b05.t1 Soares fetal liver spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:416049 5'
1539	10762	19928	1.18	7.0E-67	W85947.1	EST_HUMAN	zh56b05.t1 Soares fetal liver spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:416049 5'
2001	11204	20414	1.12	7.0E-67	7657243	NT	Homo sapiens Inositol 1,3,4-trisphosphate 5/8 Kinase (ITPK1), mRNA
2001	11204	20415	1.12	7.0E-67	7657243	NT	Homo sapiens Inositol 1,3,4-trisphosphate 5/8 Kinase (ITPK1), mRNA

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2762	9679	18816	2.8	7.0E-67	AW162232.1	EST_HUMAN	eu75d02.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782083 3' similar to gb:M37104
5777	14885	24395	1.87	7.0E-67	11425572	NT	ATP SYNTHASE COUPLING FACTOR 8, MITOCHONDRIAL PRECURSOR (HUMAN);
5777	14885	24395	1.87	7.0E-67	11425572	NT	Homo sapiens adaptor-related protein complex 2, beta 1 subunit (AP2B1), mRNA
8176	17308	26851	2.1	7.0E-67	U82486.1	NT	Homo sapiens adaptor-related protein complex 2, beta 1 subunit (AP2B1), mRNA
8300	17408	26833	1.92	7.0E-67	11430460	NT	Human cytochrome oxidase subunit VIa (COX6A1P) pseudogene, complete cds
8300	17408	26834	1.92	7.0E-67	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
8789	17716	23961	1.98	7.0E-67	AB011390.1	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
568	9818	18839	2.14	6.0E-67	X68868.1	NT	Homo sapiens gene for AF-6, complete cds
805	10044	18195	1.06	6.0E-67	Z17227.1	NT	H. sapiens mRNA for acetyl-CoA carboxylase
1280	10495	18854	0.98	6.0E-67	Y14320.1	NT	Homo sapiens mRNA for transmembrane receptor protein
3133	12368	21469	1.21	6.0E-67	4506434	NT	Homo sapiens PMP89 gene, exons 3, 4, 5, 6 & 7
3416	12641	21770	1.29	6.0E-67	4507332	NT	Homo sapiens retinoblastoma 1 (including osteosarcoma) (RB1) mRNA
3416	12641	21771	1.29	6.0E-67	4507332	NT	Homo sapiens Synapsin III (SYN3) mRNA, and translated products
4107	13314	22411	0.79	6.0E-67	AL163201.2	NT	Homo sapiens Synapsin III (SYN3) mRNA, and translated products
4107	13314	22412	0.79	6.0E-67	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
4716	13907	23008	4.23	6.0E-67	7857020	NT	Homo sapiens chromosome 21 segment HS21C001
4716	13907	23009	4.23	6.0E-67	7857020	NT	Homo sapiens chromosome 21 segment HS21C001
3187	12422	21555	2.95	5.0E-67	AF009660.1	NT	Homo sapiens chromosome 21 segment HS21C001
1338	10551	19718	0.74	4.0E-67	R00819.1	EST_HUMAN	Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region
7630	16831		2.28	4.0E-67	AA714284.1	EST_HUMAN	nm00601.s1 NCI_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1238472 3' similar to TR:O10385 O10385
2785	9884	18009	1.15	3.0E-67	AA333768.1	EST_HUMAN	PRO-POL-DUTPASE POLYPROTEIN;
3431	12656	21798	1.11	3.0E-67	BE064410.1	EST_HUMAN	EST37903 Embryo, 9 week Homo sapiens cDNA 5' end
4704	13885	22884	3.38	3.0E-67	AW869159.1	EST_HUMAN	RC4-BT0311-141198-011-H08 BT0311 Homo sapiens cDNA
4734	13925		1.01	3.0E-67	AL163278.2	NT	MR3-SN0068-040500-008-f01 SN0068 Homo sapiens cDNA
6522	16718	25183	2.27	3.0E-67	BF186098.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C0079
7811	17004		24.32	3.0E-67	AA927874.1	EST_HUMAN	hm18105.x1 NCI_CGAP_K1d11 Homo sapiens cDNA clone IMAGE:3134913 3' similar to SW:RHOP_MOUSE
183	9473	18804	1.21	2.0E-67	BE348354.1	EST_HUMAN	Q61085 GTP-RHO BINDING PROTEIN 1;
855	10091	18253	5.63	2.0E-67	AW816405.1	EST_HUMAN	om18b07.s1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1541365 3'
1113	10337		1.73	2.0E-67	AF167460.1	NT	hm16g08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3183136 3' similar to WP:F23H11.9
							CE06817;
							QV4-ST0234-181199-037-f05 ST0234 Homo sapiens cDNA
							Homo sapiens double stranded RNA activated protein kinase (PKR) gene, exons 2a, 2, 3, and 4

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Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1849	11056	20248	0.91	2.0E-67	BE303037.1	EST_HUMAN	ba72g05.y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2805978 5' similar to TR:O94892 O94892 KIAA0788 PROTEIN.;
1849	11056	20249	0.91	2.0E-67	BE303037.1	EST_HUMAN	ba72g05.y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2805978 5' similar to TR:O94892 O94892 KIAA0788 PROTEIN.;
2350	11543	20766	1.39	2.0E-67	AF308561.1	NT	Homo sapiens KRAB zinc finger protein ZFOR mRNA, complete cds
2395	11588	20806	3.97	2.0E-67	4758795	NT	Homo sapiens developmentally regulated GTP-binding protein 1 (DRG1), mRNA
3444	12669	21804	4.82	2.0E-67	AA925755.1	EST_HUMAN	z191g01.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:745392 3'
3979	13183	22301	3.33	2.0E-67	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
5720	14938	24334	4.82	2.0E-67	BF240758.1	EST_HUMAN	601875351F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4091893 5'
5785	15002	24405	2.36	2.0E-67	AB051763.1	NT	Homo sapiens mRNA for NADPH-cytochrome P-450 reductase, complete cds
5785	15002	24406	2.36	2.0E-67	AB051763.1	NT	Homo sapiens mRNA for NADPH-cytochrome P-450 reductase, complete cds
7478	18894	26167	1.8	2.0E-67	BF885788.1	EST_HUMAN	602140470F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4301705 5'
7623	18390		3.79	2.0E-67	11438448	NT	Homo sapiens KIAA0985 protein (KIAA0985), mRNA
7881	18426	25913	2.14	2.0E-67	BF377169.1	EST_HUMAN	PM2-TN0103-040600-001-002 TN0103 Homo sapiens cDNA
8685	18189	23759	2.89	2.0E-67	11418189	NT	Homo sapiens thyroid autoantigen 70kD (Ku antigen) (GZ2P1), mRNA
257	9533	18684	7.28	1.0E-67	4502168	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nehdn-11, Alzheimer disease) (APP), mRNA
715	8857	18095	1.12	1.0E-67	AA702794.1	EST_HUMAN	z80b04.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:448015 3'
4722	13913	23014	0.59	1.0E-67	BF439247.1	EST_HUMAN	na06108.x1 Soares_NSFC_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE: 3'
2142	11940	20558	1.2	8.0E-68	BE670732.1	EST_HUMAN	601448559F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3852254 5'
3851	13067	22181	5.82	8.0E-68	AA208456.1	EST_HUMAN	zq82h10.r1 Strategene hNT neuron (#837233) Homo sapiens cDNA clone IMAGE:848163 5' similar to SW:SAV_SULAC Q07590 SAV PROTEIN.;
3851	13067	22182	5.82	8.0E-68	AA208456.1	EST_HUMAN	zq82h10.r1 Strategene hNT neuron (#837233) Homo sapiens cDNA clone IMAGE:848163 5' similar to SW:SAV_SULAC Q07590 SAV PROTEIN.;
7197	18374	25858	2.52	6.0E-68	11422086	NT	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 2 (BIG2), mRNA
8973	17843		1.37	6.0E-68	BE612554.1	EST_HUMAN	601452087F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3855761 5'
812	11942	19203	1.04	5.0E-68	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
812	11942	19204	1.04	5.0E-68	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
829	10067	19220	5.46	5.0E-68	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
829	10067	19221	5.46	5.0E-68	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
2735	11914	21127	0.97	5.0E-68	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
3112	12347	21475	3.04	5.0E-68	AB037852.1	NT	Homo sapiens mRNA for KIAA1431 protein, partial cds
4162	13968		0.64	5.0E-68	4826897	NT	Homo sapiens retinoblastoma-binding protein 2 (RBBP2) mRNA
4489	13887	22778	0.75	5.0E-68	AL157645.1	EST_HUMAN	DKFZp547D207_r1 547 (synonym: htrb1) Homo sapiens cDNA clone DKFZp547D207 5'

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Table 4
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2493	11683	20899	3.92	4.0E-08	11421388	NT	Homo sapiens transcription factor NRF (NRF), mRNA
2493	11683	20800	3.92	4.0E-08	11421388	NT	Homo sapiens transcription factor NRF (NRF), mRNA
4885	14182		13.93	4.0E-08	P04406	SWISSPROT	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER
5212	14387	23472	0.72	4.0E-08	7549804	NT	Homo sapiens deloninase, iodothyronine, type II (DIO2), transcript variant 2, mRNA
5989	15271	24699	5.7	4.0E-08	11055991	NT	Homo sapiens serine carboxypeptidase 1 precursor protein (HSCP1), mRNA
5989	15271	24700	5.7	4.0E-08	11055991	NT	Homo sapiens serine carboxypeptidase 1 precursor protein (HSCP1), mRNA
6777	15972	25428	5.65	4.0E-08	D63478.2	NT	Homo sapiens mRNA for KIAA0145 protein, partial cds
6777	15972	25429	5.65	4.0E-08	D63478.2	NT	Homo sapiens mRNA for KIAA0145 protein, partial cds
7573	16778	26271	7.1	4.0E-08	4508282	NT	Homo sapiens protein tyrosine phosphatase type IVA, member 1 (PTP4A1), mRNA
7573	16778	26272	7.1	4.0E-08	4508282	NT	Homo sapiens protein tyrosine phosphatase type IVA, member 1 (PTP4A1), mRNA
3841	12882	21980	5.48	3.0E-08	AF238082.1	NT	Mus musculus G-protein coupled receptor GPR73 (Gpr73) mRNA, complete cds
6897	15903		6.45	3.0E-08	AF342323.1	EST_HUMAN	q08h02.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1850281 3' similar to contains
9188	19108		1.41	3.0E-08	AW639485.1	EST_HUMAN	THR12 THR repetitive element;
2814	14475		20.8	2.0E-08	D00522.1	NT	QV1-DT0072-010200-056-H08 DT0072 Homo sapiens cDNA
4003	13216	22320	0.89	2.0E-08	BE675766.1	EST_HUMAN	Orbitolus longicaudatus mRNA for EF-1 alpha, complete cds
4898	13878	22890	1.97	2.0E-08	AB008681.1	NT	HYPOTHETICAL 88.8 KD PROTEIN ;
6031	15239		8.84	2.0E-08	R45088.1	EST_HUMAN	Homo sapiens gene for activin receptor type IIB, complete cds
6110	15204	24623	4.55	2.0E-08	BF035316.1	EST_HUMAN	yg38g04.s1 Soares Infant brain INIB Homo sapiens cDNA clone IMAGE:34896 3'
78	9372	18502	2.89	1.0E-08	4505222	NT	601458514F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3862034 5'
301	9574	18707	11.39	1.0E-08	AW918405.1	EST_HUMAN	Homo sapiens meningioma (disrupted in balanced translocation) 1 (MN1), mRNA
2218	11413	20637	2.32	1.0E-08	AB011149.1	NT	QV4-ST0234-181189-037-f05 ST0234 Homo sapiens cDNA
2218	11413	20638	2.32	1.0E-08	AB011149.1	NT	Homo sapiens mRNA for KIAA0577 protein, complete cds
3986	13200	22308	0.97	1.0E-08	BE296032.1	EST_HUMAN	Homo sapiens mRNA for KIAA0577 protein, complete cds
5053	14235	23322	0.84	1.0E-08	AA897343.1	EST_HUMAN	601177002F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532344 5'
5348	14576	23853	1.69	1.0E-08	7682349	NT	647612.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1480518 3'
7429	16839	26132	2.83	1.0E-08	11418869	NT	Homo sapiens cell recognition molecule Caspr2 (KIAA0868), mRNA
7428	16639	26133	2.83	1.0E-08	11418869	NT	Homo sapiens phosphodiesterase 7B (PDE7B), mRNA
7478	16888	26168	2.84	1.0E-08	L78416.1	NT	Homo sapiens phosphodiesterase 7B (PDE7B), mRNA
7747	16943	26455	2.44	1.0E-08	11433277	NT	Homo sapiens MIF2 suppressor (HSM23) mRNA, complete cds
7847	17038	26554	2.74	1.0E-08	U50319.1	NT	Homo sapiens myosin IC (MYO1C), mRNA
7847	17038	26555	2.74	1.0E-08	U50319.1	NT	Human protein kinase C substrate 80K-H (PRKCSH) gene, exon 4-5
8169	17301	26845	1.98	1.0E-08	11418431	NT	Human protein kinase C substrate 80K-H (PRKCSH) gene, exon 4-5
							Homo sapiens CGI-78 protein (LOC51832), mRNA

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8169	17301	26848	1.88	1.0E-68	11418431	NT	Homo sapiens CGI-78 protein (LOC51632), mRNA
8955	8372	18502	2.07	1.0E-68	4505222	NT	Homo sapiens meningioma (disrupted in balanced translocation) 1 (MN1), mRNA
9178	18288	23688	1.69	1.0E-68	11430480	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
21	9317	18418	2.67	9.0E-69	5031978	NT	Homo sapiens pre-B-cell colony-enhancing factor (PBEF) mRNA
21	9317	18420	2.67	9.0E-69	5031978	NT	Homo sapiens pre-B-cell colony-enhancing factor (PBEF) mRNA
1035	10261	19411	3.32	9.0E-69	5031880	NT	Homo sapiens 26S proteasome-associated pad1 homolog (POH1) mRNA
1035	10261	19412	3.32	9.0E-69	5031880	NT	Homo sapiens 26S proteasome-associated pad1 homolog (POH1) mRNA
4110	13317	22416	0.89	9.0E-69	4757967	NT	Homo sapiens v-rat murine sarcoma viral oncogene homolog B1 (BRAF) mRNA
7465	16073		9.88	9.0E-69	AU117241.1	EST_HUMAN	AU117241 HEMBA1 Homo sapiens cDNA clone HEMBA1000988 5'
3364	12592		1.39	8.0E-69	AJ237744.1	NT	Homo sapiens RIBIIR gene (partial), exon 12
6814	15031	24432	5.24	7.0E-69	8989912	NT	Homo sapiens actin-related protein 3-beta (ARP3BETA), mRNA
6415	15612	25075	9.31	6.0E-69	A192764.1	EST_HUMAN	qe62h01.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1743601 3' similar to
6415	15612	25076	9.31	6.0E-69	A192764.1	EST_HUMAN	gbL11568 60S RIBOSOMAL PROTEIN L18 (HUMAN);
9101	18262		4.5	5.0E-69	AW813417.1	EST_HUMAN	qe62h01.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1743601 3' similar to
628	9777		1.22	4.0E-69	A1873630.1	EST_HUMAN	hh72e08.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2868354 3' similar to contains MER29.12
5569	14813	24187	4.72	4.0E-69	A1764973.1	EST_HUMAN	MER29 repetitive element;
5946	15162	24576	3.11	4.0E-69	4557732	NT	wm20h11.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2437126 3'
5946	15162	24576	3.11	4.0E-69	4557732	NT	wh57b08.x1 NCI_CGAP_K1411 Homo sapiens cDNA clone IMAGE:2364819 3' similar to TR:O55137
391	9885	18823	2.37	3.0E-69	BE268012.1	EST_HUMAN	Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA
618	9883	18863	1.63	3.0E-69	AF221712.1	NT	601110371F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3351352 5'
1540	10763		2.54	3.0E-69	T80514.1	EST_HUMAN	Homo sapiens Smad- and Olf-interacting zinc finger protein mRNA, partial cds
4982	14188	23259	4.28	3.0E-69	AB037732.1	NT	yd08a02.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:24880 5' similar to SP-A48836
5178	13288	22370	1.54	3.0E-69	A1765888.1	EST_HUMAN	A48836 SPEGF III-EGF REPEAT-CONTAINING FIBROPEL-LIKE PROTEIN - SEA URCHIN;
5299	14488	26927	2.26	3.0E-69	11418185	NT	Homo sapiens mRNA for KIAA1311 protein, partial cds
6313	15494	24940	8.1	3.0E-69	AF268075.1	NT	wh66g08.x1 NCI_CGAP_K1411 Homo sapiens cDNA clone IMAGE:2385758 3'
6929	16122	25589	3.67	3.0E-69	X06233.1	NT	Homo sapiens acetylase 2, mitochondrial (ACO2), mRNA
7235	18458	25844	4.89	3.0E-69	11432120	NT	Homo sapiens TRAF6-binding protein T88P mRNA, complete cds
							Human mRNA for calcium-binding protein in macrophages (MRP-14) macrophage migration inhibitory factor (MIF)-related protein
							Homo sapiens ribosomal protein S15a (RPS15A), mRNA

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7418	18030		15.58	3.0E-69	AA376398.1	EST_HUMAN	EST88807 HSC172 cells II Homo sapiens cDNA 5' end similar to similar to ribosomal protein S18
8432	17488		5.21	3.0E-69	11419157	NT	Homo sapiens HGC8.2 protein (HGC8.2), mRNA
126	8663	18802	0.88	2.0E-69	AF180252.1	NT	Homo sapiens KIAA0553 protein gene, complete cds; and alpha1b protein gene, partial cds
126	8663	18803	0.88	2.0E-69	AF180252.1	NT	Homo sapiens KIAA0553 protein gene, complete cds; and alpha1b protein gene, partial cds
410	8663	18802	4.91	2.0E-69	AF180252.1	NT	Homo sapiens KIAA0553 protein gene, complete cds; and alpha1b protein gene, partial cds
410	8663	18803	4.91	2.0E-69	AF180252.1	NT	Homo sapiens KIAA0553 protein gene, complete cds; and alpha1b protein gene, partial cds
1850	11057	20250	1.85	2.0E-69	BE257857.1	EST_HUMAN	801108444F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350074 5'
2768	12038		3.59	2.0E-69	AA431167.1	EST_HUMAN	zw7192.1 Soares_testes_NHT Homo sapiens cDNA clone IMAGE:781882 5'
1828	10839		11.27	1.0E-69	BF330124.1	EST_HUMAN	RCO-BN0305-200600-031-05 BN0305 Homo sapiens cDNA
1878	10890	20078	2.07	1.0E-69	AF053788.1	NT	Rattus norvegicus brain specific cortactin-binding protein CBP90 mRNA, partial cds
5934	15150	24560	4.11	1.0E-69	AW393989.1	EST_HUMAN	QVQ-TT0010-031199-045-c07 TT0010 Homo sapiens cDNA
6013	15263	24687	3.25	1.0E-69	AB032873.1	NT	Homo sapiens mRNA for KIAA1147 protein, partial cds
6013	15263	24688	3.25	1.0E-69	AB032873.1	NT	Homo sapiens mRNA for KIAA1147 protein, partial cds
7127	16304	28784	4.82	1.0E-69	BE245070.1	EST_HUMAN	TCBAP1E2878 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP2878
7127	16304	28785	4.82	1.0E-69	BE245070.1	EST_HUMAN	TCBAP1E2878 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP2878
7449	18657		25.72	1.0E-69	4504918	NT	Homo sapiens keratin 8 (KRT8) mRNA
8969	17458	26587	1.39	1.0E-69	BF125887.1	EST_HUMAN	601762902F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4025785 5'
8708	17724		3.22	1.0E-69	AB098984.1	EST_HUMAN	wf84608.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2360390 3' similar to contains Alu repetitive element; contains element MIR repetitive element ;
2300	12014	20714	1.88	8.0E-70	AA230303.1	EST_HUMAN	nc13d12.1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:1008023
4357	13569	22685	1.97	8.0E-70	L77588.1	NT	Homo sapiens DGS-1 mRNA, 3' end
1782	10992	20187	1.72	7.0E-70	AI497807.1	EST_HUMAN	fm89f01.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2165305 3'
1782	10992	20188	1.72	7.0E-70	AI497807.1	EST_HUMAN	fm89f01.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2165305 3'
1868	11106	20288	1.42	7.0E-70	AA282855.1	EST_HUMAN	z115h04.1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:713239 5'
2031	11232		4.82	7.0E-70	5031888	NT	Homo sapiens tumor suppressor deleted in oral cancer-related 1 (DOC-1R) mRNA
4210	13413	22508	4.25	7.0E-70	4757723	NT	Homo sapiens adenylate cyclase 3 (ADCY3) mRNA
5433	14680	23789	5.69	7.0E-70	AB032369.1	NT	Homo sapiens MIST mRNA, partial cds
5433	14680	23800	5.69	7.0E-70	AB032369.1	NT	Homo sapiens MIST mRNA, partial cds
6054	16222	24641	1.72	7.0E-70	AJ000052.1	NT	Homo sapiens gene encoding splicing factor SF1, exons 2-8
6888	15883	25342	5.2	7.0E-70	M74099.1	NT	Human displacement protein (CCAAT) mRNA
6888	15883	25343	5.2	7.0E-70	M74099.1	NT	Human displacement protein (CCAAT) mRNA
6888	15504	25058	8.49	7.0E-70	AF153715.1	NT	Homo sapiens phospholipid scramblase 1 gene, exon 1 and 5' flanking region

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8125	17259	26801	2.19	7.0E-70	11526319	NT	Homo sapiens HIR (histone cell cycle regulation defective, <i>S. cerevisiae</i>) homolog A (HIRA), mRNA
8125	17259	26802	2.19	7.0E-70	11526319	NT	Homo sapiens HIR (histone cell cycle regulation defective, <i>S. cerevisiae</i>) homolog A (HIRA), mRNA
881	10117	19279	2.56	6.0E-70	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease resistant, Alzheimer disease) (APP), mRNA
2106	11305	20519	4.61	6.0E-70	M30638.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
2474	11685	20894	1.66	6.0E-70	89233899	NT	Homo sapiens CIMP-N-acetylneuraminic acid synthase (LOC55807), mRNA
2518	12018	20920	88.43	5.0E-70	7682307	NT	Homo sapiens KIAA0792 gene product (KIAA0792), mRNA
2518	12018	20921	88.43	5.0E-70	7682307	NT	Homo sapiens KIAA0792 gene product (KIAA0792), mRNA
8378	17463		2.24	5.0E-70	BE166034.1	EST_HUMAN	MR3-HT0487-150200-115-a03 HT0487 Homo sapiens cDNA
1569	10782	18665	2.52	3.0E-70	BE071768.1	EST_HUMAN	RCO-BT0522-071289-011-at12 BT0522 Homo sapiens cDNA
1569	10782	18666	2.52	3.0E-70	BE071768.1	EST_HUMAN	RCO-BT0522-071289-011-at12 BT0522 Homo sapiens cDNA
40	8338	18443	0.74	2.0E-70	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
688	9839	19070	19.57	2.0E-70	N42161.1	EST_HUMAN	Y07a10.1 Soares melanocyte 2Nbr-IM Homo sapiens cDNA clone IMAGE:270522 5' similar to SW:D3HI_RAT P29288 3-HYDROXYISOBUTYRATE DEHYDROGENASE PRECURSOR ;
688	9839	19071	19.57	2.0E-70	N42161.1	EST_HUMAN	Y07a10.1 Soares melanocyte 2Nbr-IM Homo sapiens cDNA clone IMAGE:270522 5' similar to SW:D3HI_RAT P29288 3-HYDROXYISOBUTYRATE DEHYDROGENASE PRECURSOR ;
712	9864	19094	3.59	2.0E-70	AI246898.1	EST_HUMAN	gq51H01.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2004913 3'
1028	10254	19405	2.8	2.0E-70	8923669	NT	Homo sapiens hypothetical protein FLJ20758 (FLJ20758), mRNA
1192	10412	19568	0.59	2.0E-70	7681983	NT	Homo sapiens KIAA0193 gene product (KIAA0193), mRNA
1192	10412	19567	0.59	2.0E-70	7681983	NT	Homo sapiens KIAA0193 gene product (KIAA0193), mRNA
1413	10626	19792	1.36	2.0E-70	BE467311.1	EST_HUMAN	h2d4c12.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3212758 3'
1632	10848	20024	0.93	2.0E-70	AA180093.1	EST_HUMAN	zp45H05.1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:812441 5' similar to TR:G1041293 G1041293 D2085.5 ;
1632	10848	20025	0.93	2.0E-70	AA180093.1	EST_HUMAN	zp45H05.1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:812441 5' similar to TR:G1041293 G1041293 D2085.5 ;
1716	10928	20113	1.45	2.0E-70	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
2286	11481		29.63	2.0E-70	AA054010.1	EST_HUMAN	z48g04.1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:380214 5' similar to SW:GAG_HTLIA
2448	11639	20860	2.97	2.0E-70	AB011173.1	NT	P03345 GAG POLYPROTEIN ;
3604	12826	21946	0.8	2.0E-70	H37688.1	EST_HUMAN	Homo sapiens mRNA for KIAA0901 protein, partial cds
3809	13027	22137	1.12	2.0E-70	AL133207.2	NT	yp58b04.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:191589 5'
3918	13132	22250	2.14	2.0E-70	AL1246003.1	NT	Novel human gene mapping to chromosome X Homo sapiens Spast gene for spastin protein

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4028	13237	22342	3.74	2.0E-70	M69181.1	NT	Human nonmuscle myosin heavy chain-B (MYH10) mRNA, partial cds
5448	14872	23630	8.15	2.0E-70	X72682.1	NT	H.sapiens gene for schwannomin (CS8)
5448	14872	23631	8.15	2.0E-70	X72682.1	NT	H.sapiens gene for schwannomin (CS8)
5849	15165	24578	2.25	2.0E-70	D12625.1	NT	Human mRNA for NF1 protein isoform (neurofibromin isoform), complete cds
5858	15174	24589	10.47	2.0E-70	AF123074.1	NT	Homo sapiens cytoplasmic dynein intermediate chain 1 mRNA, complete cds
5858	15174	24590	10.47	2.0E-70	AF123074.1	NT	Homo sapiens cytoplasmic dynein intermediate chain 1 mRNA, complete cds
6087	14533	23557	1.72	2.0E-70	11422842	NT	Homo sapiens elavyltransferase 8 (N-acetylglucosaminidase alpha 2,3-sialyltransferase) (SIAT6), mRNA
6431	15828	25083	4.82	2.0E-70	M21741.1	NT	Human guanine nucleotide-binding protein alpha-subunit gene (G-s-alpha), exons 4 and 5
7638	16838	26334	3.48	2.0E-70	8923420	NT	Homo sapiens hypothetical protein FLJ20450 (FLJ20450), mRNA
7638	16838	26335	3.48	2.0E-70	8923420	NT	Homo sapiens hypothetical protein FLJ20450 (FLJ20450), mRNA
8164	17286	26830	10.05	2.0E-70	4503520	NT	Homo sapiens eukaryotic translation initiation factor 3, subunit 6 (48kD) (EIF3S6) mRNA
8787	17714	23958	2.3	2.0E-70	11430480	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
8787	17714	23959	2.3	2.0E-70	11430480	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
3370	12688		3.37	1.0E-70	4507478	NT	Homo sapiens transglutaminase 3 (E polypeptide, protein-glutamine-gamma-glutamyltransferase) (TGM3) mRNA
7508	18713	28201	19.02	1.0E-70	AV738538.1	EST_HUMAN	AV738538 CB Homo sapiens cDNA clone CBLGB10 5'
5635	14858	24242	7.21	9.0E-71	A143870.1	EST_HUMAN	q04f01.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1738008 3' similar to TR:O14045
5635	14858	24243	7.21	9.0E-71	A143870.1	EST_HUMAN	O14045 PHOSPHOTRANSFERASE ;
6100	16300	24732	2.08	9.0E-71	A1654903.1	EST_HUMAN	q04f01.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1738008 3' similar to TR:O14045
8055	16300	24732	5.42	9.0E-71	A1654903.1	EST_HUMAN	O14045 PHOSPHOTRANSFERASE ;
6704	15889		4.09	8.0E-71	AA171451.1	EST_HUMAN	wb52c05.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2309288 3' similar to TR:P97213 P97213
6245	15428	24866	8.63	7.0E-71	AA442230.1	EST_HUMAN	CDU2, CDU1, TCDD, TCDB, TCDE, TCDA, TCDC, CDD1, CDD2, CDD3, AND CDD4 GENES ;
7875	17063	20588	5.4	7.0E-71	AL163210.2	NT	wb52c05.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2309288 3' similar to TR:P97213 P97213
2177	11374	20588	28.52	5.0E-71	AF056322.1	NT	CDU2, CDU1, TCDD, TCDB, TCDE, TCDA, TCDC, CDD1, CDD2, CDD3, AND CDD4 GENES ;
4098	13307	22407	1.2	5.0E-71	AW816405.1	EST_HUMAN	zp21d11.1 Stratagene neuroepithelium (8037231) Homo sapiens cDNA clone IMAGE:610101 5' similar to
5005	14829	24205	1.82	5.0E-71	4502740	NT	TR:G1143061 G1143061 STRAIN XA34 POL ;
6390	15570	25027	21.73	5.0E-71	AF072810.1	NT	zv60h08.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:768075 5'
7043	16220		3.25	5.0E-71	X13467.1	NT	Homo sapiens chromosome 21 segment HS21C010
							Homo sapiens SP100-HMG nuclear autoantigen (SP100) mRNA, complete cds
							QV4-ST0234-181189-037-f05 ST0234 Homo sapiens cDNA
							Homo sapiens cyclin-dependent kinase 8 (CDK8) mRNA
							Homo sapiens transcription factor WSTF mRNA, complete cds
							Human PreA4 gene for Alzheimer's disease A4 amyloid protein precursor (exon 2)

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF-SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7553	16758	26262	3.73	5.0E-71	11436514	NT	Homo sapiens pro-platelet basic protein (includes platelet basic protein, beta-thromboglobulin, connective tissue-activating peptide III, neutrophil-activating peptide-2) (PPBP), mRNA
7748	16942	26454	2.43	6.0E-71	11439069	NT	Homo sapiens similar to hypothetical protein FLJ20163 (H. sapiens) (LOC633325), mRNA
8692	17680		1.78	5.0E-71	11418039	NT	Homo sapiens RNA binding motif protein 8 (RBM8), mRNA
355	9823	18752	112.04	4.0E-71	AF157628.1	NT	Equus caballus glyceraldehyde-3-phosphate dehydrogenase mRNA, partial cds
355	9823	18753	112.04	4.0E-71	AF157628.1	NT	Equus caballus glyceraldehyde-3-phosphate dehydrogenase mRNA, partial cds
2839	12078	21201	1.63	4.0E-71	4505880	NT	Homo sapiens plasminogen (PLG) mRNA
4420	13620	22715	5.57	4.0E-71	AF058322.1	NT	Homo sapiens SP100-HMG nuclear autoantigen (SP100) mRNA, complete cds
5007	14184	23283	5.98	4.0E-71	7657802	NT	Homo sapiens putative home-binding protein (SOUL), mRNA
7283	16502	25894	4.32	3.0E-71	AA557683.1	EST_HUMAN	repetitive element;
1237	10454	19613	10.52	2.0E-71	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C008
6344	14574	23651	7.58	2.0E-71	D87462.1	NT	Human mRNA for KIAA0272 gene, partial cds
6344	14574	23652	7.58	2.0E-71	D87462.1	NT	Human mRNA for KIAA0272 gene, partial cds
6072	14518	23661	57.87	2.0E-71	AL042439.1	EST_HUMAN	DKFZp434D1721_1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434D1721 5'
7222	16399	25883	4.68	2.0E-71	AF085703.1	NT	Homo sapiens short chain L-3-hydroxyacyl-CoA dehydrogenase precursor (HADHSC) gene, nuclear gene encoding mitochondrial protein, complete cds
7222	16399	25884	4.68	2.0E-71	AF085703.1	NT	Homo sapiens short chain L-3-hydroxyacyl-CoA dehydrogenase precursor (HADHSC) gene, nuclear gene encoding mitochondrial protein, complete cds
7285	16504	25995	2.75	2.0E-71	BE018477.1	EST_HUMAN	bb81a06.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3048754 5' similar to SW:R23B_HUMAN
8112	17246	26786	1.65	2.0E-71	R55628.1	EST_HUMAN	PS4727 UV EXCISION REPAIR PROTEIN PROTEIN RAD23 HOMOLOG B;
8445	17506		7.28	2.0E-71	T65489.1	EST_HUMAN	y77c11.1.1 Soares breast 2NhbBst Homo sapiens cDNA clone IMAGE:154772 5'
844	9890	19015	1.07	1.0E-71	AI077827.1	EST_HUMAN	y643a09.1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:120520 5'
949	10182	18338	2.43	1.0E-71	7706281	NT	ov15a03.s1 Soares, senescent, fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:1865916 3' similar to contains LOR1.b2 LOR1 repetitive element;
1108	10332	19482	6.48	1.0E-71	AF205890.1	NT	Homo sapiens neuronal cell death-related protein (LOC51818), mRNA
1348	10563	19728	10.22	1.0E-71	AF012872.1	NT	Homo sapiens disabled-2 gene, exons 2 through 15 and complete cds
2051	11252	20465	2.23	1.0E-71	AB017007.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
2051	11252	20466	2.23	1.0E-71	AB017007.1	NT	Homo sapiens PMS2L18 mRNA, partial cds
2653	11836	21049	4.77	1.0E-71	7657153	NT	Homo sapiens PMS2L16 mRNA, partial cds
3475	12698	21835	2	1.0E-71	AF119685.1	NT	Homo sapiens hellyenhancer-of-split related with YRPW motif-like (HEYL), mRNA
3574	12797	21922	7.32	1.0E-71	AF246218.1	NT	Homo sapiens inorganic pyrophosphatase mRNA, complete cds
3574	12797	21923	7.32	1.0E-71	AF246218.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
3574	12797	21923	7.32	1.0E-71	AF246218.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3627	12648	21968	0.89	1.0E-71	BE122850.1	EST_HUMAN	02_15 Human Epidermal Keratinocyte Subtraction Library- Upregulated Transcripts Homo sapiens cDNA clone 02_15 5' similar to Homo sapiens chromosome 19
3627	12648	21967	0.89	1.0E-71	BE122850.1	EST_HUMAN	02_15 Human Epidermal Keratinocyte Subtraction Library- Upregulated Transcripts Homo sapiens cDNA clone 02_15 5' similar to Homo sapiens chromosome 19
3722	12642	22059	1.54	1.0E-71	AF218804.1	NT	Homo sapiens attractin precursor (ATRIN) gene, exon 19
4486	13684	22757	2.57	1.0E-71	D28476.1	NT	Human mRNA for KIAA0045 gene, complete cds
4592	13786	22878	0.93	1.0E-71	H23176.1	EST_HUMAN	ym58h10.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:52528 5'
4810	13689		1.9	1.0E-71	AF077188.1	NT	Homo sapiens cullin 4A (CUL4A) mRNA, complete cds
6211	15392	24836	13.82	1.0E-71	U80753.1	NT	Homo sapiens CAGL79 mRNA, partial cds
6813	15809	25264	4.88	1.0E-71	8922811	NT	Homo sapiens hypothetical protein FLJ10898 (FLJ10898), mRNA
6813	15809	25265	4.89	1.0E-71	8922811	NT	Homo sapiens hypothetical protein FLJ10898 (FLJ10898), mRNA
7078	16253	25726	6.32	1.0E-71	AY007643.1	NT	Homo sapiens cytochrome c oxidase subunit VIIa-related protein gene, complete cds
7365	16581		6.68	1.0E-71	AV781217.1	EST_HUMAN	AV781217 MDS Homo sapiens cDNA clone MDSE1A03 5'
7459	16667	26155	2.12	1.0E-71	11418003	NT	Homo sapiens coagulation factor XIII, A1 polypeptide (F13A1), mRNA
7706	16805	26413	2.19	1.0E-71	11417191	NT	Homo sapiens leucyl/cystinyl aminopeptidase (LNPEP), mRNA
7706	16805	26414	2.19	1.0E-71	11417191	NT	Homo sapiens leucyl/cystinyl aminopeptidase (LNPEP), mRNA
8638	17746		6.70	1.0E-71	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
413	9666	18805	0.89	9.0E-72	AI857635.1	EST_HUMAN	wk95g03.x1 NCI CGAP_Lut18 Homo sapiens cDNA clone IMAGE:2423188 3' similar to TR:O88705 O88705 HYPOTHETICAL 38.6 KD PROTEIN, contains Alu repetitive element;
413	9666	18806	0.89	9.0E-72	AI857635.1	EST_HUMAN	wk95g03.x1 NCI CGAP_Lut18 Homo sapiens cDNA clone IMAGE:2423188 3' similar to TR:O88705 O88705 HYPOTHETICAL 38.6 KD PROTEIN, contains Alu repetitive element
4090	13288	22395	2.06	7.0E-72	4501868	NT	Homo sapiens acornitase 2, mitochondrial (ACO2), nuclear gene encoding mitochondrial protein, mRNA
4090	13288	22396	2.06	7.0E-72	4501868	NT	Homo sapiens acornitase 2, mitochondrial (ACO2), nuclear gene encoding mitochondrial protein, mRNA
4090	13288	22397	2.06	7.0E-72	4501868	NT	Homo sapiens acornitase 2, mitochondrial (ACO2), nuclear gene encoding mitochondrial protein, mRNA
6128	15313	24747	2.92	7.0E-72	S41684.1	NT	(pseudogene) PTHAP2=prothymosin alpha [human, Genomic, 1192 nt, segment 2 of 3]
8964	17835		1.43	7.0E-72	F26259.1	EST_HUMAN	HSPD13670 HM3 Homo sapiens cDNA clone s4000051G02
8963	15788		2.97	6.0E-72	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
65	9361	18484	1.3	6.0E-72	BF333707.1	EST_HUMAN	QV0-CS0010-150900-388-e11 CS0010 Homo sapiens cDNA
65	9361	18485	1.3	5.0E-72	BF333707.1	EST_HUMAN	QV0-CS0010-150900-388-e11 CS0010 Homo sapiens cDNA
66	9361	18484	9	5.0E-72	BF333707.1	EST_HUMAN	QV0-CS0010-150900-388-e11 CS0010 Homo sapiens cDNA
66	9361	18485	9	5.0E-72	BF333707.1	EST_HUMAN	QV0-CS0010-150900-388-e11 CS0010 Homo sapiens cDNA

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Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1147	10370		2.72	5.0E-72	L11845.1	NT	Homo sapiens alpha-tubulin mRNA, complete cds
6709	15804	25384	2.48	5.0E-72	AW161274.1	EST_HUMAN	eu80cd03.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782684 5' similar to
7795	16888	26502	3.23	5.0E-72	BF331571.1	EST_HUMAN	TR:Q69785 Q69785 HYPOTHETICAL 32.4 KD PROTEIN ; contains element MSR1 repetitive element ;
7795	16888	26503	3.23	5.0E-72	BF331571.1	EST_HUMAN	MR4-BT0598-010800-005-d05 BT0598 Homo sapiens cDNA
8523	18323		2.09	5.0E-72	BE926845.1	EST_HUMAN	MR4-BT0598-010800-005-d05 BT0598 Homo sapiens cDNA
4838	14027		1.15	4.0E-72	11034844	NT	QV1-BT0632-280800-342-a10 BT0632 Homo sapiens cDNA
8059	17194	26732	6.71	4.0E-72	H78421.1	EST_HUMAN	Homo sapiens hypothetical protein dJ1057B20.2 (dJ1057B20.2), mRNA
8178	17310	26853	3.08	4.0E-72	T81910.1	EST_HUMAN	YU28a03.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:235084 5'
							YU28d09.e1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:109849 3'
8894	17788	23921	9.76	4.0E-72	AJ277546.2	NT	Homo sapiens WEE1 gene for protein kinase and partial ZNF143 gene for zinc finger transcription factor.
20	8316	18418	1.28	3.0E-72	5031976	NT	Homo sapiens pre-B-cell colony-enhancing factor (PBEF) mRNA
913	10148		2.08	3.0E-72	AA728823.1	EST_HUMAN	af63a08.e1 Soares testis NHT Homo sapiens cDNA clone T310280 3'
1163	10385	18635	13.92	3.0E-72	U16308.1	NT	Human chondroitin sulfate proteoglycan versican V0 splice-variant precursor peptide mRNA, complete cds
1163	10385	18636	13.92	3.0E-72	U16308.1	NT	Human chondroitin sulfate proteoglycan versican V0 splice-variant precursor peptide mRNA, complete cds
1201	10421	18574	0.73	3.0E-72	U80226.1	NT	Human gamma-aminobutyric acid transaminase mRNA, partial cds
1201	10421	18575	0.73	3.0E-72	U80226.1	NT	Human gamma-aminobutyric acid transaminase mRNA, partial cds
1507	10720	18892	1.41	3.0E-72	BE242161.1	EST_HUMAN	TCAAP1E1252 Pediatric acute myelogenous leukemia cell (FAB M1) Baylar-HGSC project=TCAA Homo sapiens cDNA clone TCAAP1252
3040	12277	21405	11.08	3.0E-72	AJ228043.1	NT	Homo sapiens 859 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
3248	12479	21611	3.46	3.0E-72	8923648	NT	Homo sapiens hypothetical protein FLJ20585 (FLJ20585), mRNA
3813	13031	22141	2.14	3.0E-72	S77589.1	NT	TOR V delta 2-C alpha =T-cell receptor delta and C alpha fusion gene (alternatively spliced, splice junction)
4542	13737	22835	3.48	3.0E-72	11416198	NT	(human, precursor B-cell line REH, mRNA Partial, 211 nt)
5648	14869	24254	1.78	3.0E-72	AF073367.1	NT	Homo sapiens hypothetical protein (FLJ11127), mRNA
5648	14869	24255	1.78	3.0E-72	AF073367.1	NT	Homo sapiens growth factor receptor-bound protein 10 (GRB10) gene, exon 5
5738	14957	24358	4.53	3.0E-72	AB028004.1	NT	Homo sapiens growth factor receptor-bound protein 10 (GRB10) gene, exon 5
5738	14957	24357	4.53	3.0E-72	AB028004.1	NT	Homo sapiens mRNA for KIAA1081 protein, partial cds
5840	15158	24568	3.64	3.0E-72	4823987	NT	Homo sapiens mRNA for KIAA1081 protein, partial cds
							Homo sapiens mRNA for KIAA1081 protein, partial cds
							Homo sapiens ribosomal protein L3-like (RPL3L) mRNA
							Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (naip) and survival motor neuron protein (smn) genes, complete cds
6327	15508	24854	1.78	3.0E-72	U80017.1	NT	

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7328	16542	28031	2.65	2.0E-72	AA788277.1	EST_HUMAN	qj28b08.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391609 3' similar to gb.X02087 H.sapiens mRNA for 7SL RNA pseudogene (HUMAN);
8889	17784	23918	6.91	2.0E-72	AF182714.1	NT	Rattus norvegicus putative phosphate/pyruvate translocator mRNA, complete cds
2043	11244	20453	0.99	1.0E-72	AA846226.1	EST_HUMAN	ai83402.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1387395 3'
6559	14782	24161	4.02	1.0E-72	7657676	NT	Homo sapiens vacuolar protein sorting 41 (yeast homolog) (VPS41), mRNA
6350	15530	24980	3.92	1.0E-72	BE175434.1	EST_HUMAN	RC4-HT0578-170300-012-g02 HT0578 Homo sapiens cDNA
6350	15530	24981	3.92	1.0E-72	BE175434.1	EST_HUMAN	RC4-HT0578-170300-012-g02 HT0578 Homo sapiens cDNA
6957	16135	25605	8.43	1.0E-72	AF222742.1	NT	Homo sapiens synaptic glycoprotein SC2 (SC2) mRNA, complete cds
6957	16135	25606	8.43	1.0E-72	AF222742.1	NT	Homo sapiens synaptic glycoprotein SC2 (SC2) mRNA, complete cds
1458	10671	18943	1.08	9.0E-73	AW374968.1	EST_HUMAN	MRO-CT0063-071098-002-h11 CT0063 Homo sapiens cDNA
7524	18729		34.92	9.0E-73	11424089	NT	Homo sapiens ribosomal protein L13a (RPL13A), mRNA
1045	10270	19421	1.8	8.0E-73	AW071755.1	EST_HUMAN	ws55c06.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2501098 3' similar to TR:Q56050
3262	12495	21625	0.62	8.0E-73	11435180	NT	Q56050 HYPOTHETICAL PROTEIN MJ1656 ;
5912	16129	24538	5.01	8.0E-73	11428469	NT	Homo sapiens gephyrin (GPH), mRNA
6463	15680	25155	3.2	8.0E-73	AF113129.1	NT	Homo sapiens vacuolar ATPase isoform VA88 mRNA, complete cds
8949	17824	23904	5.07	8.0E-73	11418189	NT	Homo sapiens thyroid autoantigen 70kD (Ku antigen) (G22P1), mRNA
1142	10365	19518	0.74	7.0E-73	8923280	NT	Homo sapiens hypothetical protein FLJ20309 (FLJ20309), mRNA
3270	12503	21634	1.44	7.0E-73	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C008
4963	14150		1.27	7.0E-73	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
161	9443		2.72	6.0E-73	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
6162	15336	24773	3.59	6.0E-73	BE166574.1	EST_HUMAN	QV0-HT0494-020300-137-d03 HT0494 Homo sapiens cDNA
5303	14535	23539	2.11	4.0E-73	11422159	NT	Homo sapiens HELG protein (FAM441), mRNA
1830	11038	20234	1.22	3.0E-73	11435913	NT	Homo sapiens heme-binding protein (HEBP), mRNA
1830	11038	20235	1.22	3.0E-73	11435913	NT	Homo sapiens heme-binding protein (HEBP), mRNA
9195	17982		1.8	3.0E-73	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
9198	17984		1.4	3.0E-73	AW889091.1	EST_HUMAN	RC3-NN0066-270400-011-c04 NN0066 Homo sapiens cDNA
861	10097	19259	3.38	2.0E-73	AF139897.1	NT	Homo sapiens BASS1 (BASS1) mRNA, partial cds
1915	11120		3.14	2.0E-73	AW889091.1	EST_HUMAN	RC3-NN0066-270400-011-c04 NN0066 Homo sapiens cDNA
2260	11455		1.58	2.0E-73	U01317.1	NT	Human beta globin region on chromosome 11
3146	12381	21513	3.5	2.0E-73	4502582	NT	Homo sapiens caspase 8, apoptosis-related cysteine protease (CASP8) mRNA
3525	12749	21860	0.94	2.0E-73	7689539	NT	Homo sapiens Parkinson disease (autosomal recessive, juvenile) 2, parkin (PARK2), transcript variant 3, mRNA

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3525	12748	21881	0.94	2.0E-73	7689539	NT	Homo sapiens Parkinson disease (autosomal recessive, juvenile) 2, parkin (PARK2), transcript variant 3, mRNA
4428	13628		2.51	2.0E-73	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
5804	15082	24495	6.18	2.0E-73	AB049811.1	NT	Homo sapiens mRNA for KIAA1591 protein, partial cds
7622	16825	26321	3.98	2.0E-73	4557612	NT	Homo sapiens galactosylceramidase (Krabbe disease) (GALC), mRNA
7622	16825	26322	3.98	2.0E-73	4557612	NT	Homo sapiens galactosylceramidase (Krabbe disease) (GALC), mRNA
7649	16849	26347	1.94	2.0E-73	AB028982.1	NT	Homo sapiens mRNA for KIAA1059 protein, partial cds
8728	11120		2.68	2.0E-73	AW98081.1	EST_HUMAN	RC3-NN0066-270400-011-c04 NN0066 Homo sapiens cDNA
1763	10985	20150	2.16	1.0E-73	AU121595.1	EST_HUMAN	AU121595 MAMMA1 Homo sapiens cDNA clone MAMMA1000490 5'
7886	16421	25808	3.76	1.0E-73	BE385477.1	EST_HUMAN	601276071F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3617105 5'
748	9889	19132	1.05	8.0E-74	4557428	NT	Homo sapiens CD39-like 4 (CD39L4) mRNA
5823	14847	24228	2	8.0E-74	S83194.1	NT	Ca2+/calmodulin-dependent protein kinase IV kinase isoform [rats, brain, mRNA, 3428 nt]
5823	14847	24229	2	8.0E-74	S83194.1	NT	Ca2+/calmodulin-dependent protein kinase IV kinase isoform [rats, brain, mRNA, 3428 nt]
1819	11123	20318	4.93	7.0E-74	AJ001689.1	NT	Homo sapiens NKG2D gene, exon 10
3301	12632	21064	1.74	7.0E-74	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
8948	17823	23903	4.04	7.0E-74	BE266305.1	EST_HUMAN	601191827F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535855 5'
1130	10354	19506	4.82	8.0E-74	AF109907.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
1604	10818	19983	1.07	8.0E-74	AW263177.1	EST_HUMAN	Xn78q07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2700636 3'
2282	11477	20698	45.19	6.0E-74	BE388260.1	EST_HUMAN	601283521F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3605453 5'
2282	11477	20699	45.19	6.0E-74	BE388260.1	EST_HUMAN	601283521F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3605453 5'
2816	12055	21179	1.03	6.0E-74	AW014039.1	EST_HUMAN	UI-H-B10-ash-h-03-O-UJ.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708365 3'
2816	12055	21180	1.03	6.0E-74	AW014039.1	EST_HUMAN	UI-H-B10-ash-h-03-O-UJ.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708365 3'
3694	12914	22032	1.63	6.0E-74	BE048946.1	EST_HUMAN	hr54e11.x1 NCI_CGAP_Kd11 Homo sapiens cDNA clone IMAGE:3132332 3'
3694	12914	22033	1.63	6.0E-74	BE048946.1	EST_HUMAN	hr54e11.x1 NCI_CGAP_Kd11 Homo sapiens cDNA clone IMAGE:3132332 3'
5052	14234	23320	0.98	8.0E-74	4758135	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (S.cerevisiae CHL1-like helicase) (DDX11) mRNA
5052	14234	23321	0.98	8.0E-74	4758135	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (S.cerevisiae CHL1-like helicase) (DDX11) mRNA
5377	14808	23716	3.17	8.0E-74	11056013	NT	Homo sapiens actin filament associated protein (AFAP), mRNA
915	10150	16310	2.7	5.0E-74	AW020986.1	EST_HUMAN	df17c09.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2483704 5'
2883	11844		8.98	5.0E-74	AW362756.1	EST_HUMAN	PMO-CT0289-271099-001-r07 CT0289 Homo sapiens cDNA
5389	14827	23741	2.11	5.0E-74	11425417	NT	Homo sapiens phosphatidylinositol glycan, class L (PIGL), mRNA
5568	14793	24168	12.05	5.0E-74	X89870.1	NT	H. sapiens mRNA for TPICR18 protein

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5587	14811	24185	7.5	5.0E-74	4507868	NT	Homo sapiens VAMP (vesicle-associated membrane protein)-associated protein A (33kD) (VAPA) mRNA, and translated products
5620	14843	24221	1.93	5.0E-74	11431471	NT	Homo sapiens Interleukin 4 receptor (IL4R), mRNA
5620	14843	24222	1.93	5.0E-74	11431471	NT	Homo sapiens Interleukin 4 receptor (IL4R), mRNA
6038	15246	24668	3.78	5.0E-74	7682263	NT	Homo sapiens KIAA0716 gene product (KIAA0716), mRNA
6476	16673	25144	3.84	5.0E-74	11345483	NT	Homo sapiens hypothetical protein FLJ13222 (FLJ13222), mRNA
7321	16538	26026	2.02	5.0E-74	Y09420.1	NT	H. sapiens mRNA for HIP-1
7321	16538	26027	2.02	5.0E-74	Y09420.1	NT	H. sapiens mRNA for HIP-1
284	9558	18692	3.08	4.0E-74	D87875.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
862	10098	19280	4.8	4.0E-74	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
1832	11136	20331	2.58	4.0E-74	AB028898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
1832	11138	20332	2.58	4.0E-74	AB028898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
2040	11241	20448	8.89	4.0E-74	4508192	NT	Homo sapiens proteasome (prosome, macropain) subunit, beta type, 1 (PSMB1) mRNA
2040	11241	20450	8.89	4.0E-74	4508192	NT	Homo sapiens proteasome (prosome, macropain) subunit, beta type, 1 (PSMB1) mRNA
2102	11302	20516	1.2	4.0E-74	AB032894.1	NT	Homo sapiens mRNA for KIAA1168 protein, partial cds
3058	12292	21418	4.63	4.0E-74	AJ006976.1	NT	Homo sapiens PLP gene
3501	12726	21861	1.5	4.0E-74	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
4040	13260	22351	0.92	4.0E-74	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
4554	13749	22848	2.01	4.0E-74	7682183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
4616	13810	22801	0.75	4.0E-74	Z17227.1	NT	Homo sapiens mRNA for transmembrane receptor protein
6840	15835		21.31	3.0E-74	AA300378.1	EST_HUMAN	EST13131 Thymus tumor III Homo sapiens cDNA 5' end similar to similar to ribosomal protein L37
985	10188	18353	156.49	2.0E-74	7689491	NT	Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GAPD), mRNA
985	10188	18354	156.49	2.0E-74	7689491	NT	Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GAPD), mRNA
1183	10404	19558	1.38	2.0E-74	AF02082.1	NT	Human endogenous retrovirus HERV-K-T47D
1251	10467	19631	2.13	2.0E-74	A1950528.1	EST_HUMAN	w51607.x1 NCL CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2547204 3' similar to SW:GG85_HUMAN Q08379 GOLGIN-95, contains element MIER22 repetitive element;
1575	10788	19863	1.77	2.0E-74	4885188	NT	Homo sapiens epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog) (EGFR) mRNA
1575	10788	19864	1.77	2.0E-74	4885188	NT	Homo sapiens epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog) (EGFR) mRNA
2562	11748	20968	11.8	2.0E-74	A1557280.1	EST_HUMAN	PT2.1_15_G11.1 tumor2 Homo sapiens cDNA 3'
5030	14215	23289	2.54	2.0E-74	AL355092.1	NT	Novel human gene mapping to chromosome 22

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6030	14215	23300	2.54	2.0E-74	AL355092.1	NT	Novel human gene mapping to chromosome 22
5034	14218	23304	5.01	2.0E-74	J02983.1	NT	Human platelet glycoprotein IIb mRNA, 3' end
5571	18058	24169	1.84	2.0E-74	BE711134.1	EST_HUMAN	RC6-HT0878-220500-011-C03 HT0878 Homo sapiens cDNA
5813	18059	24212	2.23	2.0E-74	11439587	NT	Homo sapiens PDZ-73 protein (PDZ-73NY-CO-38), mRNA
5813	18059	24213	2.23	2.0E-74	11439587	NT	Homo sapiens PDZ-73 protein (PDZ-73NY-CO-38), mRNA
5838	18059	24212	2.91	2.0E-74	11439587	NT	Homo sapiens PDZ-73 protein (PDZ-73NY-CO-38), mRNA
5838	18059	24213	2.91	2.0E-74	11439587	NT	Homo sapiens PDZ-73 protein (PDZ-73NY-CO-38), mRNA
6871	18083	25561	11.58	2.0E-74	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
8064	17641		2.32	2.0E-74	AA196181.1	EST_HUMAN	zp96a08.a1 Stragene muscle 837208 Homo sapiens cDNA clone IMAGE:628018 3'
9223	18002	23888	1.34	2.0E-74	BF688568.1	EST_HUMAN	802121428F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4278559 5'
55	9352	18468	1.87	1.0E-74	7657334	NT	Homo sapiens Missipen/NIK-related kinase (MINK), mRNA
342	9810	18737	3.84	1.0E-74	AW818405.1	EST_HUMAN	QV4-ST0234-181198-037-405 ST0234 Homo sapiens cDNA
508	9758	18885	0.98	1.0E-74	8822828	NT	Homo sapiens hypothetical protein FLJ11028 (FLJ11028), mRNA
513	9764	18890	17.5	1.0E-74	X02344.1	NT	Homo sapiens beta 2 gene
608	9855	18974	2.28	1.0E-74	4508020	NT	Homo sapiens zinc finger protein 259 (ZNF259) mRNA
1007	10238	19390	1.74	1.0E-74	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
2193	11380	20613	4.9	1.0E-74	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
3104	12339	21467	2.47	1.0E-74	4758697	NT	Homo sapiens mannosidase, alpha, class 2A, member 1 (MAN2A1), mRNA
3945	13181	22277	6	1.0E-74	AL163288.2	NT	Homo sapiens chromosome 21 segment HS21C068
5228	14400	23483	1.28	1.0E-74	8659584	NT	Homo sapiens collagen, type IV, alpha 5 (Alport syndrome) (COL4A5), mRNA
5228	14400	23484	1.28	1.0E-74	8659584	NT	Homo sapiens collagen, type IV, alpha 5 (Alport syndrome) (COL4A5), mRNA
6719	15914	25374	2.79	1.0E-74	AF214582.1	NT	Homo sapiens tracheal epithelium enriched protein (PLUNC) gene, complete cds
8285	17401	26930	2.1	1.0E-74	11417856	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2), mRNA
8370	17457		4.1	1.0E-74	11417856	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2), mRNA
8519	11390	20613	1.42	1.0E-74	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
8020	17872		1.62	1.0E-74	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
2607	11791		3.57	8.0E-75	AF178228.1	NT	Homo sapiens DNA cytosine-5 methyltransferase 3B (DNMT3B) mRNA, complete cds
8888	17655		1.83	8.0E-75	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
2287	11482	20703	3.62	6.0E-75	AI817415.1	EST_HUMAN	wk38a08.x1 NCI_CGAP_P122 Homo sapiens cDNA clone IMAGE:2417854 3' similar to gb:M14123_cde4
7144	16321	25802	4.05	5.0E-75	AI638623.1	EST_HUMAN	RETROVIRUS-RELATED POL POLYPROTEIN (HUMAN);
112	9400	18529	4.44	4.0E-75	BE081333.1	EST_HUMAN	431g12.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2242390 3' similar to TR:P97361 P97361
							HYPOTHETICAL 20.1 KD PROTEIN ;
							QV1-BT0632-210200-079-602 BT0632 Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
465	9718		0.83	4.0E-75	N36757.1	EST_HUMAN	yx60h08.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:269055 5'
1738	10848	20131	1.15	4.0E-75	AW897230.1	EST_HUMAN	CMO-NN0057-150400-335-a11 NN0057 Homo sapiens cDNA
2801	12041	21182	5.26	4.0E-75	BE409484.1	EST_HUMAN	601303868F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638344 5'
3474	12688	21834	1.02	4.0E-75	8922637	NT	Homo sapiens hypothetical protein FLJ10747 (FLJ10747), mRNA
5776	14684	24394	5.66	4.0E-75	5579457	NT	Homo sapiens eukaryotic translation initiation factor 3, subunit 8 (EIF3S8), mRNA
5883	15195	24612	2.08	4.0E-75	11417948	NT	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA
5883	15195	24613	2.08	4.0E-75	11417948	NT	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA
7277	16486	25888	8.7	4.0E-75	7666505	NT	Homo sapiens myosin, heavy polypeptide 1, skeletal muscle, adult (MYH1), mRNA
8241	17370	26306	1.67	4.0E-75	AF038686.1	NT	Homo sapiens antigen NY-CO-37 (NY-CO-38) mRNA, complete cds
1010	10241	19383	3.38	3.0E-75	AF157623.1	NT	Homo sapiens HTRA serine protease (PRSS11) gene, complete cds
1011	10241	19383	2.18	3.0E-75	AF157623.1	NT	Homo sapiens HTRA serine protease (PRSS11) gene, complete cds
1804	11013	20206	2.02	3.0E-75	AB011153.1	NT	Homo sapiens mRNA for KIAA0581 protein, partial cds
2082	11282	20498	28.14	3.0E-75	4507334	NT	Homo sapiens synaptotagmin 1 (SYNJ1), mRNA
2387	11580	20797	5.08	3.0E-75	4759153	NT	Homo sapiens synaptonemal-associated protein, 28kD (SNAP28) mRNA
2686	12223	21356	0.91	3.0E-75	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
3152	12387	21519	1.02	3.0E-75	AB011153.1	NT	Homo sapiens mRNA for KIAA0581 protein, partial cds
3324	12553	21688	1.08	3.0E-75	M72383.1	NT	Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds
3324	12553	21688	1.08	3.0E-75	M72383.1	NT	Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds
3720	12940	22057	0.89	3.0E-75	M72383.1	NT	Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds
4150	13358	22459	3.01	3.0E-75	D87676.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
4429	13829	22723	0.77	3.0E-75	7662421	NT	Homo sapiens KIAA0871 protein (KIAA0871), mRNA
5215	14390		0.86	3.0E-75	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C008
5966	15288	24694	1.92	3.0E-75	11526319	NT	Homo sapiens HIR (histone cell cycle regulation defective, S. cerevisiae) homolog A (HIRA), mRNA
5988	15288	24695	1.82	3.0E-75	11526319	NT	Homo sapiens HIR (histone cell cycle regulation defective, S. cerevisiae) homolog A (HIRA), mRNA
6134	15318	24751	4.66	3.0E-75	7662209	NT	Homo sapiens KIAA0623 gene product (KIAA0623), mRNA
6134	15318	24752	4.66	3.0E-75	7662209	NT	Homo sapiens KIAA0623 gene product (KIAA0623), mRNA
6344	15525	24972	2.76	3.0E-75	4885632	NT	Homo sapiens Oncogene TIM (TIM) mRNA
6344	15525	24973	2.76	3.0E-75	4885632	NT	Homo sapiens Oncogene TIM (TIM) mRNA
2267	11462	20882	11.09	1.0E-75	AW168135.1	EST_HUMAN	yg60d02.x1 NCL_CGAP_U14 Homo sapiens cDNA clone IMAGE:2632707 3' similar to contains PTR7.1
2897	12135	21272	3.26	1.0E-75	X52221.1	NT	PTR7 repetitive element;
4888	13889	22889	1.48	1.0E-75	BE278301.1	EST_HUMAN	H.sapiens ERCC2 gene, exons 1 & 2 (partial)
							60115/633F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3504272 5'

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Table 4
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6605	15801		7.18	1.0E-75	AA389270.1	EST_HUMAN	z57h03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728485 3' similar to gb:M13832 40S RIBOSOMAL PROTEIN S17 (HUMAN);
6887	16078	25547	5.15	1.0E-75	BF313845.1	EST_HUMAN	601900294F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4123678 5'
6887	16078	25548	5.15	1.0E-75	BF313845.1	EST_HUMAN	601900294F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4123678 5'
7460	16668		5.8	1.0E-75	AA684377.1	EST_HUMAN	ac77b08.s1 Stratagene lung (8937210) Homo sapiens cDNA clone IMAGE:868599 3'
7658	16858	20359	4.08	1.0E-75	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
8574	14503	23588	2.38	1.0E-75	BE694182.1	EST_HUMAN	601437130F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3922303 5'
48	9343	18452	2.66	9.0E-76	AB52848.1	EST_HUMAN	wb30b10.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2307163 3' similar to TR:O75235 O75235 TRAP1;
48	9343	18453	2.66	9.0E-76	AB52848.1	EST_HUMAN	wb30b10.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2307163 3' similar to TR:O75235 O75235 TRAP1;
7041	16218	25693	55.5	9.0E-76	MT2937.1	NT	Human ferritin Heavy subunit mRNA, complete cds
145	9427	18561	7.27	8.0E-76	AF154830.1	NT	Homo sapiens carbamyl phosphate synthetase I mRNA, complete cds
848	10178	18334	5.48	8.0E-76	4504374	NT	Homo sapiens H factor 1 (complement) (HF1) mRNA
848	10178	18335	5.48	8.0E-76	4504374	NT	Homo sapiens H factor 1 (complement) (HF1) mRNA
2862	12100	21231	1.47	8.0E-76	7708724	NT	Homo sapiens mediator (Sur2), mRNA
5739	14958	24368	5.1	8.0E-76	11421442	NT	Homo sapiens LIM domain kinase 1 (LIMK1), mRNA
7259	16478	25971	8.45	8.0E-76	10442821	NT	Homo sapiens baculoviral IAP repeat-containing 6 (BIRC6), mRNA
8934	17815		1.97	8.0E-76	11417882	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
9030	18233	23702	1.41	8.0E-76	AL385515.1	NT	Novel human gene mapping to chromosome 22
785	10024	19174	1.91	7.0E-76	5016092	NT	Homo sapiens dihydrolipoamide dehydrogenase (E3 component of pyruvate dehydrogenase complex, 2-oxo-glutarate complex, branched chain keto acid dehydrogenase complex) (DLD) mRNA
3263	12496	21826	3.4	7.0E-76	AF036490.1	NT	Homo sapiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds
3268	12502	21833	8.15	7.0E-76	4505052	NT	Homo sapiens lymphocyte antigen 75 (LY75) mRNA, and translated products
4366	13687	22682	8.55	7.0E-76	4507184	NT	Homo sapiens septaplatin reductase (7,8-dihydrobiopterin:NADP+ oxidoreductase) (SPR) mRNA
4366	13687	22683	6.55	7.0E-76	4507184	NT	Homo sapiens septaplatin reductase (7,8-dihydrobiopterin:NADP+ oxidoreductase) (SPR) mRNA
1241	10457		8.88	6.0E-76	BE396253.1	EST_HUMAN	601312019F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3059757 5'
8001	16438	25623	3.25	6.0E-76	BE273201.1	EST_HUMAN	601142253F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3508029 5'
1812	11117	20312	11.44	5.0E-76	D63874.1	NT	Human mRNA for HMG-1, complete cds
1812	11117	20313	11.44	5.0E-76	D63874.1	NT	Human mRNA for HMG-1, complete cds
1812	11117	20314	11.44	5.0E-76	D63874.1	NT	Human mRNA for HMG-1, complete cds
3173	12408	21543	0.7	4.0E-76	BE814086.1	EST_HUMAN	QV3-BN0047-270700-283-g06 BN0047 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7082	16259	25734	3.98	4.0E-78	D81825.1	EST_HUMAN	HUM178G01B Human fetal brain (Tfujwara) Homo sapiens cDNA clone GEN-178G01 5'
7082	16259	25735	3.98	4.0E-78	D81825.1	EST_HUMAN	HUM178G01B Human fetal brain (Tfujwara) Homo sapiens cDNA clone GEN-178G01 5'
635	9880	18003	1.54	3.0E-78	BF510282.1	EST_HUMAN	UIH-BW1-anz-b-04-0-JL.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3083862 3'
635	9880	19004	1.54	3.0E-78	BF510282.1	EST_HUMAN	UIH-BW1-anz-b-04-0-JL.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3083862 3'
1678	10782	18868	10.89	3.0E-78	4503478	NT	Homo sapiens eukaryotic translation elongation factor 1 beta 2 (EEF1B2) mRNA
1578	10782	18869	10.89	3.0E-78	4503478	NT	Homo sapiens eukaryotic translation elongation factor 1 beta 2 (EEF1B2) mRNA
3407	12633	21763	5.18	3.0E-78	BF375689.1	EST_HUMAN	RC5-ST0300-180100-033-A03 ST0300 Homo sapiens cDNA
3407	12633	21764	5.18	3.0E-78	BF375689.1	EST_HUMAN	RC5-ST0300-180100-033-A03 ST0300 Homo sapiens cDNA
5294	14463	26826	2.14	3.0E-78	Z41314.1	EST_HUMAN	HSC2QD042 normalized infant brain cDNA Homo sapiens cDNA clone c-zqd04 3'
5820	15037	24438	8.16	3.0E-78	AF286598.1	NT	Homo sapiens angiotensin binding protein 1 mRNA, complete cds
6998	18174	25845	2.8	3.0E-78	AW29053.1	EST_HUMAN	xs49h01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2773009 3'
8278	18148	23752	1.8	3.0E-78	AW967984.1	EST_HUMAN	EST380059 MAGE resequences, MAGJ Homo sapiens cDNA
8382	18365	23592	4.03	3.0E-78	AW950455.1	EST_HUMAN	EST388523 MAGE resequences, MAGD Homo sapiens cDNA
288	9560	18894	1.1	2.0E-78	D84295.1	NT	Human mRNA for possible protein TPRDII, complete cds
347	9615	18741	2.83	2.0E-78	D84295.1	NT	Human mRNA for possible protein TPRDII, complete cds
347	9615	18742	2.83	2.0E-78	D84295.1	NT	Human mRNA for possible protein TPRDII, complete cds
467	9720		1.48	2.0E-78	4557682	NT	Homo sapiens immunoglobulin (CD79A) binding protein 1 (IGBP1) mRNA
587	9844	18963	1.03	2.0E-78	4503844	NT	Homo sapiens glucagon (GCG) mRNA
1038	10264	18417	0.71	2.0E-78	4758053	NT	Homo sapiens cAMP responsive element binding protein 1 (CREB1) mRNA
1522	10736	19908	2.17	2.0E-78	4504028	NT	Homo sapiens GM2 ganglioside activator protein (GM2A) mRNA
1522	10738	18909	2.17	2.0E-78	4504028	NT	Homo sapiens GM2 ganglioside activator protein (GM2A) mRNA
1897	11104	20286	1.05	2.0E-78	AA233954.1	EST_HUMAN	zs60h11.s1 Striatum schizo brain S11 Homo sapiens cDNA clone IMAGE:701825 3'
2784	12034	21158	3.2	2.0E-78	P23268	SWISSPROT	OLFATORY RECEPTOR-LIKE PROTEIN F5
3288	12489	21630	1.85	2.0E-78	AA445992.1	EST_HUMAN	zw64e02.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:780988 3' similar to SW:ITB5_HUMAN
3288	12489	21631	1.85	2.0E-78	AA445992.1	EST_HUMAN	P18084 INTEGRIN BETA-5 SUBUNIT PRECURSOR. ;
4117	8580	18994	0.81	2.0E-78	D84295.1	NT	zw64e02.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:780988 3' similar to SW:ITB5_HUMAN
4495	13693	22787	1.14	2.0E-78	11545921	NT	P18084 INTEGRIN BETA-5 SUBUNIT PRECURSOR. ;
4988	14183	23245	6.42	2.0E-78	AW879618.1	EST_HUMAN	Human mRNA for possible protein TPRDII, complete cds
5155	14334	23424	1.04	2.0E-78	5031860	NT	Homo sapiens melanoma differentiation associated protein-5 (MDA5), mRNA
5500	14728	24088	5.97	2.0E-78	AB028004.1	NT	QV3-OT0028-220300-132-b11 OT0028 Homo sapiens cDNA
7162	16339	25819	4.12	2.0E-78	11437211	NT	Homo sapiens EGF-like repeats and discoidin-like domains 3 (EDIL3), mRNA
7495	16702	26187	2.68	2.0E-78	7549807	NT	Homo sapiens mRNA for KIAA1081 protein, partial cds
							Homo sapiens similar to ribosomal protein S28 (H. sapiens) (LOC63150), mRNA
							Homo sapiens HIRA interacting protein 4 (dnaf-like) (HIRIP4), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4285	13488	22587	4.8	1.0E-76	D83874.1	NT	Human mRNA for HMG-1, complete cds
4285	13488	22588	4.8	1.0E-76	D83874.1	NT	Human mRNA for HMG-1, complete cds
5418	14848	23779	5.48	1.0E-78	BE786537.1	EST_HUMAN	601589898F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944302 5'
6053	15221	24840	4.38	9.0E-77	BE889525.1	EST_HUMAN	601612435F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913737 5'
8086	17814		1.36	9.0E-77	BE410354.1	EST_HUMAN	601302333F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638753 5'
192	9471	18602	2.94	8.0E-77	R83144.1	EST_HUMAN	Yp11h02.r1 Soares breast 3NBH8st Homo sapiens cDNA clone IMAGE:187155 5' similar to SP-ANKB_HUMAN Q01484 ANKYRIN, BRAIN VARIANT 1;
4622	13718	22813	1.3	8.0E-77	BF205181.1	EST_HUMAN	601889328F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4109503 5'
5420	14848	23782	2.57	8.0E-77	4508230	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 7 (Mox64 homolog) (PSMD7) mRNA
7925	17138	26688	2.71	8.0E-77	AA019770.1	EST_HUMAN	z682e02.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:363578 5'
7925	17138	26670	2.71	8.0E-77	AA019770.1	EST_HUMAN	z682e02.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:363578 5'
9078	17901	23901	8.5	8.0E-77	R00245.1	EST_HUMAN	ye689f04.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:123007 3' similar to contains MER10 repetitive element;
1898	11105	20297	2.31	7.0E-77	AA825755.1	EST_HUMAN	Zu01g01.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:743392 3'
2374	11567	20788	12.88	7.0E-77	4505944	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide E (25kD) (POLR2E) mRNA
2374	11567	20788	12.88	7.0E-77	4505944	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide E (25kD) (POLR2E) mRNA
287	8542	18872	8.02	6.0E-77	4504600	NT	Homo sapiens interferon (alpha, beta and omega) receptor 2 (IFNAR2) mRNA
1150	10373	18524	0.7	6.0E-77	AW957753.1	EST_HUMAN	EST3888233 IMAGE resequences, MAGE Homo sapiens cDNA
1528	10743	19016	2.44	6.0E-77	AI204088.1	EST_HUMAN	qe77h12.x1 Soares fetal lung_NbHL10W Homo sapiens cDNA clone IMAGE:1745083 3'
4949	14136	23228	0.72	6.0E-77	4557752	NT	Homo sapiens midline 1 (Opitz/BBB syndrome) (MID1) mRNA
4949	14136	23230	0.72	6.0E-77	4557752	NT	Homo sapiens midline 1 (Opitz/BBB syndrome) (MID1) mRNA
147	9429	18593	2.64	5.0E-77	AF154830.1	NT	Homo sapiens carbamyl phosphate synthetase I mRNA, complete cds
147	9429	18594	2.64	5.0E-77	AF154830.1	NT	Homo sapiens carbamyl phosphate synthetase I mRNA, complete cds
1243	10459	18618	1.8	5.0E-77	AF041015.1	NT	7 Homo sapiens glucokinase (GCK) gene, exon 2
1388	10582	18749	2.11	5.0E-77	4557250	NT	Homo sapiens dielinigrin and metalloprotease domain 10 (ADAM10) mRNA
2645	11828	21043	1.62	5.0E-77	AF162888.1	NT	Homo sapiens tousel-like kinase 1 (TLK1) mRNA, complete cds
2719	11888	21114	1.44	5.0E-77	4503160	NT	Homo sapiens cullin 1 (CUL1) mRNA
3495	12719	21856	1.39	5.0E-77	8394518	NT	Homo sapiens ubiquitin specific protease 18 (USP18) mRNA
4714	13905	23005	1.88	5.0E-77	5031680	NT	Homo sapiens EGF-like repeats and discoidin-like domains 3 (EDIL3) mRNA
4714	13905	23006	1.88	5.0E-77	5031680	NT	Homo sapiens EGF-like repeats and discoidin-like domains 3 (EDIL3) mRNA
4956	14143	23238	2.29	5.0E-77	AL043953.1	EST_HUMAN	DKFZp434G1728_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434G1728 5'
6220	15401	24842	10.02	5.0E-77	X88286.1	NT	H. sapiens mRNA for ubiquitin hydrolase
6847	18105	25571	4.08	5.0E-77	11421928	NT	Homo sapiens sorting nexin 5 (SNX5) mRNA

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6947	18105	25572	4.08	5.0E-77	11421828	NT	Homo sapiens sorting nexin 5 (SNX5), mRNA
3682	12903	22023	0.89	4.0E-77	AL449758.1	EST_HUMAN	AL449758 Homo sapiens fetal brain (Starvies GS) Homo sapiens cDNA
1942	11146	20345	1.54	3.0E-77	5730038	NT	Homo sapiens SET domain and nuclear transposase fusion gene (SETMAR) mRNA
1942	11146	20348	1.54	3.0E-77	5730038	NT	Homo sapiens SET domain and nuclear transposase fusion gene (SETMAR) mRNA
7482	18660	26148	4.65	3.0E-77	BF358917.1	EST_HUMAN	PM3-MT0078-080800-005-g03 MT0078 Homo sapiens cDNA
1360	10576	19740	1.54	2.0E-77	AV784617.1	EST_HUMAN	AV784617 MDS Homo sapiens cDNA clone MDSBTF10 5'
1435	10649	19823	8.08	2.0E-77	AW987712.1	EST_HUMAN	RC3-BN0053-170200-011-401 BN0053 Homo sapiens cDNA
2060	11281	20476	1.8	2.0E-77	L41826.1	NT	Homo sapiens CYP17 gene, 5' end
2073	11273	20483	2.86	2.0E-77	7706315	NT	Homo sapiens CGI-79 protein (LOC51634), mRNA
2554	12019	20858	1.51	2.0E-77	AB037836.1	NT	Homo sapiens mRNA for KIAA1415 protein, partial cds
2554	12019	20859	1.51	2.0E-77	AB037838.1	NT	Homo sapiens mRNA for KIAA1415 protein, partial cds
4010	13222	22323	1.48	2.0E-77	BE044318.1	EST_HUMAN	h043b05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3040113 3' similar to SW:GAG2_HUMAN P10284 RETROVIRUS-RELATED GAG POLYPROTEIN ;
4586	13780		1.9	2.0E-77	4504088	NT	SW:GAG2_HUMAN P10284 RETROVIRUS-RELATED GAG POLYPROTEIN ; nuclear gene encoding mitochondrial protein, mRNA
4779	13988	23070	6.81	2.0E-77	AA653025.1	EST_HUMAN	ns88g12.a1 NCL_CGAP_P2 Homo sapiens cDNA clone IMAGE:1188838 similar to SW:RL29_HUMAN P47914 80S RIBOSOMAL PROTEIN L28, [1]; contains element MSR1 repetitive element ;
5037	14861	24246	1.99	2.0E-77	BE298940.1	EST_HUMAN	601118952F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3029436 5'
5740	14859	24359	1.86	2.0E-77	BE787143.1	EST_HUMAN	601476802F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3879505 5'
6163	15337	24774	15.25	2.0E-77	AI839003.1	EST_HUMAN	af74609.x1 Barstead colon HPLR87 Homo sapiens cDNA clone IMAGE:2377720 3' similar to TR:Q13311 Q13311 TAX1-BINDING PROTEIN TXBP161, [1];
6828	16119	25586	4.1	2.0E-77	U50321.1	NT	Human protein kinase C substrate 80K-H (PRKCSH) gene, exon 7
6828	16119	26587	4.1	2.0E-77	U50321.1	NT	Human protein kinase C substrate 80K-H (PRKCSH) gene, exon 7
45	8341	18448	1	1.0E-77	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
45	8341	18448	1	1.0E-77	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
277	8552	18683	3.78	1.0E-77	4502168	NT	Homo sapiens amyloid beta (A4) precursor protein (protease neadn-II, Alzheimer disease) (APP), mRNA
277	9552	18684	3.78	1.0E-77	4502168	NT	Homo sapiens amyloid beta (A4) precursor protein (protease neadn-II, Alzheimer disease) (APP), mRNA
885	11880	18264	6.39	1.0E-77	4502168	NT	Homo sapiens amyloid beta (A4) precursor protein (protease neadn-II, Alzheimer disease) (APP), mRNA
885	11880	18285	6.39	1.0E-77	4502168	NT	Homo sapiens amyloid beta (A4) precursor protein (protease neadn-II, Alzheimer disease) (APP), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1885	11092	20283	1.21	1.0E-77	AW058119.1	EST_HUMAN	w63605.x1 Soares_thymus_NH7Th Homo sapiens cDNA clone IMAGE:2538160 3'
2407	11599	20820	2.84	1.0E-77	AB028024.1	NT	Homo sapiens mRNA for KIAA1101 protein, complete cds
3010	12246	21375	2.85	1.0E-77	4503300	NT	Homo sapiens 2,4-dienoyl CoA reductase 1, mitochondrial (DECR1), mRNA
4348	13548	22840	3.77	1.0E-77	7706299	NT	Homo sapiens CGI-80 protein (LOC51628), mRNA
4523	13719	22814	20.64	1.0E-77	AJ228041.1	NT	Homo sapiens 989 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
4652	13946	22837	2.36	1.0E-77	6552322	NT	Homo sapiens breast cancer 1, early onset (BRCA1), transcript variant BRCA1-exon4, mRNA
4702	13993	22692	1.01	1.0E-77	AI273014.1	EST_HUMAN	q09g04.x1 NCI_CGAP_Kid8 Homo sapiens cDNA clone IMAGE:1881110 3'
4900	14088	23181	1.31	1.0E-77	11418424	NT	Homo sapiens collagen, type XII, alpha 1 (COL12A1), mRNA
5101	14281	23365	2.43	1.0E-77	7681849	NT	Homo sapiens KIAA0005 gene product (KIAA0005), mRNA
5101	14281	23366	2.43	1.0E-77	7681849	NT	Homo sapiens KIAA0005 gene product (KIAA0005), mRNA
5627	14851	24233	1.91	1.0E-77	AF086944.1	NT	Homo sapiens dynactin 1 (DCTN1) gene, exons 27 and 28
5627	14851	24234	1.91	1.0E-77	AF086944.1	NT	Homo sapiens dynactin 1 (DCTN1) gene, exons 27 and 28
5848	15085	24475	1.88	1.0E-77	4885182	NT	Homo sapiens diaphanous (Drosophila, homolog) 1 (DIAPH1), mRNA
6105	15189	24617	12.1	1.0E-77	5881412	NT	Homo sapiens elastin (supravalvular aortic stenosis, Williams-Buren syndrome) (ELN), mRNA
6847	15084	24473	2.45	8.0E-78	AW947081.1	EST_HUMAN	RC2-ET0023-080500-012-e05 ET0023 Homo sapiens cDNA
5847	15084	24474	2.45	8.0E-78	AW947081.1	EST_HUMAN	RC2-ET0023-080500-012-e05 ET0023 Homo sapiens cDNA
85	9378	18508	1.94	8.0E-78	AU118789.1	EST_HUMAN	AU118789 HEMBA1 Homo sapiens cDNA clone HEMBA1004354 5'
85	9378	18509	1.94	8.0E-78	AU118789.1	EST_HUMAN	AU118789 HEMBA1 Homo sapiens cDNA clone HEMBA1004354 5'
3286	12517	21648	1.45	8.0E-78	BF344101.1	EST_HUMAN	602016926F1 NCI_CGAP_Brm64 Homo sapiens cDNA clone IMAGE:4152511 5'
5805	15122		2.51	8.0E-78	11432710	NT	Homo sapiens GDNF family receptor alpha 1 (GFRA1), mRNA
222	9501	18632	1.24	5.0E-78	11422488	NT	Homo sapiens hypothetical protein FLJ11316 (FLJ11316), mRNA
2528	11718	20933	8.37	5.0E-78	AW673424.1	EST_HUMAN	ba54h03.y3 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2800405 5' similar to WP.Y48B8A.6
3363	12591	21731	4.41	5.0E-78	M55586.1	NT	CE22121 ; Human collagenase type IV (CLG4) gene, exon 6
5401	14628	23742	2.51	5.0E-78	AF036536.1	NT	Homo sapiens Beas's macular dystrophy related protein mRNA, partial cds
5478	14705	24059	10.31	5.0E-78	11416585	NT	Homo sapiens transforming growth factor, beta-induced, 68KD (TGFB1), mRNA
6143	15327	24763	2.23	5.0E-78	AW953120.1	EST_HUMAN	Homo sapiens transforming growth factor, beta-induced, 68KD (TGFB1), mRNA
6797	15892	25450	8.12	5.0E-78	U60889.1	NT	Human lysosomal alpha-mannosidase (manB) gene, exon 7
6798	15993	25451	5.58	5.0E-78	BE960836.1	EST_HUMAN	Human lysosomal alpha-mannosidase (manB) gene, exon 7
1145	10368	18518	1.2	4.0E-78	AL043314.2	EST_HUMAN	601648061F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:3931887 5'
1506	10719	18891	1.36	4.0E-78	AL355841.1	NT	DKFZp434N0323_r1 434 (synonym: hbes3) Homo sapiens cDNA clone DKFZp434N0323 5'
2284	11479	20701	19.91	4.0E-78	AF107405.1	NT	Novel human gene mapping to chromosome 22
4313	13514	22607	1.61	4.0E-78	7658878	NT	Homo sapiens pre-mRNA splicing factor (SFRS3) mRNA, complete cds
7184	16371	25831	2.19	4.0E-78	11580151	NT	Homo sapiens syncytin (LOC30818), mRNA
							Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7194	18371	25862	2.19	4.0E-78	11560151	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA
7346	18562	26051	1.82	4.0E-78	11428610	NT	Homo sapiens regulatory factor X-associated ankyrin-containing protein (REFANK), mRNA
7957	17088	26628	2.18	4.0E-78	AF189148.1	NT	Homo sapiens a-CaBP1 (CABP1) mRNA, complete cds
8092	17238	26783	3.42	4.0E-78	X05844.1	NT	Human transforming growth factor-beta precursor gene exons 4-5 (and joined mature peptide)
8881	17833	23910	3.24	4.0E-78	AB011389.1	NT	Homo sapiens gene for AF-6, complete cds
104	8448	18578	2.52	3.0E-78	AF095901.1	NT	Homo sapiens eRF1 gene, complete cds
184	9448	18577	2.62	3.0E-78	AF085901.1	NT	Homo sapiens eRF1 gene, complete cds
2288	11463	20683	2.07	3.0E-78	4502142	NT	Homo sapiens apoptosis inhibitor 3 (API3) mRNA
2390	11573	20792	1.23	3.0E-78	7706705	NT	Homo sapiens SH3 and PX domain-containing protein SH3PX1 (SH3PX1), mRNA
3748	12868		1.82	3.0E-78	AU140604.1	EST_HUMAN	AU140604 PLAGE3 Homo sapiens cDNA clone PLAGE3000373 5'
3805	13023	22134	0.77	3.0E-78	4507334	NT	Homo sapiens synaptotagmin 1 (SYNJ1), mRNA
4082	13023	22134	0.89	3.0E-78	4507334	NT	Homo sapiens synaptotagmin 1 (SYNJ1), mRNA
5082	14262	23347	1.05	3.0E-78	AF080810.1	NT	Homo sapiens neuraxin III-alpha gene, partial cds
7168	16343		6.59	3.0E-78	BE144758.1	EST_HUMAN	CMO-HT0180-041099-005-c07 HT0180 Homo sapiens cDNA
7554	16769	26253	6.1	3.0E-78	BE156318.1	EST_HUMAN	QV0-HT0367-150200-114-g09 HT0367 Homo sapiens cDNA
3085	12321		5.97	2.0E-78	U04489.1	NT	Homo sapiens type IV collagen alpha 5 chain (COL4A5) gene, exon 20
3990	13204		2.23	2.0E-78	AA311872.1	EST_HUMAN	EST182583 Jurkat T-cells VI Homo sapiens cDNA 5' end
6388	15589	25028	3.78	2.0E-78	BF88800.1	EST_HUMAN	802188528F1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4298599 5'
6478	15875	25148	2.79	2.0E-78	AV714177.1	EST_HUMAN	AV714177 DC8 Homo sapiens cDNA clone DCBAWF08 5'
8815	15811	25287	2.8	2.0E-78	AI557509.1	EST_HUMAN	P12.1_16_B07.r tumor2 Homo sapiens cDNA 3'
8815	15811	25288	2.8	2.0E-78	AI557509.1	EST_HUMAN	P12.1_16_B07.r tumor2 Homo sapiens cDNA 3'
7848	18848	26344	3.63	2.0E-78	AI197837.1	EST_HUMAN	q150h05.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:1859981 3' similar to WP-RR0.1
7884	18883	26391	6.13	2.0E-78	N66951.1	EST_HUMAN	CE06325 PROTEIN KINASE;
5229	14403	23486	1.73	1.0E-78	4758843	NT	2848112.81 Soares fetal liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:266823 3'
5333	14564	23638	3.18	1.0E-78	11417304	NT	Homo sapiens nucleoporin 165kD (NUP165) mRNA
8452	17510	24019	1.3	1.0E-78	11430460	NT	Homo sapiens GAP-like protein (LOC51306), mRNA
8558	17578	23986	1.28	1.0E-78	11435803	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
8920	18263	23692	1.72	1.0E-78	AI850819.1	EST_HUMAN	Homo sapiens similar to lymphocyte activation-associated protein (H. sapiens) (LOC83140), mRNA
4709	13900	22889	4.24	9.0E-79	11525881	NT	w20808.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2298815 3'
4880	14068	23184	3.22	9.0E-79	BE000837.1	EST_HUMAN	Homo sapiens peptide YY (PYY), mRNA
5408	14838	23784	15.25	9.0E-79	AB028070.1	NT	RC2-BN0074-080300-014-c12 BN0074 Homo sapiens cDNA
							Homo sapiens mRNA for activator of S phase Kinase, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5807	15024	24424	2.48	9.0E-79	5454145	NT	Homo sapiens ubiquitin-conjugating enzyme E2E 3 (homologous to yeast UBC4/5) (UBE2E3) mRNA
6792	15987	25447	4.89	9.0E-79	J02853.1	NT	Homo sapiens casein kinase II alpha subunit mRNA, complete cds
6792	15987	25448	4.89	9.0E-79	J02853.1	NT	Homo sapiens casein kinase II alpha subunit mRNA, complete cds
7635	16838	26332	1.73	9.0E-79	AY008273.1	NT	Homo sapiens TRAF8-regulated IKK activator 1 beta Uev1A mRNA, complete cds
8045	17181	26720	3.28	9.0E-79	11423827	NT	Homo sapiens suppressor of white apricot homolog 2 (SWAP2), mRNA
8045	17181	26721	3.28	9.0E-79	11423827	NT	Homo sapiens suppressor of white apricot homolog 2 (SWAP2), mRNA
8093	17227	26784	3.83	9.0E-79	11417260	NT	Homo sapiens threonyl-tRNA synthetase (TARS), mRNA
8093	17227	26785	3.83	9.0E-79	11417260	NT	Homo sapiens threonyl-tRNA synthetase (TARS), mRNA
9170	17965	23885	1.48	9.0E-79	11417877	NT	Homo sapiens gamma-glutamyltransferase 1 (GGT1), mRNA
3723	12943	22060	0.82	8.0E-79	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
4492	13680	22782	1.36	8.0E-79	D28476.1	NT	Homo sapiens chromosome 21 segment HS21C082
4492	13680	22783	1.36	8.0E-79	D28476.1	NT	Human mRNA for KIAA0045 gene, complete cds
3219	12453	21588	20.38	7.0E-79	BE819648.1	EST_HUMAN	Human mRNA for KIAA0045 gene, complete cds
8301	17409		5.63	6.0E-78	AA989829.1	EST_HUMAN	601472766T1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:3875657 3'
8029	17166	26704	4.48	5.0E-79	AL163282.2	NT	484604.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:462558 3' similar to
3141	12376		1.06	4.0E-79	8922325	NT	TR:Q15408 Q15408 NEUTRAL PROTEASE LARGE SUBUNIT ;
318	9589	18720	1.21	3.0E-78	AF114488.1	NT	Homo sapiens chromosome 21 segment HS21C082
985	10216	18372	3.68	3.0E-78	AF232708.1	NT	Homo sapiens hypothetical protein FLJ10283 (FLJ10283), mRNA
3084	12300	21424	2.34	3.0E-79	U09410.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
5149	14328	23417	0.78	3.0E-78	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
5149	14328	23418	0.78	3.0E-78	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
5374	14803	23712	4.61	3.0E-78	AF110322.1	NT	Homo sapiens MSTP016 (MST016) mRNA, complete cds
5544	14788	24134	1.75	3.0E-78	AB020689.1	NT	Homo sapiens mRNA for KIAA0892 protein, partial cds
5500	14783	24152	3.47	3.0E-79	11426770	NT	Homo sapiens netrin 1 (NTN1), mRNA
5500	14783	24153	3.47	3.0E-79	11426770	NT	Homo sapiens netrin 1 (NTN1), mRNA
6108	15202	24819	3.01	3.0E-78	AB014520.1	NT	Homo sapiens mRNA for KIAA0820 protein, partial cds
6108	15202	24820	3.01	3.0E-78	AB014520.1	NT	Homo sapiens mRNA for KIAA0820 protein, partial cds
7437	16846	26138	1.89	3.0E-78	AF249273.1	NT	Homo sapiens Bcl-2-associated transcription factor short form mRNA, complete cds
7437	16846	26139	1.89	3.0E-78	AF249273.1	NT	Homo sapiens Bcl-2-associated transcription factor short form mRNA, complete cds
292	9568		0.81	2.0E-78	H63128.1	EST_HUMAN	601159415F2 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3511107 5'
640	9886	19011	1.14	2.0E-79	BE378926.1	EST_HUMAN	601159415F2 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3511107 5'
636	10169	19328	1.04	2.0E-79	4757841	NT	Homo sapiens BCL2-like 2 (BCL2L2) mRNA

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1042	10288		1.88	2.0E-79	AI523747.1	EST_HUMAN	th18h07.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2118885 3'
2116	11316	20531	5.52	2.0E-79	4585863	NT	Homo sapiens phosphodiesterase 8A, cGMP-specific, rod, alpha (PDE8A), mRNA
2116	11315	20532	5.52	2.0E-79	4585863	NT	Homo sapiens phosphodiesterase 8A, cGMP-specific, rod, alpha (PDE8A), mRNA
2159	11357	20575	3.99	2.0E-79	AJ271408.1	NT	Homo sapiens mRNA for Fas-associated factor, FAF1 (FAF1 gene)
2279	11474	20897	3.2	2.0E-79	AF244158.1	NT	Homo sapiens hepatocellular carcinoma-associated antigen 88 (HCA88) mRNA, complete cds
4051	13261	22364	1.07	2.0E-79	AA341506.1	EST_HUMAN	EST46988 Fetal kidney II Homo sapiens cDNA 5' end
4147	13353	22455	1.24	2.0E-79	AJ271408.1	NT	Homo sapiens mRNA for Fas-associated factor, FAF1 (FAF1 gene)
4697	13888	22688	0.68	2.0E-79	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C008
6149	15333	24770	2.41	2.0E-79	7382479	NT	Homo sapiens Rho GTPase activating protein 6 (ARHGAP6), transcript variant 4, mRNA
6149	15333	24771	2.41	2.0E-79	7382479	NT	Homo sapiens Rho GTPase activating protein 6 (ARHGAP6), transcript variant 4, mRNA
6627	15823	25285	3.2	2.0E-79	11427428	NT	Homo sapiens hypothetical protein FLJ11008 (FLJ11008), mRNA
7598	16801	26283	4.64	2.0E-79	BE064386.1	EST_HUMAN	RC4-BT0310-110300-015-F10 BT0310 Homo sapiens cDNA
7598	16801	26294	4.64	2.0E-79	BE064386.1	EST_HUMAN	RC4-BT0310-110300-015-F10 BT0310 Homo sapiens cDNA
8339	14501	23586	2.85	2.0E-79	7682357	NT	Homo sapiens KIAA0879 protein (KIAA0879), mRNA
8426	17494	24011	4.83	2.0E-79	AB020640.1	NT	Homo sapiens mRNA for KIAA0833 protein, partial cds
8668	17644	23978	3.11	2.0E-79	11418322	NT	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA
5925	18068						MRO-NN0087-260800-017-B10 NN0087 Homo sapiens cDNA
8143	17275	26819	3.21	1.0E-79	BF383071.1	EST_HUMAN	QV2-HT0540-120800-358-a05 HT0540 Homo sapiens cDNA
8454	18289		4.11	1.0E-79	BF087405.1	EST_HUMAN	ar79a04.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2151438 3'
3111	12348	21473	15.25	1.0E-80	AI460115.1	EST_HUMAN	el23a05.s1 Soares_testis_NHT Homo sapiens cDNA clone 1343648 3'
3111	12348	21474	15.25	1.0E-80	AA725848.1	EST_HUMAN	el23a05.s1 Soares_testis_NHT Homo sapiens cDNA clone 1343648 3'
7815	16818		1.66	9.0E-80	AA725848.1	EST_HUMAN	tm47d08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2161263 3'
7825	17017	26532	12.17	9.0E-80	11433824	NT	Homo sapiens solute carrier family 7 (cationic amino acid transporter, y ⁺ system), member 8 (SLC7A8), mRNA
7825	17017	26533	12.17	9.0E-80	11433824	NT	Homo sapiens solute carrier family 7 (cationic amino acid transporter, y ⁺ system), member 8 (SLC7A8), mRNA
3590	12802		4.51	8.0E-80	U84387.1	NT	Homo sapiens Y chromosome spermatogenesis candidate protein (RBM) pseudogene mRNA, partial cds
6337	15517	24964	2.95	8.0E-80	11422847	NT	Homo sapiens KIAA0724 gene product (KIAA0724), mRNA
6337	15517	24965	2.95	8.0E-80	11422847	NT	Homo sapiens KIAA0724 gene product (KIAA0724), mRNA
4974	14161	23252	0.82	7.0E-80	H04619.1	EST_HUMAN	y49d02.r1 Soares_placenta Nb2Hp Homo sapiens cDNA clone IMAGE:152067 5'
910	10145	19308	2.29	6.0E-80	AI422197.1	EST_HUMAN	if58d02.x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2103459 3' similar to SW-NUEM_HUMAN Q16785 NADH-UBIQUINONE OXIDOREDUCTASE 39 KD SUBUNIT PRECURSOR;

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Table 4
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1620	10833	20008	3.71	6.0E-80	U84888.1	NT	Homo sapiens NRD convertase mRNA, complete cds
2261	11456	20673	6.76	6.0E-80	6631094	NT	Homo sapiens minichromosome maintenance deficient (S. cerevisiae) 3 (MCM3), mRNA
2261	11456	20674	6.76	6.0E-80	6631094	NT	Homo sapiens minichromosome maintenance deficient (S. cerevisiae) 3 (MCM3), mRNA
4270	13473	22568	2.1	6.0E-80	AB032981.1	NT	Homo sapiens mRNA for KIAA1155 protein, partial cds
4270	13473	22569	2.1	6.0E-80	AB032981.1	NT	Homo sapiens mRNA for KIAA1155 protein, partial cds
6701	14920	24314	3.22	6.0E-80	AJ404468.1	NT	Homo sapiens mRNA for dyx19 heavy chain (D9AH9 gene)
6764	14963	24382	3.97	6.0E-80	11436736	NT	Homo sapiens tubby like protein 3 (TULP3), mRNA
7515	16720	26210	2.63	6.0E-80	11427366	NT	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 1 (BIG1), mRNA
7777	16972	26485	21.54	6.0E-80	AF226730.1	NT	Homo sapiens Cyt19 mRNA, complete cds
8232	17361	26899	2.16	6.0E-80	AF102265.1	NT	Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds
8308	10145	19306	1.46	6.0E-80	AI422197.1	EST_HUMAN	U58602.x1 NCI_QGAP_Bm23 Homo sapiens cDNA clone IMAGE:2103459 3' similar to SW:NUEM_HUMAN Q19785 NADH-UBIQUINONE OXIDOREDUCTASE 39 KD SUBUNIT PRECURSOR ;
8436	18173		2.28	6.0E-80	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
8848	17631		6.14	6.0E-80	AB029900.1	NT	Homo sapiens CST gene for cerebroside sulfoltransferase, exon 1, 2, 3, 4, 5
9165	18307		1.69	6.0E-80	AJ133127.1	NT	Homo sapiens mRNA for sodium-glucose cotransporter (SGLT2 gene)
995	9842	18862	2.27	6.0E-80	4506228	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 3 (PSMD3) mRNA
845	10082	19241	1.45	5.0E-80	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MINBH) mRNA, complete cds
845	10082	19242	1.45	5.0E-80	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MINBH) mRNA, complete cds
1197	10417		5.59	5.0E-80	X91647.1	NT	H. sapiens ncx1 gene (exon 12)
1455	10668		2.61	5.0E-80	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
2326	11522	20744	1	5.0E-80	U89358.1	NT	Human K3mbt protein homolog mRNA, complete cds
2394	11587	20805	7.09	5.0E-80	AB037855.1	NT	Homo sapiens mRNA for KIAA1434 protein, partial cds
2747	11928	21140	2.06	5.0E-80	4504282	NT	Homo sapiens H3 histone family, member J (H3F-J) mRNA
4016	13228	22330	1.08	5.0E-80	AB019038.1	NT	Homo sapiens HMT-1 mRNA for beta-1,4 mannosyltransferase, complete cds
4016	13228	22331	1.08	5.0E-80	AB019038.1	NT	Homo sapiens HMT-1 mRNA for beta-1,4 mannosyltransferase, complete cds
4973	14160	23251	1.16	5.0E-80	AL163286.2	NT	Homo sapiens chromosome 21 segment HS21C088
5237	14411	23491	2.76	5.0E-80	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
6841	16046	25511	8.8	4.0E-80	F25915.1	EST_HUMAN	HSPD13155 HM3 Homo sapiens cDNA clone s4000045F03
221	9500		17.47	3.0E-80	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
4719	13910	23012	1.02	3.0E-80	BF083009.1	EST_HUMAN	PMO-GN0018-040900-002-E03 GN0018 Homo sapiens cDNA
4926	14117		12.26	3.0E-80	BE817465.1	EST_HUMAN	QV4-BN0263-040600-241-g10 BN0263 Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5579	14803	24178	2	3.0E-80	A1091676.1	EST_HUMAN	cc23a12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:1667054 3' similar to TR:O35790 O35790 PIG-L.;
1767	10877	20169	6.28	2.0E-80	R35321.1	EST_HUMAN	y65a08.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:38080 5'
1828	11036	20232	1.53	2.0E-80	A1444821.1	EST_HUMAN	RET487 subtracted retina cDNA library Homo sapiens cDNA clone RET487
2022	11223	20431	5.67	2.0E-80	AL043118.2	EST_HUMAN	DKFZp434D1323_r1_434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434D1323 5'
6818	18012	25478	2.2	2.0E-80	AW864270.1	EST_HUMAN	EST376343 MAGe resequences, MAGH Homo sapiens cDNA
7448	16854	26145	6.59	2.0E-80	AA393362.1	EST_HUMAN	z170f12.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:727727 5' similar to TR:G191315
345	8613		2.45	1.0E-80	AL163303.2	NT	G191315 ANDROGEN-DEPENDENT EXPRESSED PROTEIN. ;
809	10048	19189	1.37	1.0E-80	AF231920.1	NT	Homo sapiens chromosome 21 segment HS21C103
1624	11128		2.64	1.0E-80	AI732658.1	EST_HUMAN	Homo sapiens chromosome 21 unknown mRNA
4458	13654	22748	1.38	1.0E-80	AF077188.1	NT	nn01f12.x5 NCI_CGAP_Cc8 Homo sapiens cDNA clone IMAGE:1076495 3' similar to contains OFR.11 OFR repetitive element;
4835	14024	23118	0.6	1.0E-80	N96520.1	EST_HUMAN	Homo sapiens cullin 4A (CUL4A) mRNA, complete cds
5350	14590		3.73	1.0E-80	BE386915.1	EST_HUMAN	z339g07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:284972 5' similar to contains Alu repetitive element
5841	14865	24248	5.71	1.0E-80	L10347.1	NT	601274305F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3815433 5'
6323	15504	24950	2.87	1.0E-80	A1848731.1	EST_HUMAN	Human pro-alpha1 type II collagen (COL2A1) gene exons 1-54, complete cds
6323	16604	24951	2.87	1.0E-80	A1848731.1	EST_HUMAN	wq25c05.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2472286 3'
7245	18465	25955	2.04	1.0E-80	11841278	NT	wq25c06.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2472286 3'
7245	18465	25958	2.04	1.0E-80	11841278	NT	Homo sapiens similar to rat myomegalin (LOC84182), mRNA
8724	17678	23950	2.02	1.0E-80	11417801	NT	Homo sapiens similar to rat myomegalin (LOC84182), mRNA
7276	16495	25888	3.34	8.0E-81	A1251782.1	EST_HUMAN	Homo sapiens meningoangioma (disrupted in balanced translocation) 1 (MN1), mRNA
7276	16495	25887	3.34	8.0E-81	A1251752.1	EST_HUMAN	qh80g05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1854286 3'
7713	16812	28420	6.93	8.0E-81	BE394525.1	EST_HUMAN	qh80g05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1854286 3'
2173	11370	20691	1.83	7.0E-81	AA011080.1	EST_HUMAN	601310531F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3832070 5'
6189	16388	24808	2.88	7.0E-81	A1822115.1	EST_HUMAN	z621d10.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:359635 5' similar to SW-KRHA_RABIT Q02957 KERATIN, GLYCINE/TYROSINE-RICH OF HAIR. [1], contains element MER22 repetitive element;
4381	13582	22683	5.13	6.0E-81	BE256829.1	EST_HUMAN	z891c08.x5 Soares_fetal_lung_NbHL18W Homo sapiens cDNA clone IMAGE:286818 3'
4381	13582	22684	5.13	6.0E-81	BE256829.1	EST_HUMAN	601111970F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352840 5'
5316	14548	23617	1.74	6.0E-81	4501848	NT	601111970F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352840 5'
5316	14548	23618	1.74	6.0E-81	4501848	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
8867	17767	23637	1.88	6.0E-81	BF676022.1	EST_HUMAN	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8867	17767	23838	1.88	6.0E-81	BF679022.1	EST_HUMAN	802153666F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4284601 5'
2183	11380	20804	4.15	5.0E-81	BE268042.1	EST_HUMAN	801126505F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3345480 5'
8113	17247	26787	2.62	5.0E-81	8506834	NT	Homo sapiens hypothetical protein (FLJ11045), mRNA
225	8504	18634	0.69	4.0E-81	AF252257.1	NT	Homo sapiens CRP2 binding protein mRNA, partial cds
709	8951	19080	0.68	4.0E-81	AI521435.1	EST_HUMAN	th80612.x1 NCI_CGAP_OV23 Homo sapiens cDNA clone IMAGE:2122702 3' similar to TR:Q85560 Q85560
3135	12370	21501	4.19	4.0E-81	AB037768.1	NT	Homo sapiens mRNA for KIAA1345 protein, partial cds
4142	13348	22447	2.53	4.0E-81	AF263306.1	NT	Homo sapiens rab3 interacting protein variant 2 mRNA, partial cds
4142	13348	22448	2.53	4.0E-81	AF263306.1	NT	Homo sapiens rab3 interacting protein variant 2 mRNA, partial cds
6554	15750	25211	2.38	4.0E-81	X06888.1	NT	Human mRNA for amyloid A4(751) protein
6838	15833	25294	3.01	4.0E-81	U20197.1	NT	Human cone photoreceptor cGMP-phosphodiesterase alpha' subunit gene, exons 2 and 3
6838	15833	25295	3.01	4.0E-81	U20197.1	NT	Human cone photoreceptor cGMP-phosphodiesterase alpha' subunit gene, exons 2 and 3
6839	16029	23494	3.59	4.0E-81	AB018001.1	NT	Homo sapiens mRNA for Death-associated protein kinase 2, complete cds
7740	16038	26444	3.01	4.0E-81	4759085	NT	Homo sapiens vesicle trafficking protein sec22b (SEC22B) mRNA
7740	16038	26445	3.01	4.0E-81	4759085	NT	Homo sapiens vesicle trafficking protein sec22b (SEC22B) mRNA
8331	18239	23709	4.54	4.0E-81	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
8331	18239	23707	4.54	4.0E-81	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
9055	17887	23897	4.02	4.0E-81	11417874	NT	Homo sapiens transcobalamin II; macrocytic anemia (TCN2), mRNA
1274	10489	19848	12.21	3.0E-81	Y18000.1	NT	Homo sapiens NF2 gene
1274	10489	19847	12.21	3.0E-81	Y18000.1	NT	Homo sapiens NF2 gene
2339	11632	20755	11.44	3.0E-81	AF077188.1	NT	Homo sapiens cullin 4A (CUL4A) mRNA, complete cds
2948	12186	21318	6.63	3.0E-81	4508280	NT	Homo sapiens pleiotrophin (heparin binding growth factor 8, neurite growth-promoting factor 1) (PTN) mRNA
2948	12186	21319	6.63	3.0E-81	4508280	NT	Homo sapiens pleiotrophin (heparin binding growth factor 8, neurite growth-promoting factor 1) (PTN) mRNA
2788	12026	21152	2.43	2.0E-81	BE784636.1	EST_HUMAN	601474072F1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:3877121 5'
2788	12026	21153	2.43	2.0E-81	BE784636.1	EST_HUMAN	601474072F1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:3877121 5'
3755	12874	22090	0.83	2.0E-81	AW611542.1	EST_HUMAN	hg85c01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2852384 3'
4682	13874	22874	1.91	2.0E-81	5453871	NT	Homo sapiens platelet-derived growth factor receptor-like (PDGFR) mRNA
8207	12974	22090	2.87	2.0E-81	AW611542.1	EST_HUMAN	hg85c01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2852384 3'
3632	12853	21972	1.31	1.0E-81	AW980658.1	EST_HUMAN	EST372729 MAGe resequences, MAGF Homo sapiens cDNA
4516	13712	22805	2.89	1.0E-81	AA040370.1	EST_HUMAN	z445f09.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:485825 5' similar to PIR:S52437 S52437 CDP-diacylglycerol synthase - fruit fly;
4648	13840	22830	7.9	1.0E-81	BE047686.1	EST_HUMAN	tz45c04.y1 NCI_CGAP_Brm52 Homo sapiens cDNA clone IMAGE:2281528 5'

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression, Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5164	14343	23432	3.88	1.0E-81	9986844	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
5263	14482	26925	3.55	1.0E-81	U87928.1	NT	Human acetylcholinesterase (AC02) gene, exon 3
5367	14597	23874	3.93	1.0E-81	11432868	NT	Homo sapiens polymerase (DNA directed), gamma (POLG), mRNA
5397	14597	23875	3.93	1.0E-81	11432866	NT	Homo sapiens polymerase (DNA directed), gamma (POLG), mRNA
5511	14738	24098	3.39	1.0E-81	U52351.1	NT	Homo sapiens arm-repeat protein NPRAP/neurotrophin (CTNND2) mRNA, partial cds
5511	14738	24100	3.39	1.0E-81	U52351.1	NT	Homo sapiens arm-repeat protein NPRAP/neurotrophin (CTNND2) mRNA, partial cds
6403	15584	25041	7.33	1.0E-81	11432866	NT	Homo sapiens polymerase (DNA directed), gamma (POLG), mRNA
7008	16186	25658	2.87	1.0E-81	BE958278.1	EST_HUMAN	601645051F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3830228 5'
7008	16186	25660	2.87	1.0E-81	BE958278.1	EST_HUMAN	601645051F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3830228 5'
7081	16238	25711	6.11	1.0E-81	BE564387.1	EST_HUMAN	601343180F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685483 5'
7114	16281	25772	2.9	1.0E-81	AA830784.1	EST_HUMAN	act14d08.s1 Stratagene HeLa cell s3 837218 Homo sapiens cDNA clone IMAGE:856427 3' similar to SW:YB386_YEAST P38128 HYPOTHETICAL 60.5 KD PROTEIN IN RPS101-RPS13 INTERGENIC REGION. ;
7514	16719	26209	2.12	1.0E-81	8923698	NT	Homo sapiens golgin-like protein (GLP), mRNA
7555	16855	26354	2.19	1.0E-81	AW844988.1	EST_HUMAN	MRO-CT0008-250599-019 CT0008 Homo sapiens cDNA
7555	16855	26355	2.19	1.0E-81	AW844988.1	EST_HUMAN	MRO-CT0008-250599-019 CT0008 Homo sapiens cDNA
7821	12853	21972	3.15	1.0E-81	AW860858.1	EST_HUMAN	EST372729 MAGE resequences, MAGF Homo sapiens cDNA
8054	17180	26730	2.23	1.0E-81	BF204263.1	EST_HUMAN	601867714F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4110459 5'
8550	17573	23984	3.86	1.0E-81	11418138	NT	Homo sapiens phorbol (similar to apolipoprotein B mRNA editing protein) (DJ742C19.2), mRNA
12	9308	18410	4.82	8.0E-82	AF161408.1	NT	Homo sapiens HSPC288 mRNA, partial cds
108	9308	18410	3.84	8.0E-82	AF161408.1	NT	Homo sapiens HSPC288 mRNA, partial cds
268	9543	18673	1.81	8.0E-82	U08988.1	NT	Human CRFB4 gene, partial cds
824	10682	18214	2.49	8.0E-82	U08988.1	NT	Human CRFB4 gene, partial cds
887	10132	19284	0.74	8.0E-82	U08988.1	NT	Human CRFB4 gene, partial cds
1482	10685	19870	1.58	8.0E-82	AB037748.1	NT	Homo sapiens mRNA for KIAA1327 protein, partial cds
1633	10847	20026	1.59	8.0E-82	6715601	NT	Homo sapiens glutathione peroxidase 5 (epididymal androgen-related protein) (GPX5), transcript variant 2, mRNA
4228	13432	22528	0.78	8.0E-82	8829432	NT	Homo sapiens hypothetical protein FLJ20461 (FLJ20461), mRNA
1451	10884		1.81	7.0E-82	BF035327.1	EST_HUMAN	601458531F1 NIH_MGC_98 Homo sapiens cDNA clone IMAGE:3882088 5'
2722	11801	21117	1.57	7.0E-82	AU144050.1	EST_HUMAN	AU144050 HEMBA1 Homo sapiens cDNA clone HEMBA1000762 3'
4105	13312	22410	0.71	5.0E-82	AA515512.1	EST_HUMAN	m89e11.s1 NCL_CGAP_C03 Homo sapiens cDNA clone IMAGE:925198 3'
1846	10860	20041	59.94	4.0E-82	AF031484.1	NT	Homo sapiens alpha-tubulin isoform 1 mRNA, complete cds
8207	17338	26878	5.01	4.0E-82	AI637300.1	EST_HUMAN	wp75e09.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2467824 3' similar to TR:O75276 O75276 PKD1 ;

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8807	17728		6.52	4.0E-82	AF028701.2	NT	Homo sapiens presenilin-1 gene, exons 1 and 2
282	9557	18680	20.38	3.0E-82	4502168	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
710	9952	19091	2.58	3.0E-82	BE005705.1	EST_HUMAN	RC2-BN0120-010400-013-02 BN0120 Homo sapiens cDNA
787	10038	18187	4.71	3.0E-82	5174702	NT	Homo sapiens transforming growth factor beta-activated kinase-binding protein 1 (TAB1), mRNA
880	10118	19278	4.98	3.0E-82	4502168	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
1068	10284		38.43	3.0E-82	AA725848.1	EST_HUMAN	ai23605.s1 Soares_testis_NHT Homo sapiens cDNA clone 1343848 3'
1363	10578	19745	0.98	3.0E-82	AW875073.1	EST_HUMAN	RC9-PT0001-190100-021-802 PT0001 Homo sapiens cDNA
1462	10675	19848	2.85	3.0E-82	AL183285.2	NT	Homo sapiens chromosome 21 segment HS21C085
1865	11072	20283	1.69	3.0E-82	BE813232.1	EST_HUMAN	RC1-BN0005-260700-018-g04 BN0005 Homo sapiens cDNA
3239	12473		2.30	3.0E-82	5453811	NT	Homo sapiens neurotrophic tyrosine kinase, receptor, type 2 (NTRK2) mRNA
6508	15704	25170	2.69	3.0E-82	11425208	NT	Homo sapiens ankyrin-like with transmembrane domains 1 (ANKTM1), mRNA
804	9651	18989	1.37	2.0E-82	AB023216.1	NT	Homo sapiens mRNA for KIAA0999 protein, partial cds
804	9851	18970	1.37	2.0E-82	AB023216.1	NT	Homo sapiens mRNA for KIAA0999 protein, partial cds
1681	10874	20058	1.4	2.0E-82	AL046390.1	EST_HUMAN	DKFZp434M117_r1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434M117 5'
2935	12173	21307	0.79	2.0E-82	AL183201.2	NT	Homo sapiens chromosome 21 segment HS21C001
3831	13048	22158	1.43	2.0E-82	D87875.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
3989	13212	22318	0.87	2.0E-82	U78833.1	NT	Human integral membrane serine protease Sepsinase mRNA, complete cds
4218	13421	22518	0.99	2.0E-82	4504118	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
4555	13750	22849	1.56	2.0E-82	AB028019.1	NT	Homo sapiens mRNA for KIAA1098 protein, partial cds
4555	13750	22850	1.56	2.0E-82	AB028019.1	NT	Homo sapiens mRNA for KIAA1098 protein, partial cds
4886	14074	23172	2.13	2.0E-82	AF045555.1	NT	Homo sapiens wbscr1 (WBSCR1) and wbscr5 (WBSCR5) genes, complete cds, alternatively spliced and replication factor C subunit 2 (RFC2) gene, complete cds
5110	14280	23378	1.23	2.0E-82	4507580	NT	Homo sapiens tumor necrosis factor receptor superfamily, member 5 (TNFRSF5) mRNA
5110	14290	23377	1.23	2.0E-82	4507580	NT	Homo sapiens tumor necrosis factor receptor superfamily, member 5 (TNFRSF5) mRNA
5427	14864	23781	2.59	2.0E-82	AB018270.1	NT	Homo sapiens mRNA for KIAA0727 protein, partial cds
5741	14960	24360	5.35	2.0E-82	AF234882.1	NT	Homo sapiens FMAA1 splice variant a (FMAA1) mRNA, complete cds
7824	17016	26531	1.74	2.0E-82	11417105	NT	Homo sapiens 3-hydroxy-3-methylglutaryl-Coenzyme A reductase (HMGCR), mRNA
7858	17046	26584	5.19	2.0E-82	U80738.1	NT	Homo sapiens CAGF9 mRNA, partial cds
7858	17046	26585	5.19	2.0E-82	U80738.1	NT	Homo sapiens CAGF9 mRNA, partial cds
8361	17452		2.21	2.0E-82	N94950.1	EST_HUMAN	zb31d10.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:305203 3'
8927	17810		3.89	2.0E-82	AA011278.1	EST_HUMAN	z101g09.r1 Soares_fetal_liver_spleen_1NFLS S1 Homo sapiens cDNA clone IMAGE:426588 5'
9241	18012		1.86	2.0E-82	11418097	NT	Homo sapiens SRY (sex determining region Y)-box 10 (SOX10), mRNA

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
589	9848	18984	1.53	1.0E-82	11648621	NT	Homo sapiens melanoma differentiation associated protein-5 (MDA5), mRNA
1216	10434		1.61	1.0E-82	BE885106.1	EST_HUMAN	601510859F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912207 5'
1282	10507	19686	1.54	1.0E-82	BE084386.1	EST_HUMAN	RC4-BT0310-110300-015-f10 BT0310 Homo sapiens cDNA
1283	10508	19687	1.26	1.0E-82	AB011110.2	NT	Homo sapiens mRNA for KIAA0538 protein, partial cds
7331	16547	26037	2.65	1.0E-82	AL183208.2	NT	Homo sapiens chromosome 21 segment HS21C009
7578	16783	26276	1.95	1.0E-82	AL183246.2	NT	Homo sapiens chromosome 21 segment HS21C046
6885	15880	25339	4.85	9.0E-83	BF672220.1	EST_HUMAN	602150403F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4291581 5'
1418	10631	19799	8.92	8.0E-83	BE363973.1	EST_HUMAN	601273348F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3814382 5'
1658	11947	20052	10.45	8.0E-83	N68951.1	EST_HUMAN	za48f12.s1 Soares fetal liver spleen 1NPLS Homo sapiens cDNA clone IMAGE:288823 3'
1365	10580	19746	1.95	7.0E-83	AW385528.1	EST_HUMAN	QV4-LT0018-271289-068-h11 LT0018 Homo sapiens cDNA
2817	12056		1.49	7.0E-83	AA594655.1	EST_HUMAN	nc12h01.s1 NCI_CQAP_Phe1 Homo sapiens cDNA clone IMAGE:1100497 3' similar to contains Alu repetitive element
4830	14019		7.39	7.0E-83	BF221813.1	EST_HUMAN	7p37a07.x1 NCI_CQAP_Py28 Homo sapiens cDNA clone IMAGE:3847893 3' similar to TR:Q9Y318 Q9Y318
409	9682	18801	1.41	6.0E-83	M33320.1	NT	DJ207H1.1 ; Human platelet Glycoprotein Iib (GPIIb) gene, exons 2-29
1767	10686	20163	2.7	6.0E-83	AW573088.1	EST_HUMAN	ht31h03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2833528 3' similar to
2882	12219	21354	0.72	6.0E-83	AW816405.1	EST_HUMAN	SW:YBEB_HAEIN_P44471 HYPOTHETICAL PROTEIN H0034. ;
3016	12262		1.47	6.0E-83	AF231919.1	NT	QV4-ST0234-181189-037-f05 ST0234 Homo sapiens cDNA
3537	12780	21891	0.91	6.0E-83	11430241	NT	Homo sapiens chromosome 21 unknown mRNA
5323	14555	23625	1.89	6.0E-83	4507866	NT	Homo sapiens VAMP (vesicle-associated membrane protein)-associated protein A (33kD) (VAPA) mRNA, and translated products
8291	15472	24913	1.99	6.0E-83	11422024	NT	Homo sapiens met proto-oncogene (hepatocyte growth factor receptor) (MET), mRNA
6884	16162	25633	3.82	6.0E-83	4505314	NT	Homo sapiens myomesin (M-protein) 2 (185kD) (MYOM2), mRNA
7007	16185	25657	3.15	6.0E-83	11430847	NT	Homo sapiens pre-mRNA splicing factor similar to S. cerevisiae Prp18 (PRP18), mRNA
7007	16185	25658	3.15	6.0E-83	11430847	NT	Homo sapiens pre-mRNA splicing factor similar to S. cerevisiae Prp18 (PRP18), mRNA
8082	17187		6.3	6.0E-83	AA486105.1	EST_HUMAN	ab14e10.s1 Stratagene lung (#837210) Homo sapiens cDNA clone IMAGE:840810 3' similar to contains THR12 THR repetitive element ;
8311	17416		4.28	6.0E-83	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
954	10187		2.23	5.0E-83	U17883.1	NT	Human succinate dehydrogenase iron-protein subunit (sdhB) gene, exon 5
2017	11850		19.94	5.0E-83	AF008305.1	NT	Homo sapiens 26S proteasome regulatory subunit (SUG2) mRNA, complete cds
3817	12838	21957	1.19	5.0E-83	AL133207.2	NT	Novel human gene mapping to chromosome X
3884	13100	22217	0.67	5.0E-83	4895180	NT	Homo sapiens deoxyribonuclease I (DNASE1), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4425	13825	22720	0.69	5.0E-83	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
5109	14289	23374	12.48	5.0E-83	4557013	NT	Homo sapiens catalase (CAT) mRNA
5109	14289	23375	12.48	5.0E-83	4557013	NT	Homo sapiens catalase (CAT) mRNA
5177	14355	23442	1.07	5.0E-83	AB037832.1	NT	Homo sapiens mRNA for KIAA1411 protein, partial cds
846	8892	19017	3.73	4.0E-83	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
1005	10238		4.72	3.0E-83	AA368311.1	EST_HUMAN	EST78542 Placenta I Homo sapiens cDNA similar to similar to endogenous retrovirus ERV9
2732	11911		1.22	3.0E-83	AA632654.1	EST_HUMAN	np87c07.s1 NCI CGAP_Thy1 Homo sapiens cDNA clone IMAGE:1133282 similar to contains THR12 THR repetitive element;
1789	10979	20188	1.36	2.0E-83	AA693492.1	EST_HUMAN	cd84g05.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1621592 3' similar to TR:Q92614
1789	10979	20189	1.36	2.0E-83	AA693492.1	EST_HUMAN	cd84g05.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1621592 3' similar to TR:Q92614
1893	11100	20291	7.4	2.0E-83	N66951.1	EST_HUMAN	Q92614 MYELOBLAST KIAA0218. ;
2803	12043	21184	1.24	2.0E-83	BE828684.1	EST_HUMAN	za48f12.s1 Soares_fetal_liver spleen INFLS Homo sapiens cDNA clone IMAGE:285823 3'
3236	12470		2.65	2.0E-83	11430834	NT	RC8-ET0046-280600-013-H12 ET0048 Homo sapiens cDNA
3758	12975		0.63	2.0E-83	AL163202.2	NT	Homo sapiens ad (Drosophila)-like 1 (SALL1), mRNA
4329	13530	22824	4.20	2.0E-83	AF202879.1	NT	Homo sapiens chromosome 21 segment HS21C002
4653	13947	22838	5.89	2.0E-83	7706398	NT	Homo sapiens hematopoietic progenitor cell antigen CD34 precursor (CD34) mRNA, partial cds
4653	13947	22839	5.89	2.0E-83	7706398	NT	Homo sapiens ankyrin repeat-containing protein ASB-2 (LOC51676), mRNA
6288	15447	24888	5.44	2.0E-83	AF129533.1	NT	Homo sapiens F-box protein Fbx3 (FBL3B) mRNA, partial cds
6585	16761	26223	3.51	2.0E-83	AF011620.1	NT	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1
6595	16761	26224	3.51	2.0E-83	AF011620.1	NT	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1
7428	16638	26129	4.43	2.0E-83	11438448	NT	Homo sapiens KIAA0985 protein (KIAA0985), mRNA
7500	16707	26183	2.3	2.0E-83	AL134462.1	EST_HUMAN	DKFZp547J135.1 547 (synonym: hfor1) Homo sapiens cDNA clone DKFZp547J135 5'
7500	16707	26184	2.3	2.0E-83	AL134462.1	EST_HUMAN	DKFZp547J135.1 547 (synonym: hfor1) Homo sapiens cDNA clone DKFZp547J135 5'
8988	17838		4.39	2.0E-83	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
1416	10628	19798	2.16	1.0E-83	4504326	NT	Homo sapiens hydroxacyl-Coenzyme A dehydrogenase/3-ketacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit (HADHB) mRNA
1416	10628	19797	2.16	1.0E-83	4504326	NT	Homo sapiens hydroxacyl-Coenzyme A dehydrogenase/3-ketacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit (HADHB) mRNA
1887	11190	20400	1.81	1.0E-83	4503652	NT	Homo sapiens fatty-acid-Coenzyme A ligase, very long-chain 1 (FACVL1) mRNA
2618	11802	21019	1.72	1.0E-83	BE83660.1	EST_HUMAN	601507375F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3908754 5'
3850	13068	22180	5.44	1.0E-83	AF053768.1	NT	Rattus norvegicus brain specific cortactin-binding protein CBP80 mRNA, partial cds

Table 4

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4230	13433	22527	3.15	1.0E-83	Z25822.1	NT	H. sapiens gene for mitochondrial dodecenoyl-CoA delta-isoomerase, exon 3
4908	14088	23189	2.7	1.0E-83	4502168	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
5883	18178	24585	1.87	1.0E-83	AI027614.1	EST_HUMAN	ov98b08.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1845431 3' similar to gb:M64241 QM PROTEIN (HUMAN);
3778	12887	22113	4.49	7.0E-84	BE901209.1	EST_HUMAN	601676023F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958853 5'
1302	10517	19874	3.88	6.0E-84	BE838884.1	EST_HUMAN	RC2-FN0119-200800-011-g05 FN0119 Homo sapiens cDNA
1302	10517	19875	3.88	6.0E-84	BE838884.1	EST_HUMAN	RC2-FN0119-200800-011-g05 FN0119 Homo sapiens cDNA
2382	11555	20777	3.84	6.0E-84	AA776574.1	EST_HUMAN	ee88a03.s1 Strabegene schizo brain S11 Homo sapiens cDNA clone IMAGE:971020 3'
5298	14484		3.16	6.0E-84	AL042863.2	EST_HUMAN	DKFZp434H0322_r1 434 (synonym: hba3) Homo sapiens cDNA clone DKFZp434H0322 5'
5449	14675	23634	1.65	6.0E-84	AA897339.1	EST_HUMAN	ea47g03.s1 Soares NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:1480500 3' similar to gb:M14338 VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN);
6282	15463	24905	3.1	6.0E-84	BE810371.1	EST_HUMAN	PMO-LT0019-100800-004-F02 LT0019 Homo sapiens cDNA
6490	15887	26163	2.42	6.0E-84	BE770189.1	EST_HUMAN	PM4-FT0064-160800-004-e10 FT0054 Homo sapiens cDNA
8007	17202		2.15	6.0E-84	AW36812.1	EST_HUMAN	IL0-BT0168-091169-139-e06 BT0168 Homo sapiens cDNA
721	8883	19102	3.3	5.0E-84	AA382811.1	EST_HUMAN	EST80094 Testis I Homo sapiens cDNA 5' end
2978	12213		2.48	5.0E-84	AF109718.1	NT	Homo sapiens chromosome 3 subtelomeric region
8078	17213	28745	2.34	5.0E-84	11428740	NT	Homo sapiens regulatory factor X, 3 (influences HLA class II expression) (RFX3), mRNA
1415	10828	19795	3.31	4.0E-84	AI885321.1	EST_HUMAN	wa78c04.x1 Soares NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:2302086 3' similar to SW:NRDC_HUMAN O43847 NARDILYSIN PRECURSOR;
4889	14158	23248	1.1	4.0E-84	4505928	NT	Homo sapiens polymerase (DNA-directed), alpha (70kD) (POLA2), mRNA
4870	14157	23249	1.59	4.0E-84	AF063601.2	NT	Homo sapiens myosin light chain kinase isoform 2 (MLCK) mRNA, complete cds
5775	14993	24393	2.02	4.0E-84	AF058850.1	NT	Homo sapiens histone deacetylase 3 (HDAC3) gene, complete cds
6355	15535	24989	14.25	4.0E-84	11421326	NT	Homo sapiens KIAA0783 gene product (KIAA0783), mRNA
7482	16889	28184	5.84	4.0E-84	AB032858.1	NT	Homo sapiens mRNA for KIAA1130 protein, partial cds
321	9592	18723	1.64	3.0E-84	AF026200.1	NT	Homo sapiens Bach1 protein homolog mRNA, partial cds
1930	11134	20328	1.3	3.0E-84	5453855	NT	Homo sapiens pericentriolar material 1 (PCM1) mRNA
1975	11178	20386	2.89	3.0E-84	AL068880.1	NT	Novel human mRNA containing Zinc finger C2H2 type domains
3568	12791	21917	1.11	3.0E-84	AB028898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
3730	12849	22087	5.34	3.0E-84	AF014459.1	NT	Homo sapiens X-linked juvenile retinoschisis precursor protein (XLRSP) mRNA, complete cds
7455	16883		11.6	3.0E-84	AI983801.1	EST_HUMAN	wu20d05.x1 Soares Ducrenae_colon_NHCD Homo sapiens cDNA clone IMAGE:2520585 3' similar to gb:L05093 60S RIBOSOMAL PROTEIN L18A (HUMAN);
2075	11275	20491	7.28	2.0E-84	BE695397.1	EST_HUMAN	GM1-BT0785-190800-272-b08 BT0785 Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2075	11275	20492	7.28	2.0E-84	BE685397.1	EST_HUMAN	CM1-BT0785-180800-272-508 BT0785 Homo sapiens cDNA
2894	12132	21268	10.41	2.0E-84	AF036943.1	NT	Homo sapiens myelin transcription factor 1-like (MYT1-L) mRNA, complete cds
2818	12154	21289	1.58	2.0E-84	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
8583	17586	24003	3.31	2.0E-84	BF448000.1	EST_HUMAN	nae30a02.x1 Lupski_sympathetic_trunk Homo sapiens cDNA clone IMAGE:4090251 3' similar to TR:Q8UGS3 Q8UGS3 DJ756023.1;
8583	17585	24004	3.31	2.0E-84	BF448000.1	EST_HUMAN	nae30a02.x1 Lupski_sympathetic_trunk Homo sapiens cDNA clone IMAGE:4090251 3' similar to TR:Q8UGS3 Q8UGS3 DJ756023.1;
317	8588	18719	1.58	1.0E-84	AF114488.1	NT	Homo sapiens Intersectin short isoform (ITSN) mRNA, complete cds
558	8808	18831	12.88	1.0E-84	4507952	NT	Homo sapiens tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide (YWHAZ) mRNA
727	8889		1.24	1.0E-84	11427631	NT	Homo sapiens complement component 5 (C5), mRNA
1300	10516	18672	2.6	1.0E-84	AA884378.1	EST_HUMAN	am85b11.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1628885 3'
2021	11222	20430	2.87	1.0E-84	BE392137.1	EST_HUMAN	601308006F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3826257 5'
2190	11387	20609	2.2	1.0E-84	11427197	NT	Homo sapiens pericentriolar material 1 (PCM1), mRNA
3732	12652	22069	3.02	1.0E-84	AA720851.1	EST_HUMAN	rw12606.s1 NCI_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1239108 3'
4410	13610	22707	5.57	1.0E-84	AJ228041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
4710	13901	23000	3.61	1.0E-84	AL043314.2	EST_HUMAN	DKFZp434N0323_r1_434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434N0323 5'
4710	13901	23001	3.61	1.0E-84	AL043314.2	EST_HUMAN	DKFZp434N0323_r1_434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434N0323 5'
4833	13610	22707	3.37	1.0E-84	AJ228041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
6124	15308	24741	2.67	1.0E-84	AL048784.1	NT	Novel human gene mapping to chromosome 13
6334	15500	24945	2.39	1.0E-84	11430846	NT	Homo sapiens NGFI-A binding protein 1 (ERG1 binding protein 1) (NAB1), mRNA
6831	16124		4.77	1.0E-84	5031984	NT	Homo sapiens nuclear transport factor 2 (placental protein 15) (PP15) mRNA
7013	14492	23581	2.88	1.0E-84	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
7013	14492	23582	2.88	1.0E-84	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
8453	17511		2.18	1.0E-84	11417812	NT	Homo sapiens putative receptor P2X-like 1, orphan receptor (P2RXL1), mRNA
8573	17560	23669	4.24	1.0E-84	11418185	NT	Homo sapiens aconitase 2, mitochondrial (ACO2), mRNA
974	10208		1.55	9.0E-85	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
1080	10305	19455	2.89	9.0E-85	U51432.1	NT	Homo sapiens nuclear protein Skip mRNA, complete cds
1080	10305	19456	2.89	9.0E-85	U51432.1	NT	Homo sapiens nuclear protein Skip mRNA, complete cds
1557	10771	19843	8.88	9.0E-85	M33282.1	NT	Human plasminogen gene, exon 7
1557	10771	19844	8.88	9.0E-85	M33282.1	NT	Human plasminogen gene, exon 7
1649	10883	20045	2.34	9.0E-85	7857020	NT	Homo sapiens DKFZp434P211 protein (DKFZp434P211), mRNA
3783	13003	22118	1.05	9.0E-85	7018418	NT	Homo sapiens nuclear GTPase (HUMAUNTIG), mRNA
4238	13441	22533	1.04	9.0E-85	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4794	13983	23087	1.89	9.0E-85	M33784.1	NT	Human ornithine decarboxylase gene, complete cds
4794	13983	23088	1.89	9.0E-85	M33784.1	NT	Human ornithine decarboxylase gene, complete cds
4897	14085	23178	1.12	9.0E-85	5901879	NT	Homo sapiens heat shock transcription factor 2 binding protein (HSF2BP), mRNA
4834	14121	23216	1.2	9.0E-85	AL163288.2	NT	Homo sapiens chromosome 21 segment HS21C088
1144	10367	19518	10.12	7.0E-85	LO5094.1	NT	Homo sapiens ribosomal protein L27 mRNA, complete cds
8156	17288		11.61	7.0E-85	AF113210.1	NT	Homo sapiens MSTP030 mRNA, complete cds
7854	17083	26823	3.24	8.0E-85	11438573	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 10 (RNA helicase) (DDX10), mRNA
7854	17083	26824	3.24	8.0E-85	11438573	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 10 (RNA helicase) (DDX10), mRNA
2301	11496	20716	6.3	5.0E-85	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
5419	14847	23780	2.28	5.0E-85	BF035674.1	EST_HUMAN	601458846F1 NIH_MGC 88 Homo sapiens cDNA clone IMAGE:3882402 5'
5419	14847	23781	2.28	5.0E-85	BF035674.1	EST_HUMAN	601458846F1 NIH_MGC 88 Homo sapiens cDNA clone IMAGE:3882402 5'
7679	16878	26384	2.18	5.0E-85	AF224689.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
8205	14497		3.22	5.0E-85	AF211189.1	NT	Homo sapiens T-type calcium channel alpha1 subunit Alpha1-e isoform (CACNA1I) mRNA, complete cds
7220	16387		2.61	4.0E-85	BE079283.1	EST_HUMAN	RC1-BT0823-120200-011-c07 BT0823 Homo sapiens cDNA
1308	10522	18681	0.77	3.0E-85	AF086157.1	NT	Homo sapiens protein phosphatase 2A BR gamma subunit gene, exon 6
1760	10882	20144	35.52	3.0E-85	T97495.1	EST_HUMAN	yes3g09.r1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:121504 5'
4305	13506	22602	1.15	3.0E-85	BE267189.1	EST_HUMAN	601189704F2 NIH_MGC 7 Homo sapiens cDNA clone IMAGE:3633618 5'
4820	14108	23203	1.43	3.0E-85	11024695	NT	Homo sapiens F-box only protein 24 (FBXO24), mRNA
4820	14108	23204	1.43	3.0E-85	11024695	NT	Homo sapiens F-box only protein 24 (FBXO24), mRNA
4887	14174	23284	1.03	3.0E-85	7363442	NT	Homo sapiens olfactory receptor, family 12, subfamily D, member 2 (OR12D2), mRNA
5727	14945	24341	5.2	3.0E-85	7862308	NT	Homo sapiens KIAA0783 gene product (KIAA0783), mRNA
5727	14945	24342	5.2	3.0E-85	7862308	NT	Homo sapiens KIAA0783 gene product (KIAA0783), mRNA
6085	15255		7.81	3.0E-85	AJ404488.1	NT	Homo sapiens mRNA for dynein heavy chain (DNAH9 gene)
6768	15953	25411	5.03	3.0E-85	11430889	NT	Homo sapiens phospholipase C, epsilon (PLCE), mRNA
8039	17175	26715	2.38	3.0E-85	5031860	NT	Homo sapiens EGF-like repeats and discoidin-like domains 3 (EDIL3), mRNA
8094	17910		3.91	3.0E-85	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
970	10202	19358	0.64	2.0E-85	7657266	NT	Homo sapiens KIAA0929 protein Mox2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
1047	10273	19426	2.37	2.0E-85	AF248540.1	NT	Homo sapiens intersectin 2 (SH3D1B) mRNA, complete cds
1408	10821	19785	1.02	2.0E-85	7708205	NT	Homo sapiens CGI-201 protein (LOC51340), mRNA

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1424	10637	19808	10.87	2.0E-85	5174775	NT	Homo sapiens apolipoprotein C-II (APOC2) mRNA
1424	10637	19807	10.87	2.0E-85	5174775	NT	Homo sapiens apolipoprotein C-II (APOC2) mRNA
2197	11394	20618	1.78	2.0E-85	U10525.1	NT	Human DNA polymerase beta gene, exons 12 and 13
2775	10560		7.76	2.0E-85	7857468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
2987	12224	21357	2.02	2.0E-85	M30838.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
4326	13527	22621	6.55	2.0E-85	4505880	NT	Homo sapiens plasminogen (PLG) mRNA
4932	14120	23215	1.04	2.0E-85	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
6845	18034	25498	2.59	2.0E-85	A1760820.1	EST_HUMAN	w187h08.x1 NCI_CGAP_Kd12 Homo sapiens cDNA clone IMAGE:2388431 3' similar to contains element
2251	11448		2.28	1.0E-85	BE784308.1	EST_HUMAN	MSR1 repetitive element
2357	11550	20771	8.25	1.0E-85	BE618392.1	EST_HUMAN	601591418F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3945818 5'
2357	11550	20772	8.25	1.0E-85	BE618392.1	EST_HUMAN	601462817F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866021 5'
7009	16187	25681	3.36	1.0E-85	BE257917.1	EST_HUMAN	601108738F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350553 5'
7488	18705	26180	2.91	1.0E-85	AA778785.1	EST_HUMAN	245f03.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:463245 3'
7488	18705	26181	2.91	1.0E-85	AA778785.1	EST_HUMAN	245f03.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:463245 3'
7688	18773	26285	2.74	1.0E-85	BF311552.1	EST_HUMAN	601887003F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4128440 5'
7688	18773	26286	2.74	1.0E-85	BF311552.1	EST_HUMAN	601887003F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4128440 5'
7631	18832	26329	2.84	1.0E-85	Y00052.1	NT	Human mRNA for T-cell cyclophilin
8458	17679	23951	3.47	1.0E-85	11417882	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
8730	17679	23951	4.77	1.0E-85	11417882	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
1432	10645		36.13	9.0E-86	BE274217.1	EST_HUMAN	601120778F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2887680 5'
6722	14940	24338	2.69	8.0E-86	11424140	NT	Homo sapiens similar to CDC28 protein kinase 1 (H. sapiens) (LOC63041), mRNA
945	10178	19332	1.29	7.0E-86	AA860801.1	EST_HUMAN	aj88f08.s1 Soares_parathyroid_tumor_NHHPA Homo sapiens cDNA clone IMAGE:1403559 3'
945	10178	19333	1.29	7.0E-86	AA860801.1	EST_HUMAN	aj88f08.s1 Soares_parathyroid_tumor_NHHPA Homo sapiens cDNA clone IMAGE:1403559 3'
6076	14522	23565	6.39	7.0E-86	11421737	NT	Homo sapiens Tax1 (human T-cell leukemia virus type I) binding protein 1 (TAX1BP1), mRNA
6888	16883	26364	3.63	7.0E-86	L38557.1	NT	Homo sapiens gene, exon 15
7633	18738	26228	2.69	7.0E-86	11417012	NT	Homo sapiens galactose oxidase (GALC) gene, exon 15
7633	18738	26228	2.69	7.0E-86	11417012	NT	Homo sapiens similar to transcription factor CA150 (H. sapiens) (LOC63170), mRNA
1301	10516	19673	3.14	8.0E-86	4505492	NT	Homo sapiens acylglutamate dehydrogenase (liponamide) (OGDH) mRNA
216	9495	19829	1.96	4.0E-86	BE547173.1	EST_HUMAN	601072594F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3458830 5'
5675	14895	24287	11.54	4.0E-86	BE295843.1	EST_HUMAN	601176955F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531953 5'
7783	9495	19829	1.88	4.0E-86	BE547173.1	EST_HUMAN	601072594F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3458830 5'
4276	13479	22577	1.08	3.0E-86	BE867703.1	EST_HUMAN	601443262F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847455 5'
5487	14713	24070	7.08	3.0E-86	AW340848.1	EST_HUMAN	x292h12.x1 NCI_CGAP_Luz24 Homo sapiens cDNA clone IMAGE:2871719 3'

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Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7141	16318	26800	2.86	3.0E-86	BE886478.1	EST_HUMAN	601508986F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3911303 5'
7141	16318	25801	2.86	3.0E-86	BE886479.1	EST_HUMAN	601508986F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3911303 5'
7073	16408	25893	10.4	3.0E-86	AI859240.1	EST_HUMAN	U18502.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2251371 3'
8427	18171		2.01	3.0E-86	BE410354.1	EST_HUMAN	601302333F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3636753 5'
271	9548	18675	2.25	2.0E-86	AA308284.1	EST_HUMAN	EST177232 Jurkat T-cells V1 Homo sapiens cDNA 5' end
420	9873		2.72	2.0E-86	AL183203.2	NT	Homo sapiens chromosome 21 segment HS21C003
1188	10418	16571	2.57	2.0E-86	N58977.1	EST_HUMAN	yz18a08.r1 Soares_multiple_sclerosis_2NBHMSF Homo sapiens cDNA clone IMAGE:283478 5'
2158	11356	20574	18.73	2.0E-86	8635487	NT	Human endogenous retrovirus, complete genome
3363	12620	21751	1.49	2.0E-86	AW968142.1	EST_HUMAN	EST178216 MAGe sequences, MAGI Homo sapiens cDNA
3727	12846	22063	3.14	2.0E-86	AF159776.1	NT	Homo sapiens lysophosphatidic acid acyltransferase-delta (LPAAT-delta) mRNA, complete cds
3727	12848	22084	3.14	2.0E-86	AF159776.1	NT	Homo sapiens lysophosphatidic acid acyltransferase-delta (LPAAT-delta) mRNA, complete cds
4017	13228		2.63	2.0E-86	AW515742.1	EST_HUMAN	Ud87g08.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2916542 3'
4789	13688	23095	4.21	2.0E-86	AF058490.1	NT	Homo sapiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds
5093	14273	23356	0.94	2.0E-86	4505778	NT	Homo sapiens phosphatase kinase, alpha 1 (muscle) (PHKA1), mRNA
							Homo sapiens butyrobetaine (gamma), 2-oxoglutarate dioxygenase (gamma-butyrobetaine hydroxylase) (BBOX), mRNA
6846	15841	25301	3.57	2.0E-86	11437135	NT	Homo sapiens butyrobetaine (gamma), 2-oxoglutarate dioxygenase (gamma-butyrobetaine hydroxylase) (BBOX), mRNA
6846	15841	25302	3.57	2.0E-86	11437135	NT	Homo sapiens butyrobetaine (gamma), 2-oxoglutarate dioxygenase (gamma-butyrobetaine hydroxylase) (BBOX), mRNA
7196	16373	25854	3.67	2.0E-86	11545848	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NPAS3), mRNA
7196	16373	25855	3.67	2.0E-86	11545848	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NPAS3), mRNA
7479	16687	26169	1.82	2.0E-86	4759051	NT	Homo sapiens ribosomal protein S6 kinase, 80kD, polypeptide 5 (RPS8KA5) mRNA
8000	17793	23924	4.33	2.0E-86	11418189	NT	Homo sapiens thyroid autoantigen 70kD (Ku antigen) (G22P1), mRNA
9077	17802		2.64	2.0E-86	AB011398.1	NT	Homo sapiens gene for AF-4, complete cds
							Homo sapiens NADH dehydrogenase (ubiquinone) Fe-S protein 1 (75kD) (NADH-coenzyme Q reductase) (NDUFS1) mRNA
1577	10790	19898	2.82	1.0E-86	4828855	NT	Homo sapiens fibulin 5 (FBLN5) mRNA
3128	12381	21490	1.41	1.0E-86	5453849	NT	Human gamma-glutamyl transpeptidase mRNA, complete cds
3201	12436	21671	2.53	1.0E-86	L20492.1	NT	Homo sapiens chromosome 21 segment HS21C009
3265	12498	21628	1.13	1.0E-86	AL183208.2	NT	Homo sapiens chromosome 21 segment HS21C009
3265	12498	21628	1.13	1.0E-86	AL183209.2	NT	Homo sapiens chromosome 21 segment HS21C009
3921	13137	22255	0.97	1.0E-86	7706161	NT	Homo sapiens hypothetical protein (LOC51318), mRNA
3921	13137	22256	0.97	1.0E-86	7706161	NT	Homo sapiens hypothetical protein (LOC51318), mRNA
4251	13454	22546	8.26	1.0E-86	AL183300.2	NT	Homo sapiens chromosome 21 segment HS21C100
4623	13817	22907	0.62	1.0E-86	4507334	NT	Homo sapiens synaptotagmin 1 (SYNJ1), mRNA
4637	14124	23219	1.42	1.0E-86	AF100751.1	NT	Homo sapiens FK506-binding protein FKBP23 isoform mRNA, complete cds

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Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5468	14694	24047	3.61	1.0E-88	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
8132	14694	24047	2.91	1.0E-88	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
5370	14800		1.74	9.0E-87	AI150703.1	EST_HUMAN	qb577c08.x1 Scores fetal Heart_NbHH19W Homo sapiens cDNA clone IMAGE:1706128 3' similar to SW:K1CJ_MOUSE P02535 KERATIN, TYPE I CYTOSKELETAL 10;
6272	15452	24891	2.05	9.0E-87	4757721	NT	Homo sapiens a disintegrin and metalloprotease domain 22 (ADAM22), mRNA
6272	15452	24892	2.05	9.0E-87	4757721	NT	Homo sapiens a disintegrin and metalloprotease domain 22 (ADAM22), mRNA
485	9738	18371	78.74	8.0E-87	X62245.1	NT	O.cuniculus mRNA for elongation factor 1 alpha
2258	11453	20971	2.01	7.0E-87	BF063211.1	EST_HUMAN	7h85f02.x1 NCI_CGAP_Co18 Homo sapiens cDNA clone IMAGE:3322779 3'
2258	11453	20972	2.01	7.0E-87	BF063211.1	EST_HUMAN	7h85f02.x1 NCI_CGAP_Co18 Homo sapiens cDNA clone IMAGE:3322779 3'
7088	16273	25750	3.8	7.0E-87	AL043314.2	EST_HUMAN	DKFZp434N0323_1 434 (synonym: hba3) Homo sapiens cDNA clone DKFZp434N0323 5'
7088	16273	25751	3.8	7.0E-87	AL043314.2	EST_HUMAN	DKFZp434N0323_1 434 (synonym: hba3) Homo sapiens cDNA clone DKFZp434N0323 5'
7468	16874	26156	11.33	7.0E-87	K03002.1	NT	Human mRNA from chromosome 15 gene with homology to MHC-HLA-SB-1 Intron A
7468	16874	26157	11.33	7.0E-87	K03002.1	NT	Human mRNA from chromosome 15 gene with homology to MHC-HLA-SB-1 Intron A
3500	12724	21880	0.67	6.0E-87	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
7312	16530		8.07	6.0E-87	11432444	NT	Homo sapiens similar to SET translocation (myeloid leukemia-associated) (H. sapiens) (LOC63102), mRNA
1168	10388	19539	6.71	5.0E-87	AA392811.1	EST_HUMAN	EST198094 Testis 1 Homo sapiens cDNA 5' end
8732	10388	19539	2.59	5.0E-87	AA392811.1	EST_HUMAN	EST198094 Testis 1 Homo sapiens cDNA 5' end
973	10205	19360	1.04	4.0E-87	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1180	10401	19554	18.34	4.0E-87	AB037835.1	NT	Homo sapiens mRNA for KIAA1414 protein, partial cds
1999	11202	20413	2.08	4.0E-87	AB007825.1	NT	Homo sapiens mRNA for KIAA0458 protein, partial cds
2049	11250	20461	0.99	4.0E-87	R78133.1	EST_HUMAN	y80f10.r1 Scores placenta Nb2HP Homo sapiens cDNA clone IMAGE:145579 5' similar to contains Alu repetitive element;
2049	11250	20461	0.99	4.0E-87	R78133.1	EST_HUMAN	y80f10.r1 Scores placenta Nb2HP Homo sapiens cDNA clone IMAGE:145579 5' similar to contains Alu repetitive element;
2388	11579	20765	1.67	4.0E-87	7708298	NT	Homo sapiens CGI-60 protein (LOC51626), mRNA
2388	11579	20766	1.67	4.0E-87	7708298	NT	Homo sapiens CGI-60 protein (LOC51626), mRNA
3441	12688	21800	1.43	4.0E-87	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (t(11q23;q24) myeloid/lymphoid); translocated to, 4 (MLL T4) mRNA
5418	14844	23776	6.4	4.0E-87	O00321	SWISSPROT	ETS-RELATED PROTEIN 71 (ETS TRANSLOCATION VARIANT 2)
5685	14905	24288	4.8	4.0E-87	BE247284.1	EST_HUMAN	TCBAP1E4051 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4051
7724	16923	26432	3.91	4.0E-87	M60878.1	NT	Human von Willebrand factor pseudogene corresponding to exons 23 through 34
8258	17385	26918	3.1	4.0E-87	11417339	NT	Homo sapiens similar to heat shock 70kD protein 98 (mortalin-2) (H. sapiens) (LOC63184), mRNA

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Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8831	18223	23695	1.48	4.0E-87	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
8831	18223	23696	1.48	4.0E-87	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
8894	17855		21.93	4.0E-87	11417812	NT	Homo sapiens purinergic receptor P2X-like 1, orphan receptor (P2RXL1), mRNA
2731	11910	21124	5.33	2.0E-87	4885420	NT	Homo sapiens high-mobility group (nucleosome chromosomal) protein 4 (HMG4) mRNA
2800	12138		1.12	2.0E-87	BF327820.1	EST_HUMAN	QV0-BN0148-050600-254-e03 BN0148 Homo sapiens cDNA
3787	12985	22101	0.7	2.0E-87	AU116935.1	EST_HUMAN	AU116935 HEMBA1 Homo sapiens cDNA clone HEMBA1000307 5'
5517	14742	24108	10.95	2.0E-87	BE734180.1	EST_HUMAN	601569041F1 NIH_MGC 21 Homo sapiens cDNA clone IMAGE:3843730 5'
5517	14742	24109	10.95	2.0E-87	BE734180.1	EST_HUMAN	601569041F1 NIH_MGC 21 Homo sapiens cDNA clone IMAGE:3843730 5'
5800	15017		5.29	2.0E-87	BE567183.1	EST_HUMAN	601341383F1 NIH_MGC 53 Homo sapiens cDNA clone IMAGE:3883348 5'
6276	18466	24897	30.73	2.0E-87	N48128.1	EST_HUMAN	y21e07.1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:243398 5'
6370	15550	25006	34.08	2.0E-87	N48128.1	EST_HUMAN	y21e07.1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:243398 5'
6598	15794	23252	14.69	2.0E-87	X52851.1	NT	Human cyclophilin gene for cyclophilin (EC 5.2.1.8)
1190	11945		2.22	1.0E-87	7705983	NT	Homo sapiens putative glycosyl transfer protein (LOC51054), mRNA
1434	10847	19819	2.01	1.0E-87	AW361977.1	EST_HUMAN	PM2-CT0265-141089-001-g04 CT0265 Homo sapiens cDNA
1434	10847	19820	2.01	1.0E-87	AW361977.1	EST_HUMAN	PM2-CT0265-141089-001-g04 CT0265 Homo sapiens cDNA
3690	12911	22030	18.53	1.0E-87	Y00052.1	NT	Human mRNA for T-cell cyclophilin
3714	12834	22052	2.67	1.0E-87	4758827	NT	Homo sapiens neurodin III (NRPX3) mRNA
5762	14981	24378	2	1.0E-87	AF073371.1	NT	Homo sapiens growth factor receptor-bound protein 10 (GRB10) gene, exon 8
5762	14981	24380	2	1.0E-87	AF073371.1	NT	Homo sapiens growth factor receptor-bound protein 10 (GRB10) gene, exon 8
6499	15698	25160	12.4	1.0E-87	AF214562.1	NT	Homo sapiens tracheal epithelium enriched protein (PLUNC) gene, complete cds
6874	18152	25623	2.81	1.0E-87	BE818183.1	EST_HUMAN	RC8-BN0276-050700-012-E02 BN0276 Homo sapiens cDNA
6874	18152	25624	2.81	1.0E-87	BE818183.1	EST_HUMAN	RC8-BN0276-050700-012-E02 BN0276 Homo sapiens cDNA
7570	16775		1.88	1.0E-87	D10083.1	NT	Homo sapiens RGH1 gene, retrovirus-like element
7608	16811	28308	1.88	1.0E-87	5031660	NT	Homo sapiens EGF-like repeats and discordin Like domains 3 (EDIL3), mRNA
7608	16811	28307	1.88	1.0E-87	5031660	NT	Homo sapiens EGF-like repeats and discordin Like domains 3 (EDIL3), mRNA
8827	18371		1.67	1.0E-87	7867632	NT	Homo sapiens sulfotransferase-related protein (SULTX3), mRNA
1114	10338	19468	7.21	9.0E-88	AF167465.1	NT	Homo sapiens double stranded RNA activated protein kinase (PKR) gene, exon 12
1357	10572	19737	2.4	9.0E-88	AB037820.1	NT	Homo sapiens mRNA for KIAA1399 protein, partial cds
1357	10572	19738	2.4	9.0E-88	AB037820.1	NT	Homo sapiens mRNA for KIAA1399 protein, partial cds
2091	11291	20503	2.43	9.0E-88	7861701	NT	Homo sapiens DKFZP586P1522 protein (DKFZP586P1522), mRNA
3806	12827	21947	1.22	9.0E-88	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
4255	13458	22550	3.4	9.0E-88	X91929.1	NT	H.sapiens ECE-1 gene (exon 9)
4255	13458	22551	3.4	9.0E-88	X91929.1	NT	H.sapiens ECE-1 gene (exon 9)

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5028	14213	23297	1.01	9.0E-88	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
1788	11005		3.42	5.0E-88	7681887	NT	Homo sapiens KIAA0063 gene product (KIAA0063), mRNA
2603	11787	21008	6.14	5.0E-88	N89399.1	EST_HUMAN	K9719F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone K9719 5' similar to ZINC FINGER PROTEIN HZF1
2858	12186	21330	0.78	5.0E-88	AF114488.1	NT	Homo sapiens Intersectin short isoform (ITSN) mRNA, complete cds
2872	12208	21346	1.02	5.0E-88	AF114488.1	NT	Homo sapiens Intersectin short isoform (ITSN) mRNA, complete cds
2872	12208	21347	1.02	5.0E-88	AF114488.1	NT	Homo sapiens Intersectin short isoform (ITSN) mRNA, complete cds
3387	12695		2.78	5.0E-88	AI693217.1	EST_HUMAN	wd88h08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2338788 3' similar to contains Alu repetitive element; contains element MER22 MER22 repetitive element
3509	12733	21871	0.68	5.0E-88	AF114488.1	NT	Homo sapiens Intersectin short isoform (ITSN) mRNA, complete cds
4748	13839	23043	0.74	5.0E-88	AF114488.1	NT	Homo sapiens Intersectin short isoform (ITSN) mRNA, complete cds
5887	15269	24696	2.41	5.0E-88	H10832.1	EST_HUMAN	ym06b10.r1 Scores Infant brain 1N1B Homo sapiens cDNA clone IMAGE:47128 5'
8572	11005		1.59	5.0E-88	7681887	NT	Homo sapiens KIAA0063 gene product (KIAA0063), mRNA
8214	11005		1.4	5.0E-88	7681887	NT	Homo sapiens KIAA0063 gene product (KIAA0063), mRNA
1337	10552	19717	1.15	4.0E-88	BF091229.1	EST_HUMAN	PM1-TN0028-050900-004-f10 TN0028 Homo sapiens cDNA
1337	10552	19718	1.16	4.0E-88	BF091228.1	EST_HUMAN	PM1-TN0028-050900-004-f10 TN0028 Homo sapiens cDNA
8181	15363	24803	1.71	4.0E-88	11416585	NT	Homo sapiens transforming growth factor, beta-induced, 68kD (TGFB1), mRNA
7484	16891	26174	1.8	4.0E-88	4502684	NT	Homo sapiens cell division cycle 10 (homologous to CDC10 of S. cerevisiae) (CDC10) mRNA
8023	17160	26696	2.62	4.0E-88	7681947	NT	Homo sapiens KIAA0152 gene product (KIAA0152), mRNA
8023	17160	26697	2.52	4.0E-88	7681947	NT	Homo sapiens KIAA0152 gene product (KIAA0152), mRNA
739	8980	19121	0.91	3.0E-88	11545800	NT	Homo sapiens hypothetical protein FLJ21634 (FLJ21634), mRNA
1781	10991		2.73	3.0E-88	4508020	NT	Homo sapiens zinc finger protein 259 (ZNF259) mRNA
2898	12137	21275	6.07	3.0E-88	N60851.1	EST_HUMAN	za48f12.s1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:285823 3'
4226	13428	22520	0.91	3.0E-88	4501912	NT	Homo sapiens a disintegrin and metalloproteinase domain 23 (ADAM23) mRNA
4226	13429	22521	0.91	3.0E-88	4501912	NT	Homo sapiens a disintegrin and metalloproteinase domain 23 (ADAM23) mRNA
4474	13872		4.18	3.0E-88	11428300	NT	Homo sapiens hypothetical protein FLJ20220 (FLJ20220), mRNA
5328	14560	23032	2.81	3.0E-88	11428367	NT	Homo sapiens velsin-containing protein (VCP), mRNA
5483	14709	24085	3.48	3.0E-88	8968888	NT	Homo sapiens polycythemia rubra vera 1; cell surface receptor (PRV1), mRNA
5538	14782	24129	3.92	3.0E-88	11420697	NT	Homo sapiens vral simian leukemia viral oncogene homolog A (ras related) (RALA), mRNA
6111	15205	24624	14.23	3.0E-88	AF278285.1	NT	Homo sapiens putative anion transporter 1 mRNA, complete cds
6308	15489	24934	6.98	3.0E-88	11438400	NT	Homo sapiens retinoblastoma-binding protein 2 (RBBP2), mRNA
8432	15929	25094	15.11	3.0E-88	11421728	NT	Homo sapiens growth differentiation factor 5 (cartilage-derived morphogenetic protein-1) (GDF5), mRNA

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8558	17580		3.87	3.0E-88	11417974	NT	Homo sapiens transcobalamin II; macrocytic anemia (TCN2), mRNA
1043	10269	18419	1.37	2.0E-88	7305198	NT	Homo sapiens Caldesin, presenilin-binding protein, EF hand transcription factor (CSEN), mRNA
1601	10815	18991	1.56	2.0E-88	AF246219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
1722	10834	20117	5.7	2.0E-88	AF246219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
4417	13817	22713	2.08	2.0E-88	5031688	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
5621	14844	24223	5.34	1.0E-88	AW139568.1	EST_HUMAN	Homo sapiens dyx11c1, axonemal, light polypeptide 4 (DNAL4), mRNA
5621	14844	24224	5.34	1.0E-88	AW139568.1	EST_HUMAN	UI-H-B11-ess-d-04-Q-UJ.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2718750 3'
5953	15169	24582	23.77	1.0E-88	AB007877.1	NT	UI-H-B11-ess-d-04-Q-UJ.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2718750 3'
5953	15169	24583	23.77	1.0E-88	AB007877.1	NT	Homo sapiens KIAA0417 mRNA, complete cds
8158	15341	24778	4.02	1.0E-88	AA488981.1	EST_HUMAN	Homo sapiens KIAA0417 mRNA, complete cds
6850	16128	25596	2.94	1.0E-88	AL043314.2	EST_HUMAN	aa54a11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:824732 3' similar to WP:B0272.2 CE00851;
7981	16416	25903	3.87	1.0E-88	AA891479.1	EST_HUMAN	DKFZp434N0323_r1 434 (synonym: hbs3) Homo sapiens cDNA clone DKFZp434N0323 5'
8760	17717		5.85	1.0E-88	AL163246.2	NT	os91g03.s1 NCI_CGAP_GC3 Homo sapiens cDNA clone IMAGE:1612758 3' similar to gb:M16342 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEINS C1/C2 (HUMAN);
7525	16730	26220	8.72	9.0E-89	11421238	NT	Homo sapiens chromosome 21 segment HS21C046
2692	11872	21087	0.96	8.0E-89	BE311557.1	EST_HUMAN	Homo sapiens transglutinin 2 (TAGLN2), mRNA
439	9683	18831	1.05	7.0E-89	7657213	NT	601142409F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3506186 5'
439	9683	18832	1.05	7.0E-89	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
4904	14082	23185	2.94	7.0E-89	4557390	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
4951	14138	23232	6.21	7.0E-89	AL045748.1	EST_HUMAN	Homo sapiens complement component 8, beta polypeptide (C8B), mRNA
7791	16985	26500	2.88	7.0E-89	M59783.1	NT	DKFZp434E248_r1 434 (synonym: hbs3) Homo sapiens cDNA clone DKFZp434E248 5'
9240	18011		1.78	7.0E-89	U87927.1	NT	Human aldose reductase (AR) gene, segment 2
1030	10256	19407	1.83	6.0E-89	5803114	NT	Human ascorbate hydratase (ACO2) gene, exon 2
2180	11377	20569	4.97	6.0E-89	4506124	NT	Homo sapiens inner membrane protein, mitochondrial (mitofilin) (IMMT), mRNA
2397	11590	20807	7.83	6.0E-89	4507798	NT	Homo sapiens serine/threonine-protein kinase PRP4 homolog (PRP4), mRNA
2397	11590	20808	7.83	6.0E-89	4507798	NT	Homo sapiens ubiquitin-conjugating enzyme E2L3 (UBE2L3), mRNA
3468	12722	21958	0.65	6.0E-89	7681817	NT	Homo sapiens ubiquitin-conjugating enzyme E2L3 (UBE2L3), mRNA
4478	13676	22765	1.37	6.0E-89	7681737	NT	Homo sapiens HSPC159 protein (HSPC159), mRNA
4639	13833	22921	3.22	6.0E-89	AB007868.2	NT	Homo sapiens HSPC019 protein (HSPC019), mRNA
4639	13833	22922	3.22	6.0E-89	AB007868.2	NT	Homo sapiens mRNA for KIAA0406 protein, partial cds
5214	14388	23474	1.53	6.0E-89	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
5214	14388	23475	1.53	6.0E-89	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5105	14285	23369	2.93	5.0E-89	BE244323.1	EST_HUMAN	TCBAP2E0383 Pediatric pre-B cell acute lymphoblastic leukemia Bay/for-HGSC project=TCBA Homo sapiens cDNA clone TCBAP0383
5105	14285	23370	2.93	5.0E-89	BE244323.1	EST_HUMAN	TCBAP2E0383 Pediatric pre-B cell acute lymphoblastic leukemia Bay/for-HGSC project=TCBA Homo sapiens cDNA clone TCBAP0383
7700	16886	28408	1.84	4.0E-89	AI788672.1	EST_HUMAN	w601c03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2348452 3'
2830	12068	21191	2.07	3.0E-89	AW976181.1	EST_HUMAN	EST388280 MAGI resequences, MAGN Homo sapiens cDNA
8885	17848	23886	2.42	3.0E-89	AV705749.1	EST_HUMAN	AV705749 ADB Homo sapiens cDNA clone AD88GA01 5'
125	9687	18807	1.11	2.0E-89	7706670	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
125	9687	18808	1.11	2.0E-89	7706670	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
414	9687	18807	0.69	2.0E-89	7706670	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
414	9687	18808	0.69	2.0E-89	7706670	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
638	9787	18910	0.78	2.0E-89	AB037763.1	NT	Homo sapiens mRNA for KIAA1342 protein, partial cds
2834	12073	21195	1.58	2.0E-89	AI222065.1	EST_HUMAN	qg8c08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843022 3' similar to gb:J04131
3527	12761	21883	0.94	2.0E-89	AA759149.1	EST_HUMAN	GAMMA-GLUTAMYL TRANSPEPTIDASE 1 PRECURSOR (HUMAN); contains Alu repetitive element
3527	12761	21884	0.64	2.0E-89	AA759149.1	EST_HUMAN	ah70e03.s1 Soares_testis_NHT Homo sapiens cDNA clone 1320888 3'
4127	13333	22431	1.28	2.0E-89	AF088897.1	NT	ah70e03.s1 Soares_testis_NHT Homo sapiens cDNA clone 1320888 3'
4135	13341	22441	5.58	2.0E-89	X59742.1	NT	Homo sapiens topoisomerase-related function protein (TRF4-2) mRNA, partial cds
4135	13341	22442	5.58	2.0E-89	X59742.1	NT	H.sapiens HCK gene for tyrosine kinase (PTK), exons 10-11
4342	13544	22635	1.7	2.0E-89	AL163203.2	NT	H.sapiens HCK gene for tyrosine kinase (PTK), exons 10-11
4500	13688	22792	1.09	2.0E-89	AJ007378.1	NT	Homo sapiens chromosome 21 segment HS21C003
5040	14224	23308	0.95	2.0E-89	11545821	NT	Homo sapiens GGT gene, exon 5
5381	14591		56	2.0E-89	BE541744.1	EST_HUMAN	Homo sapiens melanoma differentiation associated protein-5 (MDA5), mRNA
6432	14659	23768	2.85	2.0E-89	AB007548.1	NT	601085998F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3452423 5'
6364	15544	24899	4.77	2.0E-89	U81004.1	NT	Homo sapiens gene for LECT2, complete cds
6436	15633	25098	2.36	2.0E-89	11428801	NT	Human GT24 (GT24) mRNA, partial cds
7913	17128	26658	3.35	2.0E-89	11434411	NT	Homo sapiens solute carrier family 24 (sodium/potassium/calcium exchanger), member 2 (SLC24A2), mRNA
8104	17238	26776	5.65	2.0E-89	11433673	NT	Homo sapiens Integrin, alpha 3 (antigen CD49C, alpha 3 subunit of VLA-3 receptor) (ITGA3), mRNA
8208	17339	26878	2.84	2.0E-89	U10692.1	NT	Homo sapiens cell adhesion molecule with homology to L1CAM (close homologue of L1) (CHL1), mRNA
8259	17386		2.22	2.0E-89	11417260	NT	Human Mage-7 antigen (MAGE7) pseudogene, complete cds
							Homo sapiens threonyl-RNA synthetase (TARS), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8107	17241	28780	6.99	1.0E-89	BF188052.1	EST_HUMAN	hr81d09.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3134897 3' similar to TR:O54778 O54778 SOLUTE CARRIER FAMILY 22 - LIKE 2 PROTEIN ;
8107	17241	28781	6.99	1.0E-89	BF188052.1	EST_HUMAN	hr81d09.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3134897 3' similar to TR:O54778 O54778 SOLUTE CARRIER FAMILY 22 - LIKE 2 PROTEIN ;
1070	10296	19445	2.31	8.0E-00	AL183248.2	NT	Homo sapiens chromosome 21 segment HS21C048
1071	10296	19445	2.97	8.0E-00	AL183248.2	NT	Homo sapiens chromosome 21 segment HS21C048
1338	11981	19718	3.38	8.0E-00	BE070561.1	EST_HUMAN	7c38f09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284583 3'
1338	11981	19720	3.38	8.0E-00	BE070561.1	EST_HUMAN	7c38f09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284583 3'
848	10083		2.87	7.0E-00	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
3032	12268	21305	1.22	6.0E-00	X91926.1	NT	H. sapiens ECE-1 gene (exon 6)
3032	12268	21306	1.22	6.0E-00	X91926.1	NT	H. sapiens ECE-1 gene (exon 6)
4212	13415	22510	6.66	6.0E-00	8922398	NT	Homo sapiens hypothetical protein FLJ10388 (FLJ10388), mRNA
4212	13415	22511	6.66	6.0E-00	8922398	NT	Homo sapiens hypothetical protein FLJ10388 (FLJ10388), mRNA
5647	14870	24256	3.59	6.0E-00	U77700.1	NT	Homo sapiens HsGCN1 mRNA, partial cds
5647	14870	24257	3.59	6.0E-00	U77700.1	NT	Homo sapiens HsGCN1 mRNA, partial cds
6570	15768	25227	6.84	6.0E-00	4504794	NT	Homo sapiens HsGCN1 mRNA, partial cds
6570	15768	25228	6.84	6.0E-00	4504794	NT	Homo sapiens HsGCN1 mRNA, partial cds
158	9440		24.41	5.0E-00	AB035344.1	NT	Homo sapiens TGL6 gene, exon 1-10b
1200	10420	19573	1.75	5.0E-00	U80226.1	NT	Human gamma-aminobutyric acid transaminase mRNA, partial cds
2521	11709	20925	1.83	5.0E-00	AF114487.1	NT	Homo sapiens Intersectin long isoform (ITSN) mRNA, complete cds
4537	13732	22630	2.47	5.0E-00	4506354	NT	Homo sapiens pregnancy-zone protein (PZP) mRNA
4912	13906	22697	1.1	5.0E-00	AA705222.1	EST_HUMAN	z82g10.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:481442 3'
4912	13906	22698	1.1	5.0E-00	AA705222.1	EST_HUMAN	z82g10.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:481442 3'
5488	14712	24069	3.24	5.0E-00	Z16411.1	NT	H. sapiens mRNA encoding phospholipase c
5558	14712	24069	2.51	5.0E-00	Z16411.1	NT	H. sapiens mRNA encoding phospholipase c
6171	15353	24791	2.22	5.0E-00	AF113708.1	NT	Homo sapiens angiotensin 4 (ANG4) mRNA, partial cds
6171	15353	24792	2.22	5.0E-00	AF113708.1	NT	Homo sapiens angiotensin 4 (ANG4) mRNA, partial cds
6318	15499	24944	7.67	5.0E-00	4557258	NT	Homo sapiens adenylyate cyclase 9 (ADCY9) mRNA
6557	15753	25216	4.78	5.0E-00	11345483	NT	Homo sapiens hypothetical protein FLJ13222 (FLJ13222), mRNA
7195	16372	25853	4.96	5.0E-00	11433721	NT	Homo sapiens ATPase, aminophospholipid transporter-like, Class I, type 8A, member 2 (ATP8A2), mRNA
9048	17921		1.36	5.0E-00	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
9095	17911		1.72	5.0E-00	A1523386.1	EST_HUMAN	ar78h05.x1 Barstead aorta HPLRB8 Homo sapiens cDNA clone IMAGE:2128761 3'

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Table 4
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
307	9580	18712	1.78	4.0E-60	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
307	9580	18713	1.78	4.0E-60	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
1084	10318	18470	2.95	4.0E-60	4505318	NT	Homo sapiens myosin phosphatase, target subunit 1 (MYPT1), mRNA
1084	10877	20062	8.83	4.0E-60	X99033.1	NT	H. sapiens gene encoding discoidin receptor tyrosine kinase, exon 18
2813	12053	21175	1.1	4.0E-60	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
2813	12053	21178	1.1	4.0E-60	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
2888	12225	21358	1.5	4.0E-60	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
2888	12226	21358	1.5	4.0E-60	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
4858	13853	22950	4.47	4.0E-60	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
4808	13888	23104	1.63	4.0E-60	AB033070.1	NT	Homo sapiens mRNA for KIAA1244 protein, partial cds
4833	14022	23116	1.9	4.0E-60	M85687.1	NT	Human prothormone converting enzyme (NEC2) gene, exon 8
6231	14405	23488	1.03	4.0E-60	5728777	NT	Homo sapiens collagen, type XI, alpha 1 (COL12A1), mRNA
8884	12053	21175	1.35	4.0E-60	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
8884	12053	21176	1.35	4.0E-60	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
8148	17280	26825	52.24	3.0E-60	BE563833.1	EST_HUMAN	601335244F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3688147 5'
218	9497	18831	3.74	2.0E-60	BE537913.1	EST_HUMAN	601067378F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453834 5'
1181	10402	18555	8.41	2.0E-60	5031748	NT	Homo sapiens high-mobility group (nonhistone chromosomal) protein 17 (HMG17), mRNA
1181	10402	18556	8.41	2.0E-60	5031748	NT	Homo sapiens high-mobility group (nonhistone chromosomal) protein 17 (HMG17), mRNA
3830	13047	22157	2.29	2.0E-60	AI138213.1	EST_HUMAN	gc54c02.x1 Soares_placenta_869weeks_2NbhP8b69W Homo sapiens cDNA clone IMAGE:1713410 3'
4894	13885	22886	1.12	2.0E-60	AB006627.1	NT	similar to SW:OLF3_MOUSE P23275 OLFACTORY RECEPTOR OR3.;
4831	14119	23214	9.77	2.0E-60	5728855	NT	Homo sapiens mRNA for KIAA0288 gene, partial cds
5558	14791	24163	4.85	2.0E-60	AW872688.1	EST_HUMAN	Homo sapiens GRB2-related adaptor protein (GRAP) mRNA
7012	16180	26683	6.27	2.0E-60	11427320	NT	ba49d05.y3 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2898881 5' similar to TR:075208 O75208 HYPOTHETICAL 35.5 KD PROTEIN.;
7012	16180	26684	6.27	2.0E-60	11427320	NT	Homo sapiens similar to laminin receptor 1 (87KD, ribosomal protein SA) (H. sapiens) (LOC83484), mRNA
8008	18441	25829	3.88	2.0E-60	11024711	NT	Homo sapiens similar to laminin receptor 1 (87KD, ribosomal protein SA) (H. sapiens) (LOC83484), mRNA
281	9558	18889	4.74	1.0E-60	4502166	NT	Homo sapiens myosin, heavy polypeptide 4, skeletal muscle (MYH4), mRNA
379	11839	18779	1.31	1.0E-60	AF231920.1	NT	Homo sapiens amyloid beta (A4) precursor protein (protease resistant-II, Alzheimer disease) (APP), mRNA
380	11838	18778	1.24	1.0E-60	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
702	8944	19079	1.82	1.0E-60	AJ237589.1	NT	Homo sapiens chromosome 21 unknown mRNA

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
702	9944	18080	1.92	1.0E-00	AJ237589.1	NT	Homo sapiens mRNA for T-box transcription factor (TBX20 gene), partial
737	9978	19118	11.4	1.0E-00	AF284750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
737	9978	19119	11.4	1.0E-00	AF284750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1118	10342		1.49	1.0E-00	4507828	NT	Homo sapiens Kruppel-like factor 7 (ubiquitous) (KLF7), mRNA
1313	10529	19890	3.36	1.0E-00	AF098154.1	NT	Homo sapiens protein phosphatase 2A BR gamma subunit gene, exon 3
1313	10529	19891	3.36	1.0E-00	AF098154.1	NT	Homo sapiens protein phosphatase 2A BR gamma subunit gene, exon 3
1643	10857		3.08	1.0E-00	BE3798894.1	EST_HUMAN	601159593F2 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:35111118 5'
1898	11073	20264	2.95	1.0E-00	11420514	NT	Homo sapiens similar to SALL1 (sal (Drosophila)-like (LOC57167), mRNA
2805	12045	21167	6.75	1.0E-00	6005720	NT	Homo sapiens chromosome 8 open reading frame 2 (C8ORF2), mRNA
3835	13052	22163	1.47	1.0E-00	AB020710.1	NT	Homo sapiens mRNA for KIAA0803 protein, partial cds
3835	13052	22164	1.47	1.0E-00	AB020710.1	NT	Homo sapiens mRNA for KIAA0803 protein, partial cds
4415	13615	22711	1.76	1.0E-00	AF167340.1	NT	Homo sapiens soluble interleukin 1 receptor accessory protein (IL1RAP) gene, exon 8, alternative exons 8 and complete cds, alternatively spliced
6282	14435	23509	1.28	1.0E-00	AB037820.1	NT	Homo sapiens mRNA for KIAA1399 protein, partial cds
5282	14435	23510	1.28	1.0E-00	AB037820.1	NT	Homo sapiens mRNA for KIAA1399 protein, partial cds
5523	14748	24115	2.08	1.0E-00	AB014533.1	NT	Homo sapiens mRNA for KIAA0633 protein, partial cds
6385	15545	25000	2.56	1.0E-00	11426758	NT	Homo sapiens solute carrier family 1 (high affinity aspartate/glutamate transporter), member 6 (SLC1A6), mRNA
6725	15920	25378	3.54	1.0E-00	11422088	NT	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 2 (BIG2), mRNA
6859	16049	25314	2.42	1.0E-00	11422108	NT	Homo sapiens CGI-15 protein (LOC51008), mRNA
6859	16049	25315	2.42	1.0E-00	11422109	NT	Homo sapiens CGI-15 protein (LOC51008), mRNA
9036	17880	23894	1.51	1.0E-00	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
9036	17880	23895	1.51	1.0E-00	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
4178	13382	22483	5.53	8.0E-01	D12234.1	EST_HUMAN	HUM000S381 Liver HepG2 cell line. Homo sapiens cDNA clone s381 3'
3451	12876	21811	1.9	5.0E-01	AA702794.1	EST_HUMAN	zib0b04.s1 Soares_fetal_liver spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:448015 3'
4822	14011	23109	1.46	5.0E-01	7110634	NT	Homo sapiens chromosome 22 open reading frame 5 (C22ORF5), mRNA
4822	14011	23110	1.46	5.0E-01	7110634	NT	Homo sapiens chromosome 22 open reading frame 5 (C22ORF5), mRNA
9068	17895		1.23	5.0E-01	A1183586.1	EST_HUMAN	qe70f11.x1 Soares_fetal_lung_NbHL18W Homo sapiens cDNA clone IMAGE:1744365 3' similar to contains MIR.b2 MIR repetitive element:
3166	12401	21535	1.56	4.0E-01	AF158776.1	NT	Homo sapiens isophosphatidic acid acyltransferase-delta (LPAAT-delta) mRNA, complete cds
3166	12401	21536	1.56	4.0E-01	AF158776.1	NT	Homo sapiens isophosphatidic acid acyltransferase-delta (LPAAT-delta) mRNA, complete cds
7504	18711	26169	6.21	4.0E-01	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
8509	17545	23983	2.28	4.0E-01	M77994.1	EST_HUMAN	EST01579 Hippocampus, Striatum (cat. #836205) Homo sapiens cDNA clone HHCMC60 similar to Retrovirus-related gag polyprotein

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8509	17545	24031	2.28	4.0E-01	M77994.1	EST_HUMAN	EST01579 Hippocampus, Striatum (cat. #836205) Homo sapiens cDNA clone HHCMS60 similar to
1585	10809	19885	1.4	3.0E-01	11430193	NT	Retrovirus-related gag polyprotein
1595	10809	19888	1.4	3.0E-01	11430193	NT	Homo sapiens solute carrier family 4, anion exchanger, member 3 (SLC4A3), mRNA
3313	12543	21677	1.41	3.0E-01	AL163283.2	NT	Homo sapiens solute carrier family 4, anion exchanger, member 3 (SLC4A3), mRNA
3439	12684	21797	3.24	3.0E-01	AB033104.1	NT	Homo sapiens chromosome 21 segment HS21C083
3439	12684	21798	3.24	3.0E-01	AB033104.1	NT	Homo sapiens mRNA for KIAA1278 protein, partial cds
3770	12988	22104	0.97	3.0E-01	AF084530.1	NT	Homo sapiens mRNA for KIAA1278 protein, partial cds
4590	13784	22876	5.52	3.0E-01	M30938.1	NT	Homo sapiens cyclin-D binding Myb-like protein mRNA, complete cds
4899	14188	23275	3.31	3.0E-01	AL163285.2	NT	Human Ku (p70/p80) subunit mRNA, complete cds
4969	14188	23276	3.31	3.0E-01	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
5789	15006		3.05	3.0E-01	4502740	NT	Homo sapiens chromosome 21 segment HS21C085
5921	15138	24549	3.58	3.0E-01	11497611	NT	Homo sapiens cyclin-dependent kinase 6 (CDK6) mRNA
5921	15138	24550	3.58	3.0E-01	11497611	NT	Homo sapiens gamma-aminobutyric acid (GABA) B receptor, 1 (GABBR1), transcript variant 2, mRNA
6351	15531	24982	4.48	3.0E-01	U86959.1	NT	Homo sapiens gamma-aminobutyric acid (GABA) B receptor, 1 (GABBR1), transcript variant 2, mRNA
6351	15531	24983	4.48	3.0E-01	U86959.1	NT	Human L-type calcium channel beta-1 subunit (CACNLB1) gene, exons 10 and 11
8768	17704	23955	1.33	3.0E-01	AF240786.1	NT	Human L-type calcium channel beta-1 subunit (CACNLB1) gene, exons 10 and 11
9124	14490	23535	4.48	3.0E-01	AF169555.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
9124	14490	23536	4.48	3.0E-01	AF169555.1	NT	genes, complete cds
50	8347	18460	2.75	1.0E-01	AL163284.2	NT	Homo sapiens beta-ureidopropionase (BUP1) gene, exon 8
1262	10468	19632	9.01	1.0E-01	AW449748.1	EST_HUMAN	Homo sapiens beta-ureidopropionase (BUP1) gene, exon 8
6015	15285	24689	1.89	1.0E-01	BF348182.1	EST_HUMAN	Human sapiens chromosome 21 segment HS21C084
6015	15285	24690	1.89	1.0E-01	BF348182.1	EST_HUMAN	UI-H-B13-ake-d-01-0-J1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2735280 3'
8875	18306		1.69	1.0E-01	H15212.1	EST_HUMAN	602022088F1 NCI_CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4157804 5'
1248	10465	19626	19.2	8.0E-02	AJ001689.1	NT	602022088F1 NCI_CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4157804 5'
1248	10465	19627	19.2	8.0E-02	AJ001689.1	NT	Yn30e03.r1 Scores Infant brain 1NIB Homo sapiens cDNA clone IMAGE:48587 5'
5426	14953	23790	3.81	9.0E-02	U03007.1	NT	Homo sapiens NKX2D gene, exon 10
5463	14718	24078	1.9	8.0E-02	11427148	NT	Homo sapiens NKX2D gene, exon 10
5850	15068	24478	3.85	9.0E-02	AF310105.1	NT	Human Nat K+ ATPase alpha-subunit mRNA, partial cds
6848	16035	25499	2.27	9.0E-02	11422088	NT	Homo sapiens hypothetical protein FLJ20260 (FLJ20260), mRNA
92	8385	18514	3.46	8.0E-02	W26367.1	EST_HUMAN	Homo sapiens NALP1 mRNA, complete cds
							Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 2 (BIG2), mRNA
							2813 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
280	9584	18987	6.09	8.0E-02	BE386363.1	EST_HUMAN	601273513F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3814887 5'
1780	11000	20195	1.06	8.0E-02	11434722	NT	Homo sapiens diacylglycerol kinase, gamma (80KD) (DGKG), mRNA
1780	11000	20198	1.06	8.0E-02	11434722	NT	Homo sapiens diacylglycerol kinase, gamma (80KD) (DGKG), mRNA
4207	13410	22504	0.94	8.0E-02	AA09157.1	EST_HUMAN	om13602.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1540922 3' similar to contains L1.b2 L1 repetitive element;
5132	14310	23401	0.77	8.0E-02	AW157571.1	EST_HUMAN	au83h08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782911 3' similar to
8808	15804	25280	4.9	8.0E-02	L04193.1	NT	TR:O60302 O60302 KIAA0555 PROTEIN, contains element MER22 repetitive element;
8808	15804	25281	4.9	8.0E-02	L04193.1	NT	Human lens membrane protein (mp19) gene, exon 11
8791	15886	25446	3.28	8.0E-02	AB014511.1	NT	Human lens membrane protein (mp19) gene, exon 11
7382	16597	26085	5.33	8.0E-02	AF074393.1	NT	Homo sapiens mRNA for KIAA0811 protein, partial cds
7900	17118	28848	2.27	8.0E-02	4503340	NT	Homo sapiens nuclear mitogen- and stress-activated protein kinase-1 (MSK1) mRNA, complete cds
8859	17762	23835	1.7	8.0E-02	11434704	NT	Homo sapiens dihydrodipicamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex) (DLST) mRNA
26	8022	19425	1.35	7.0E-02	AB031007.1	NT	Homo sapiens fragile X mental retardation, autosomal homolog 1 (FXR1), mRNA
241	11983	19849	0.97	7.0E-02	AB018301.1	NT	Homo sapiens DNA, MHC class I region, 7.1 ancestral haplotype
241	11983	18850	0.97	7.0E-02	AB018301.1	NT	Homo sapiens mRNA for KIAA0758 protein, partial cds
588	9845		1.47	7.0E-02	AF007822.1	NT	Homo sapiens cytoplasmic Sepsase truncated isoform mRNA, complete cds
1287	10502	19663	1.21	7.0E-02	4502384	NT	Homo sapiens B-cell CLL/lymphoma 7b (BCL7B) mRNA
2153	11351	20587	8.03	7.0E-02	5031570	NT	Homo sapiens ARP2 (actin-related protein 2, yeast) homolog (ACTR2), mRNA
2153	11351	20588	8.03	7.0E-02	5031570	NT	Homo sapiens ARP2 (actin-related protein 2, yeast) homolog (ACTR2), mRNA
2530	11718	20935	9.05	7.0E-02	AF167706.1	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds
2884	11888	21078	8.58	7.0E-02	6005738	NT	Homo sapiens NRAS-related gene (D1S155E), mRNA
2709	11888	21105	2.57	7.0E-02	AB031007.1	NT	Homo sapiens DNA, MHC class I region, 7.1 ancestral haplotype
3319	14487	21881	0.74	7.0E-02	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
3319	14487	21882	0.74	7.0E-02	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
4586	13780	22872	1.34	7.0E-02	S71824.1	NT	N-CAM=145 kDa neural cell adhesion molecule [human, small cell lung cancer cell line OS2-R, mRNA, 2860 nt]
4586	13780	22873	1.34	7.0E-02	S71824.1	NT	N-CAM=145 kDa neural cell adhesion molecule [human, small cell lung cancer cell line OS2-R, mRNA, 2880 nt]
5194	14370	23457	0.95	7.0E-02	4508118	NT	Homo sapiens prospero-related homeobox 1 (PROX1) mRNA
5305	14537	23541	5.59	7.0E-02	AA448208.1	EST_HUMAN	zw68d12.r1 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:781175 5'
1587	10780		1.21	5.0E-02	BE380882.1	EST_HUMAN	601283012F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3805018 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2721	11900	21118	2.78	3.0E-92	BE09714.1	EST_HUMAN	601501242F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3902839 5'
5603	14827	24203	5.34	3.0E-92	AA378336.1	EST_HUMAN	EST191020 Synovial sarcoma Homo sapiens cDNA 5' end similar to ribosomal protein S13
7349	18565	26054	4.3	3.0E-92	X15804.1	NT	Human mRNA for alpha-actinin
7349	18565	26055	4.3	3.0E-92	X15804.1	NT	Human mRNA for alpha-actinin
27	9323	18428	1.34	2.0E-92	4501898	NT	Homo sapiens actinin A receptor, type IIB (ACVR2B) mRNA
144	9428	18560	13.1	2.0E-92	AF154830.1	NT	Homo sapiens carbamyl phosphate synthetase I mRNA, complete cds
183	9482	18582	3.22	2.0E-92	11422948	NT	Homo sapiens hypothetical protein dJ482O23.2 (dJ482O23.2), mRNA
183	9482	18583	3.22	2.0E-92	11422948	NT	Homo sapiens hypothetical protein dJ482O23.2 (dJ482O23.2), mRNA
757	9898	19144	3.85	2.0E-92	BE289180.1	EST_HUMAN	601118337F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028304 5'
757	9898	19145	3.85	2.0E-92	BE289180.1	EST_HUMAN	601118337F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028304 5'
1889	10901		1.47	2.0E-92	S78853.1	NT	mitg-mas-related [human, Genomic, 2416 nt]
1805	11111	20305	1.45	2.0E-92	AB181119.1	EST_HUMAN	wk27d07 x1 NCJ_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2413549 3' similar to TR:Q12844
1805	11111	20305	1.45	2.0E-92	AB181119.1	EST_HUMAN	Q12844 BREAKPOINT CLUSTER REGION PROTEIN ;
1905	11111	20306	1.45	2.0E-92	AB181119.1	EST_HUMAN	wk27d07 x1 NCJ_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2413549 3' similar to TR:Q12844
2015	11217	20426	8.59	2.0E-92	4509880	NT	Q12844 BREAKPOINT CLUSTER REGION PROTEIN ;
2021	11805	21022	24.63	2.0E-92	6912457	NT	Homo sapiens syndecan 4 (amphiglycan, ryndocan) (SDC4) mRNA
2782	10844	20022	2.37	2.0E-92	11418424	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
2782	10844	20023	2.37	2.0E-92	11418424	NT	Homo sapiens collagen, type XII, alpha 1 (COL12A1), mRNA
3591	12812	21832	1.29	2.0E-92	AF231919.1	NT	Homo sapiens collagen, type XII, alpha 1 (COL12A1), mRNA
3591	12812	21833	1.29	2.0E-92	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
3696	12897	22008	5.14	2.0E-92	5903180	NT	Homo sapiens chromosome 21 unknown mRNA
4274	13477	22574	1.37	2.0E-92	M10976.1	NT	Homo sapiens stress-induced-phosphoprotein 1 (Hsp70/Hsp90-organizing protein) (STIP1), mRNA
4768	13955	23056	0.84	2.0E-92	AF138523.1	NT	Human endogenous retroviral DNA (4-1), complete proviral segment
5017	14204		3.73	2.0E-92	AL040437.1	EST_HUMAN	Homo sapiens bile salt export pump (BSEP) mRNA, complete cds
5248	14421		0.95	2.0E-92	4759169	NT	DKFZp434C0414_r1 434 (synonym: htss3) Homo sapiens cDNA clone DKFZp434C0414 5'
5941	15157	24568	2.81	2.0E-92	AB028991.1	NT	Homo sapiens steroid regulatory element binding transcription factor 2 (SREBF2) mRNA
7344	16580	26048	7.05	2.0E-92	11434900	NT	Homo sapiens mRNA for KIAA1088 protein, partial cds
7703	16802	28410	1.75	2.0E-92	AW838290.1	EST_HUMAN	Homo sapiens thyroid stimulating hormone receptor (TSHR), mRNA
7703	16802	28411	1.75	2.0E-92	AW838290.1	EST_HUMAN	GM44-L10026-161298-082-g06 L10026 Homo sapiens cDNA
8878	17774	23943	2.73	2.0E-92	AB029016.1	NT	GM44-L10026-161298-082-g08 L10026 Homo sapiens cDNA
8887	17791	23923	1.35	2.0E-92	AF106856.1	NT	Homo sapiens mRNA for KIAA1083 protein, partial cds
9153	11805	21022	29.98	2.0E-92	6912457	NT	Homo sapiens adenylosuccinate lyase gene, complete cds
							Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8269	18312	23600	1.48	2.0E-02	AF106650.1	NT	Homo sapiens adenylsuccinate lyase gene, complete cds
1817	11025	20219	1.38	1.0E-02	R78078.1	EST_HUMAN	y80e08.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:145574 5'
1817	11025	20220	1.38	1.0E-02	R78078.1	EST_HUMAN	y80e08.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:145574 5'
2041	11242	20451	68.35	1.0E-02	4506868	NT	Homo sapiens ribosomal protein, large, P1 (RPLP1) mRNA
1898	11201	20412	3.07	9.0E-03	AU121681.1	EST_HUMAN	AU121681 MAMMA1 Homo sapiens cDNA clone MAMMA1000738 5'
2009	11212		43.7	9.0E-03	AA316723.1	EST_HUMAN	EST188414 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to ribosomal protein L28
2609	11793		1.25	9.0E-03	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CAONA1E) gene, exons 7-49, and partial cds, alternatively spliced
3593	12814	21805	1.08	9.0E-03	BE388571.1	EST_HUMAN	601281887F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3603832 5'
4328	13528	22823	1.11	9.0E-03	AU121681.1	EST_HUMAN	AU121681 MAMMA1 Homo sapiens cDNA clone MAMMA1000738 5'
8167	17289		18.88	9.0E-03	11418526	NT	Homo sapiens ribosomal protein L10a (RPL10A), mRNA
6828	16146	24566	2.48	8.0E-03	BF036384.1	EST_HUMAN	601460521F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3863908 5'
250	9526	18686	7.52	7.0E-03	AF231918.1	NT	Homo sapiens chromosome 21 unknown mRNA
3041	12278	21408	0.85	6.0E-03	11526170	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
1388	10602	19767	1.49	5.0E-03	AB014511.1	NT	Homo sapiens mRNA for KIAA0611 protein, partial cds
1411	10824	19789	11.81	5.0E-03	AI674184.1	EST_HUMAN	wc08e08.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2314670 3'
1411	10824	19790	11.81	5.0E-03	AI674184.1	EST_HUMAN	wc08e08.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2314670 3'
3199	12434	21569	5.83	5.0E-03	X04201.1	NT	Human skeletal muscle 1.3 kb mRNA for tropomyosin
6382	15562	25018	3.42	5.0E-03	AF087136.1	NT	Homo sapiens protein phosphatase-1 regulatory subunit 7 (PPP1R7) gene, exon 11, complete cds and alternatively spliced product
6971	18149	25820	2.22	5.0E-03	AF274883.1	NT	Homo sapiens secretory pathway component Sec31B-1 mRNA, alternatively spliced, complete cds
7402	18615	28105	2.16	5.0E-03	11439588	NT	Homo sapiens nucleobindin 2 (NUCB2), mRNA
8774	18037	23844	2.01	5.0E-03	11417877	NT	Homo sapiens gamma-glutamyltransferase 1 (GGT1), mRNA
87	8390		5.23	4.0E-03	AA458933.1	EST_HUMAN	z60e09.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:785688 3' similar to SW:CLPA_RAT P37397 CALPONIN, ACIDIC ISOFORM;
451	9704	18841	0.84	4.0E-03	4557878	NT	Homo sapiens interferon gamma receptor 1 (IFNGR1) mRNA
451	9704	18842	0.84	4.0E-03	4557878	NT	Homo sapiens interferon gamma receptor 1 (IFNGR1) mRNA
781	10020	19169	3.31	4.0E-03	7657454	NT	Homo sapiens pascadillo (zabrafish) homolog 1, containing BRCT domain (PES1), mRNA
781	10020	19170	3.31	4.0E-03	7657454	NT	Homo sapiens pascadillo (zabrafish) homolog 1, containing BRCT domain (PES1), mRNA
1191	10411	19585	2.02	4.0E-03	8923658	NT	Homo sapiens hypothetical protein FLJ20731 (FLJ20731), mRNA
1948	11150	20352	4.8	4.0E-03	AF047877.1	NT	Homo sapiens dystrophin (DMD) gene, deletion breakpoints 1-3 in intron 5
2209	11408	20630	1.21	4.0E-03	AF157476.1	NT	Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3542	12765	21898	0.82	4.0E-03	7705398	NT	Homo sapiens tumor antigen SLP-8p (HCC8), mRNA
4025	13236	22341	1.62	4.0E-03	4504654	NT	Homo sapiens interleukin 18 receptor 1 (IL18R1), mRNA
5047	12765	21898	0.85	4.0E-03	7705398	NT	Homo sapiens tumor antigen SLP-8p (HCC8), mRNA
5508	14733	24095	4.77	4.0E-03	T48884.1	EST_HUMAN	y694c12.1 Stratagene liver (H937224) Homo sapiens cDNA clone IMAGE:78938 5' similar to similar to SP-A44391 A44391 SERUM RESPONSE ELEMENT-BINDING PROTEIN SRE-ZBP - HUMAN
7693	16892	26401	18.41	4.0E-03	AV692051.1	EST_HUMAN	AV692051 GK6 Homo sapiens cDNA clone GKDRF07 5'
3631	12852	21970	15.84	3.0E-03	BF680630.1	EST_HUMAN	602248554F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4332036 5'
3631	12852	21971	15.84	3.0E-03	BF680630.1	EST_HUMAN	602248554F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4332036 5'
4220	13423		1.43	3.0E-03	AF225898.1	NT	Homo sapiens tensin mRNA, complete cds
5103	14283		1.05	3.0E-03	AF231981.1	NT	Homo sapiens long chain polyunsaturated fatty acid elongation enzyme (HELO1) mRNA, complete cds
7378	16595	28082	5.39	3.0E-03	AI824829.1	EST_HUMAN	wb02a05.x1 NC1 CGAP GC8 Homo sapiens cDNA clone IMAGE:2304489 3'
195	9476	18608	50.31	2.0E-03	AB015610.1	NT	Chlorococcus aethiops mRNA for ribosomal protein S4X, complete cds
195	9475	18607	50.31	2.0E-03	AB015610.1	NT	Chlorococcus aethiops mRNA for ribosomal protein S4X, complete cds
328	8588	18729	9.28	2.0E-03	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
329	8589	18729	8.05	2.0E-03	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
2100	11300	20514	2.1	2.0E-03	U40763.1	NT	Human Cdk-associated RS cyclophilin CAR5-Cyp mRNA, complete cds
2449	11840	20861	3.05	2.0E-03	BE252982.1	EST_HUMAN	801117588F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3358220 5'
5175	14353	23441	0.97	2.0E-03	BE263201.1	EST_HUMAN	801116810F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3357243 5'
5403	14631	23743	4.28	2.0E-03	AW084385.1	EST_HUMAN	EST378458 IMAGE resequences, MAGH Homo sapiens cDNA
8663	17640		1.69	2.0E-03	AA126735.1	EST_HUMAN	d20c10.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:503346 3'
8749	17892		1.73	2.0E-03	L41825.1	NT	Homo sapiens CYP17 gene, 5' and
9025	17875		4.17	2.0E-03	BF035327.1	EST_HUMAN	801458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
103	8396	18525	2.48	1.0E-03	AF238897.1	NT	Homo sapiens CTR1 pseudogene
103	8396	18528	2.48	1.0E-03	AF238897.1	NT	Homo sapiens CTR1 pseudogene
524	9775	18800	11.32	1.0E-03	7857016	NT	Homo sapiens hypothetical protein (DJ328E19.C1.1), mRNA
807	9854	18973	4.39	1.0E-03	AI146755.1	EST_HUMAN	y64408.x1 NC1 CGAP_CLL1 Homo sapiens cDNA clone IMAGE:1672503 3' similar to TR:Q82384 Q82384
882	10118	19280	10.07	1.0E-03	D81675.1	NT	ZINC FINGER PROTEIN. ;
1244	10460	19619	8.18	1.0E-03	8923270	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
1244	10460	19620	8.18	1.0E-03	8923270	NT	Homo sapiens hypothetical protein FLJ20291 (FLJ20291), mRNA
1353	10568	19732	2.25	1.0E-03	AF167708.1	NT	Homo sapiens hypothetical protein FLJ20291 (FLJ20291), mRNA
							Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2308	11500	20721	5.98	1.0E-03	AF231981.1	NT	Homo sapiens long chain polyunsaturated fatty acid elongation enzyme (HELO1) mRNA, complete cds
2428	11617	20839	12.19	1.0E-03	AF055086.1	NT	Homo sapiens MHC class 1 region
2472	11683		2.57	1.0E-03	AL137200.1	NT	Novel human gene mapping to chromosome 1
2774	10518	19678	2.76	1.0E-03	BE287369.1	EST_HUMAN	601177688F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532965 5'
2774	10518	19677	2.75	1.0E-03	BE287369.1	EST_HUMAN	601177688F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532965 5'
2884	12122	21255	3.73	1.0E-03	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
3182	12417		2.24	1.0E-03	AF231981.1	NT	Homo sapiens long chain polyunsaturated fatty acid elongation enzyme (HELO1) mRNA, complete cds
4421	13621	22718	3.49	1.0E-03	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
5474	14701	24055	1.97	1.0E-03	U78509.1	NT	Homo sapiens glucocorticoid receptor (GRL) gene, intron D, exon 5, and intron E
5474	14701	24058	1.97	1.0E-03	U78509.1	NT	Homo sapiens glucocorticoid receptor (GRL) gene, intron D, exon 5, and intron E
5624	14848	24230	10.31	1.0E-03	4557792	NT	Homo sapiens neurofibromin 1 (neurofibromatosis, von Recklinghausen disease, Watson disease) (NF1) mRNA
5894	15277	24707	2.01	1.0E-03	11431560	NT	Homo sapiens protein kinase C, beta 1 (PRKCB1), mRNA
6185	15367	24807	3.71	1.0E-03	D42072.1	NT	Human mRNA for NF1 N-isoform-exon11, complete cds
6547	15743	25204	2.45	1.0E-03	AB037832.1	NT	Homo sapiens mRNA for KIAA1411 protein, partial cds
6894	15800	25088	2.82	1.0E-03	AB040918.1	NT	Homo sapiens mRNA for KIAA1485 protein, partial cds
6954	16132	25000	4.68	1.0E-03	X13474.1	NT	Human PrsA4 gene for Alzheimer's disease A4 amyloid protein precursor (exon 9)
6954	16132	25601	4.68	1.0E-03	X13474.1	NT	Human PrsA4 gene for Alzheimer's disease A4 amyloid protein precursor (exon 9)
8312	18101	23807	2.74	1.0E-03	A286282.1	EST_HUMAN	qim03g12.x1 NCI_CGAP_Lu6 Homo sapiens cDNA clone IMAGE:1880758 3' similar to WP:1984.4 CE13742;
8330	17812		1.26	1.0E-03	AJ230125.1	NT	Homo sapiens GGT1 gene, exon 1
9018	17870		3.25	1.0E-03	11417856	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2), mRNA
9200	18353		1.46	1.0E-03	AF240788.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
9839	13155	22272	2.41	6.0E-04	AF142482.1	NT	Homo sapiens transcription enhancer factor-5 mRNA, complete cds
9143	17949		1.5	6.0E-04	11418351	NT	Homo sapiens mitogen-activated protein kinase 12 (MAPK12), mRNA
5379	14808	23719	4.05	5.0E-04	AB014512.1	NT	Homo sapiens mRNA for KIAA0612 protein, partial cds
5379	14808	23720	4.05	5.0E-04	AB014512.1	NT	Homo sapiens mRNA for KIAA0612 protein, partial cds
5887	14807	24300	4.88	5.0E-04	AA722434.1	EST_HUMAN	z987g06.a1 Soares_fetal_heart_Nb2HF19W Homo sapiens cDNA clone IMAGE:409584 3'
6092	15283	24725	1.76	5.0E-04	AID15800.1	EST_HUMAN	q853d05.a1 Soares_fetal_heart_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1623369 3'
7544	16749	26242	2.23	5.0E-04	11423962	NT	Homo sapiens adenylate kinase 2 (AK2), mRNA
7544	16749	26243	2.23	5.0E-04	11423962	NT	Homo sapiens adenylate kinase 2 (AK2), mRNA

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8638	18358	23608	8.17	6.0E-94	T89398.1	EST_HUMAN	yd88b04.s1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:116239 3'
8227	18005		1.88	5.0E-94	9558724	NT	Homo sapiens cleavage and polyadenylation specific factor 1, 160kD subunit (CPSF1), mRNA
1808	11018		17.14	4.0E-94	L05094.1	NT	Homo sapiens ribosomal protein L27 mRNA, complete cds
2618	11803	21020	1.96	4.0E-94	4506008	NT	Homo sapiens protein phosphatase 1, regulatory subunit 10 (PPP1R10) mRNA
3652	12873	21991	1.02	4.0E-94	AW197851.1	EST_HUMAN	xn88f12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2701679 3'
3652	12873	21992	1.02	4.0E-94	AW197851.1	EST_HUMAN	xn88f12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2701679 3'
4728	13920	23023	4.08	4.0E-94	AI591312.1	EST_HUMAN	hw11f10.x1 NCL_CGAP_Bm52 Homo sapiens cDNA clone IMAGE:2289403 3' similar to TR:Q15265 Q15265 PROTEIN TYROSINE PHOSPHATASE;
5956	15074	24488	1.89	4.0E-94	11440870	NT	Homo sapiens solute carrier family 22 (organic cation transporter), member 1-like (SLC22A1L), mRNA
5858	15074	24487	1.89	4.0E-94	11440870	NT	Homo sapiens solute carrier family 22 (organic cation transporter), member 1-like (SLC22A1L), mRNA
7889	16424	25811	1.88	4.0E-94	11545792	NT	Homo sapiens hypothetical protein FLJ12455 (FLJ12455), mRNA
617	9882	18982	1.1	3.0E-94	AB022785.1	NT	Homo sapiens ASH2L gene, complete cds, similar to Drosophila ash2 gene
728	9970	19108	0.9	3.0E-94	4502508	NT	Homo sapiens complement component 5 (C5) mRNA
1713	10925	20109	2.41	3.0E-94	AF167708.1	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds
1713	10925	20110	2.41	3.0E-94	AF167708.1	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds
1742	10954	20137	3.37	3.0E-94	4557558	NT	Homo sapiens E1A binding protein p300 (EP300) mRNA
4171	13376	22474	0.66	3.0E-94	AA464805.1	EST_HUMAN	zw63g08.r1 Soares_fetus_Nb2Hf8_9w Homo sapiens cDNA clone IMAGE:774782 5'
4308	13509	22604	1.2	3.0E-94	AA781838.1	EST_HUMAN	ai59h08.s1 Soares_testis_NHT Homo sapiens cDNA clone 1375163 3'
5528	14750	24117	3.33	3.0E-94	11498288	NT	Homo sapiens zinc finger protein 277 (ZNF277), mRNA
5849	15066	24478	5.57	3.0E-94	11528228	NT	Homo sapiens chromosome 21 open reading frame 18 (C21ORF18), mRNA
6849	16944	25305	5.17	3.0E-94	AB014579.1	NT	Homo sapiens mRNA for KIAA0879 protein, partial cds
6858	16138	25607	3.97	3.0E-94	AF087842.1	NT	Homo sapiens glycogenin-1L mRNA, complete cds
7685	16984	26368	1.79	3.0E-94	4757821	NT	Homo sapiens axonal transport of synaptic vesicles (ATSV) mRNA
151	9433	18567	1.86	1.0E-94	BE295714.1	EST_HUMAN	601175762F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531038 5'
3054	12280	21415	2.17	1.0E-94	BE253433.1	EST_HUMAN	601111686F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352559 5'
3054	12280	21416	2.17	1.0E-94	BE253433.1	EST_HUMAN	601111686F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352559 5'
4352	13554	22650	1.54	1.0E-94	9506892	NT	Homo sapiens hypothetical protein (FLJ20748), mRNA
7010	16188	25682	2.51	1.0E-94	BE780478.1	EST_HUMAN	601468748F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3872089 5'
7634	16835	26331	3.18	1.0E-94	U65590.1	NT	Homo sapiens IL-1 receptor antagonist IL-1Ra (IL-1RN) gene, alternatively spliced forms, complete cds
7864	17054	26575	2.47	1.0E-94	AI272244.1	EST_HUMAN	ep22c02.x1 Schiller oligodendrogloma Homo sapiens cDNA clone IMAGE:1958122 3' similar to TR:Q62845 Q62845 NEURAL CELL ADHESION PROTEIN BIG-2 PRECURSOR.;

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8763	9433	18567	1.42	1.0E-04	BE295714.1	EST_HUMAN	601175762F1 NH_MGC_17 Homo sapiens cDNA clone IMAGE:3531038 6'
9084	9433	18567	1.69	1.0E-04	BE295714.1	EST_HUMAN	601175762F1 NH_MGC_17 Homo sapiens cDNA clone IMAGE:3531038 5'
1471	10884	19859	8.53	8.0E-05	AF027302.1	NT	Homo sapiens TNF-alpha stimulated ABC protein (ABC50) mRNA, complete cds
3119	12354	21482	1.11	9.0E-05	7682027	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
3119	12354	21483	1.11	8.0E-05	7682027	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
6544	15740	25201	2.66	8.0E-05	AF274753.1	NT	Homo sapiens progressive ankylosis-like protein (ANK) mRNA, complete cds
148	9428	18562	8.86	8.0E-05	AF154830.1	NT	Homo sapiens carbamyl phosphate synthetase I mRNA, complete cds
4533	13728	22825	1.87	8.0E-05	AI700898.1	EST_HUMAN	we08e04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2340606 3' similar to gb:K00558
4533	13728	22828	1.87	8.0E-05	AI700898.1	EST_HUMAN	TUBULIN ALPHA-1 CHAIN (HUMAN);
6180	15362	24801	1.66	8.0E-05	11428528	NT	we08e04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2340608 3' similar to gb:K00558
6180	15362	24802	1.66	8.0E-05	11428528	NT	TUBULIN ALPHA-1 CHAIN (HUMAN);
6528	15724	25189	2.69	8.0E-05	AF032897.1	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 11 (PSMD11), mRNA
6869	16091	25558	2.63	8.0E-05	11420944	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 11 (PSMD11), mRNA
6869	16091	25559	2.63	8.0E-05	11420944	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 11 (PSMD11), mRNA
7024	16201	25679	2.45	8.0E-05	6174844	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 11 (PSMD11), mRNA
7033	16210		3.18	8.0E-05	AB037816.1	NT	Homo sapiens channel subunit (HERG-3) mRNA, complete cds
7302	16321	26012	1.85	8.0E-05	AF112152.1	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
8018	17157	26693	2.51	8.0E-05	10804024	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
8988	17850		15.84	8.0E-05	AA029050.1	EST_HUMAN	Homo sapiens proline dehydrogenase (proline oxidase) (PRODH) mRNA
280	8555	18887	9.86	7.0E-05	D87875.1	NT	Homo sapiens mRNA for KIAA1395 protein, partial cds
280	8555	18888	9.86	7.0E-05	D87875.1	NT	Homo sapiens developmental arteries and neural crest EGF-like protein mRNA, complete cds
4360	13562	22858	7.94	7.0E-05	M89708.1	NT	Homo sapiens HCF-binding transcription factor Zhangfei (ZF), mRNA
4407	13607		1.32	7.0E-05	AL163248.2	NT	z084801.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:744848 3' similar to contains L1.1 L1
7456	16664	26153	1.9	3.0E-05	R83180.1	EST_HUMAN	repetitive element;
1621	10834	20009	3.28	2.0E-05	7682027	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
1621	10834	20010	3.28	2.0E-05	7682027	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
1910	11115	20311	3.87	2.0E-05	4507512	NT	Homo sapiens Ly-6-like protein (CD59) mRNA, complete cds
1913	11118	20315	1.83	2.0E-05	BE383873.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C048
2380	11663	20800	1.13	2.0E-05	6453865	NT	yp87g11.1 Soares fetal liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:194488 6'
2390	11563	20801	1.13	2.0E-05	5453865	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
							Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
							Homo sapiens tissue inhibitor of metalloproteinase 3 (Soraby fundus dystrophy, pseudoinflammatory) (TIMP3) mRNA
							mRNA
							601312161F1 NH_MGC_44 Homo sapiens cDNA clone IMAGE:3658882 6'
							Homo sapiens G protein-coupled receptor 19 (GPR19) mRNA
							Homo sapiens G protein-coupled receptor 19 (GPR19) mRNA

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2428	11819	20840	3.71	2.0E-05	AF240788.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
2478	11888	20887	11.4	2.0E-05	4758423	NT	Homo sapiens glycine cleavage system protein H (aminomethyl carrier) (GCSH) mRNA
3121	12356	21485	3.34	2.0E-05	AF015452.1	NT	Homo sapiens Usurpin-gamma mRNA, complete cds
3539	12782	21892	2.98	2.0E-05	7705900	NT	Homo sapiens unconventional myosin-15 (LOC51168), mRNA
3539	12782	21893	2.98	2.0E-05	7705900	NT	Homo sapiens unconventional myosin-15 (LOC51168), mRNA
3595	12816	21938	1.25	2.0E-05	AB037807.1	NT	Homo sapiens mRNA for KIAA1388 protein, partial cds
3731	12951	22068	0.85	2.0E-05	AI200284.1	EST_HUMAN	qm01c02.x1 Soares_NIHMPu_S1 Homo sapiens cDNA clone IMAGE:1880546 3' similar to WP:T23G7.4
4355	13557	22652	1.79	2.0E-05	7657185	NT	CE03705 ;
5064	14244	23331	3.37	2.0E-05	7681979	NT	Homo sapiens hypothetical protein (HS322B1A), mRNA
5121	14300	23388	1.7	2.0E-05	AA447831.1	EST_HUMAN	Homo sapiens KIAA0187 gene product (KIAA0187), mRNA
5121	14300	23389	1.7	2.0E-05	AA447831.1	EST_HUMAN	zxt1d07.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:788157 5'
5431	14858	23796	4.23	2.0E-05	7705764	NT	zxt1d07.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:788157 5'
5431	14858	23797	4.23	2.0E-05	7705764	NT	Homo sapiens CGI-48 protein (LOC51086), mRNA
5731	14850	24349	4.34	2.0E-05	M59724.1	NT	Homo sapiens CGI-48 protein (LOC51086), mRNA
5910	15127	24538	2.53	2.0E-05	AF257737.1	NT	Homo sapiens CGI-48 protein (LOC51086), mRNA
6815	18010	25473	3.61	2.0E-05	11421795	NT	Homo sapiens CGI-48 protein (LOC51086), mRNA
7311	16528	26020	2.34	2.0E-05	4757853	NT	Human muscle-type phosphofructokinase (PFK-M) gene, exon 7
8735	17681	23953	2.2	2.0E-05	AF240788.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
9164	17958	23884	5.88	2.0E-05	11418164	NT	Homo sapiens ribophorin II (RPN2), mRNA
5498	14724	24082	7.75	1.0E-05	AA284851.1	EST_HUMAN	Homo sapiens bone morphogenetic protein receptor, type IA (BMPRI1A) mRNA
5498	14724	24083	7.75	1.0E-05	AA284851.1	EST_HUMAN	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
6286	15477	24819	3.3	1.0E-05	BF370000.1	EST_HUMAN	Homo sapiens adenylosuccinate lyase (ADSL), mRNA
6286	15477	24820	3.3	1.0E-05	BF370000.1	EST_HUMAN	Homo sapiens adenylosuccinate lyase (ADSL), mRNA
6527	16723	25188	2.63	9.0E-06	BE887269.1	EST_HUMAN	Homo sapiens ovary tumor NihHOT Homo sapiens cDNA clone IMAGE:714007 5' similar to
448	11987	18838	1.64	8.0E-06	BE907607.1	EST_HUMAN	zxt3h04.r1 Soares ovary tumor NihHOT Homo sapiens cDNA clone IMAGE:714007 5' similar to
448	11987	18839	1.64	8.0E-06	BE907607.1	EST_HUMAN	TR:G1067084 G1067084 F59H2.6 ;
5444	14870	22220	2.59	8.0E-06	AW838047.1	EST_HUMAN	zxt3h04.r1 Soares ovary tumor NihHOT Homo sapiens cDNA clone IMAGE:714007 5' similar to
3887	13103	20847	0.88	7.0E-06	AF231920.1	NT	TR:G1067084 G1067084 F59H2.6 ;
2226	11421	20847	1.36	6.0E-06	BE171984.1	EST_HUMAN	TR:G1067084 G1067084 F59H2.6 ;

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3290	12521	21652	0.88	8.0E-08	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
3457	12682	21816	19.61	8.0E-08	M26873.1	NT	Human glyceraldehyde-3-phosphate dehydrogenase pseudogene 3'end
8078	17214	26746	1.88	6.0E-08	7682289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
8078	17214	26747	1.88	6.0E-08	7682289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
8118	17252	26793	2.29	6.0E-08	8923839	NT	Homo sapiens myosin, heavy polypeptide 2, skeletal muscle, adult (MYH2), mRNA
325	9598	18725	2.91	5.0E-08	AB032988.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
852	10088	19248	3.55	5.0E-08	AB032988.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
852	10088	19249	3.55	5.0E-08	AB032988.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
2581	11767		8.37	5.0E-08	11416787	NT	Homo sapiens phosphodiesterase 8A, cGMP-specific, rod, alpha (PDE8A), mRNA
2892	12229	21381	0.65	5.0E-08	6912735	NT	Homo sapiens transient receptor potential channel 5 (TRPC5), mRNA
4925	14113		1.74	5.0E-08	X60812.1	NT	H. sapiens DNA for monocarboxylic acid type A (7) (partial)
5892	15274	24703	3.98	5.0E-08	11424389	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
5892	15274	24704	3.98	5.0E-08	11424389	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
6495	15692	25156	2.88	5.0E-08	M68347.1	NT	Human type IV collagenase (CLG4B) gene, exon 5
6495	15692	25157	2.88	5.0E-08	M68347.1	NT	Human type IV collagenase (CLG4B) gene, exon 5
4173	13377		18.09	3.0E-08	H68956.1	EST_HUMAN	yr87h12 r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:212327 5'
421	9874		2.93	2.0E-08	4503098	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
755	8898	18141	2.93	2.0E-08	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
4768	13958	23059	1.08	2.0E-08	BE148074.1	EST_HUMAN	RC3-HT0230-040500-110-g02 HT0230 Homo sapiens cDNA
8758	15954		6.71	2.0E-08	AV689481.1	EST_HUMAN	AV689481 GKC Homo sapiens cDNA clone GKCFCMD07 5'
8416	17489		2.01	2.0E-08	AW249440.1	EST_HUMAN	2818351.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2818351 5'
677	8921	19052	2.99	1.0E-08	Y18890.1	NT	Human endogenous retrovirus type K (HERV-K), gag, pol and env genes
1751	10983	20145	3.39	1.0E-08	AW955054.1	EST_HUMAN	EST387124 MAGC resequences, MAGC Homo sapiens cDNA
1751	10983	20146	3.39	1.0E-08	AW955054.1	EST_HUMAN	EST387124 MAGC resequences, MAGC Homo sapiens cDNA
2231	11951	20853	1.03	1.0E-08	U51472.2	NT	Felis catus superfast myosin heavy chain (sMyHC) mRNA, complete cds
6888	15861	25340	28.75	1.0E-08			Homo sapiens similar to ectonucleotide pyrophosphatase/phosphodiesterase 3 (H. sapiens) (LOC83214), mRNA
8403	14488	23533	1.38	1.0E-08	11419429	NT	Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA
8403	14488	23534	1.38	1.0E-08	4828863	NT	Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA
6315	15495		3.65	8.0E-07	BE141849.1	EST_HUMAN	IL5-HT0117-011098-004-D07 HT0117 Homo sapiens cDNA
7844	17084	28613	2.09	6.0E-07	X15804.1	NT	Human mRNA for alpha-actinin
6467	15864	25135	2.41	5.0E-07	AL043314.2	EST_HUMAN	DKFZp434N0323_r1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434N0323 5'
6506	15702	25188	13.07	5.0E-07	AA418028.1	EST_HUMAN	zv07e12.s1 Soares_NHHMPu_S1 Homo sapiens cDNA clone IMAGE:787768 3' similar to TR:G1304125 G1304125 PMS4 mRNA;

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6983	16161	25632	3.44	5.0E-07	BF154912.1	EST_HUMAN	RCO-BT0812-250800-032-a09 BT0812 Homo sapiens cDNA
8080	17215	26748	2.4	5.0E-07	BE148597.1	EST_HUMAN	MRO-HT0241-150500-010-502 HT0241 Homo sapiens cDNA
8080	17215	26749	2.4	5.0E-07	BE148597.1	EST_HUMAN	MRO-HT0241-150500-010-502 HT0241 Homo sapiens cDNA
847	10180	18338	1.69	4.0E-07	BE004436.1	EST_HUMAN	CMO-BIN0108-170300-293-a08 BIN0108 Homo sapiens cDNA
1874	11081	20271	1.08	4.0E-07	5453572	NT	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 2 (BIG2), mRNA
6007	16257	24881	6.08	4.0E-07	Y11339.2	NT	Homo sapiens mRNA for GalNAc alpha-2, 6-sialyltransferase 1, long form
6007	16257	24882	6.08	4.0E-07	Y11339.2	NT	Homo sapiens mRNA for GalNAc alpha-2, 6-sialyltransferase 1, long form
7722	16921	26429	1.74	4.0E-07	11863122	NT	Homo sapiens AXL receptor tyrosine kinase (AXL), transcript variant 1, mRNA
7722	16921	26430	1.74	4.0E-07	11863122	NT	Homo sapiens AXL receptor tyrosine kinase (AXL), transcript variant 1, mRNA
8806	17604		6	4.0E-07	11418318	NT	Homo sapiens G-2 and S-phase expressed 1 (GTSE1), mRNA
247	8524	18654	0.98	3.0E-07	AB032898.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
884	10120	19282	8.01	3.0E-07	4502168	NT	Homo sapiens amyloid beta (A4) precursor protein (protease resistant) (APP), mRNA
884	10120	19283	8.01	3.0E-07	4502168	NT	Homo sapiens amyloid beta (A4) precursor protein (protease resistant) (APP), mRNA
1443	11895	19832	2.27	3.0E-07	4758813	NT	Homo sapiens N-myc (and STAT) interactor (NMI), mRNA
2402	11852	20813	3.91	3.0E-07	U38255.1	NT	Human beta-prime-tubulin (BAM22) gene, exon 7
3227	12481	21593	1.34	3.0E-07	5174478	NT	Homo sapiens perlecanin (PCNT) mRNA
4789	13978	23082	31.26	1.0E-07	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
5840	18057	24464	2.46	1.0E-07	BE568488.1	EST_HUMAN	601339520F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3681821 5'
7294	16513	26005	4.29	1.0E-07	11427757	NT	Homo sapiens KIAA0849 gene product (KIAA0849), mRNA
7294	16513	26006	4.29	1.0E-07	11427757	NT	Homo sapiens KIAA0849 gene product (KIAA0849), mRNA
7857	17047	26566	3.58	1.0E-07	AA53761.1	EST_HUMAN	nk28g02.s1 NCI_CGAP_Cot11 Homo sapiens cDNA clone IMAGE:1014982 3'
8004	16439	25928	18.38	1.0E-07	11426272	NT	Homo sapiens ribosomal protein S15 (RPS15), mRNA
8004	16439	25927	18.38	1.0E-07	11426272	NT	Homo sapiens ribosomal protein S15 (RPS15), mRNA
911	10146	19007	3.5	9.0E-08	BE080973.1	EST_HUMAN	PM4-BT0724-010400-008-a12 BT0724 Homo sapiens cDNA
1283	10498	19658	0.67	9.0E-08	8393092	NT	Homo sapiens cat eye syndrome critical region gene 1 (CECR1), mRNA
6247	14420	23497	1.46	9.0E-08	11419594	NT	Homo sapiens FSH primary response (LRPR1, rat) homolog 1 (FSHPRH1), mRNA
6434	15631	25098	11.48	9.0E-08	4758119	NT	Homo sapiens death-associated protein (DAP), mRNA
6434	15631	25097	11.48	9.0E-08	4758119	NT	Homo sapiens death-associated protein (DAP), mRNA
7674	18779	26273	2.68	9.0E-08	AB023222.1	NT	Homo sapiens mRNA for KIAA1005 protein, partial cds
7574	18779	26274	2.68	9.0E-08	AB023222.1	NT	Homo sapiens mRNA for KIAA1005 protein, partial cds
8621	10146	19307	2.6	9.0E-08	BE080973.1	EST_HUMAN	PM4-BT0724-010400-008-a12 BT0724 Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
25	9321		1.5	8.0E-88	AJ251158.1	NT	Homo sapiens partial MICB gene for MHC class I chain-related protein B, exons 2-3 and joined CDS
1701	10913	20100	3.45	8.0E-88	AB017007.1	NT	Homo sapiens PMS2L16 mRNA, partial cds
1701	10918	20101	3.45	8.0E-88	AB017007.1	NT	Homo sapiens PMS2L16 mRNA, partial cds
3778	12896	22112	7.09	8.0E-88	J04469.1	NT	Human mitochondrial creatine kinase (CKMT) gene, complete cds
2144	11342	20560	1.34	3.0E-88	AJ403124.1	EST_HUMAN	AJ403124 3.4 (downregulated in larynx carcinoma) Homo sapiens cDNA clone l8
2668	11763	20973	3.6	3.0E-88	AB014607.1	NT	Homo sapiens mRNA for KIAA0707 protein, partial cds
2708	11885		6.43	3.0E-88	AA077488.1	EST_HUMAN	7B18H01 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B18H01
6082	15252	24675	1.94	3.0E-88	11419210	NT	Homo sapiens activator of S phase kinase (ASK), mRNA
6082	15252	24676	1.94	3.0E-88	11419210	NT	Homo sapiens activator of S phase kinase (ASK), mRNA
7035	16212	25688	2.7	3.0E-88	AJ403124.1	EST_HUMAN	AJ403124 3.4 (downregulated in larynx carcinoma) Homo sapiens cDNA clone l8
7035	16212	25689	2.7	3.0E-88	AJ403124.1	EST_HUMAN	AJ403124 3.4 (downregulated in larynx carcinoma) Homo sapiens cDNA clone l8
7528	16791	26221	2.58	3.0E-88	U59309.1	NT	Human fumarate precursor (FH) mRNA, nuclear gene encoding mitochondrial protein, complete cds
8213	17894		3.36	3.0E-88	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
743	8884	18127	0.75	2.0E-88	BE261894.1	EST_HUMAN	801149486F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3502245 5'
2047	11248	20458	3.98	2.0E-88	BE264281.1	EST_HUMAN	801172858F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3528134 5'
2204	11401	20828	2.69	2.0E-88	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
2342	11635	20758	0.91	2.0E-88	AF248540.1	NT	Homo sapiens intersecin 2 (SH3D1B) mRNA, complete cds
2342	11635	20759	0.91	2.0E-88	AF248540.1	NT	Homo sapiens intersecin 2 (SH3D1B) mRNA, complete cds
3088	12332	21458	1.3	2.0E-88	AB032377.1	NT	Homo sapiens hCHK1 gene for checkpoint kinase, exon 2
3088	12332	21459	1.3	2.0E-88	AB032377.1	NT	Homo sapiens hCHK1 gene for checkpoint kinase, exon 2
4084	13293	22392	1.45	2.0E-88	8923308	NT	Homo sapiens hypothetical protein FLJ20333 (FLJ20333), mRNA
4284	13487	22588	0.64	2.0E-88	AF032697.1	NT	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
4333	13534	22825	3.89	2.0E-88	4758331	NT	Homo sapiens fatty acid-Coenzyme A ligase, long-chain 4 (FACL4) mRNA
4843	14032	23123	1.04	2.0E-88	AF218602.1	NT	Homo sapiens attractin precursor (ATRIN) gene, exon 18
4843	14032	23124	1.04	2.0E-88	AF218602.1	NT	Homo sapiens attractin precursor (ATRIN) gene, exon 18
5384	14613	23728	5.47	2.0E-88	7706512	NT	Homo sapiens PDZ domain-containing guanine nucleotide exchange factor 1 (LOC51735), mRNA
6658	15853	25312	3.8	2.0E-88	11428813	NT	Homo sapiens SH3-domain GRB2-like 2 (SH3GL2), mRNA
6658	15853	25313	3.8	2.0E-88	11428813	NT	Homo sapiens SH3-domain GRB2-like 2 (SH3GL2), mRNA
8626	17019	23971	4.63	2.0E-88	11435947	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
411	9884	18804	60.73	1.0E-88	AI862007.1	EST_HUMAN	hw38804.x1 NCL CGAP_U11 Homo sapiens cDNA clone IMAGE:2261743 3' similar to SW-RL28_HUMAN P2318 60S RIBOSOMAL PROTEIN L23A. ;
461	9714	18849	2.16	1.0E-88	AW988611.1	EST_HUMAN	PMO-BN0065-100300-001-c08 BN0065 Homo sapiens cDNA

Table 4

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1768	10876	20165	45.72	1.0E-08	N49818.1	EST_HUMAN	Y23105.r1 Soares fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:243585 5' similar to PIR:S54204 S54204 ribosomal protein L29 - human;
5342	14572	23848	3.57	1.0E-08	AA195854.1	EST_HUMAN	z088-09.r1 Stratagene muscle 837209 Homo sapiens cDNA clone IMAGE:828240 5' similar to TR:G808562 G808562 NEBULIN;
6764	15859	25413	3.58	1.0E-08	AF141349.1	NT	Homo sapiens beta-tubulin mRNA, complete cds
6764	15959	25414	3.58	1.0E-08	AF141349.1	NT	Homo sapiens beta-tubulin mRNA, complete cds
5680	14900	24294	4.01	9.0E-08	AW1868635.1	EST_HUMAN	EST1380711 IMAGE resequences, MAGJ Homo sapiens cDNA
7682	16881	26388	2.78	9.0E-08	AI479829.1	EST_HUMAN	tr68h07.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2163421 3' similar to SW:BIID_HUMAN P55857 BH3 INTERACTING DOMAIN DEATH AGONIST;
7682	16881	26388	2.78	9.0E-08	AI479829.1	EST_HUMAN	tr68h07.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2163421 3' similar to SW:BIID_HUMAN P55857 BH3 INTERACTING DOMAIN DEATH AGONIST;
7952	17091	26621	2.22	9.0E-08	AA134604.1	EST_HUMAN	z080402.r1 Stratagene lung carcinoma 837218 Homo sapiens cDNA clone IMAGE:565443 5' similar to TR:G862894 G862894 GPI-ANCHORED PROTEIN P137;
5595	14809	24183	9.29	7.0E-08	AF035808.1	NT	Homo sapiens oscillin (hln) gene, exon 5
8134	17267	26811	2.84	7.0E-08	AF001886.1	NT	Homo sapiens NK-receptor (KIR-G2) gene, linker region exon
478	9730	18804	0.88	6.0E-09	U10991.1	NT	Human G2 protein mRNA, partial cds
2097	11287	20509	2.73	6.0E-08	11430555	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, (LOC51232), mRNA
2097	11287	20510	2.73	6.0E-08	11430555	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, (LOC51232), mRNA
4780	13951	23052	1.05	6.0E-08	4502680	NT	Homo sapiens CD34 antigen (CD34) mRNA
5228	14402	23485	0.95	6.0E-08	8923244	NT	Homo sapiens hypothetical protein FLJ20772 (FLJ20772), mRNA
6705	15600	25361	2.55	8.0E-08	AB036426.1	NT	Homo sapiens NDST4 mRNA for N-deacetylase/N-sulfotransferase 4, complete cds
6735	15630	25389	4.2	6.0E-08	AF080255.1	NT	Homo sapiens lodestar protein mRNA, complete cds
6735	15630	25390	4.2	6.0E-08	AF080255.1	NT	Homo sapiens lodestar protein mRNA, complete cds
7307	16525	26016	4.48	6.0E-08	11526289	NT	Homo sapiens BH3 interacting domain death agonist (BID), mRNA
929	10163	18319	0.59	5.0E-08	U35484.1	NT	Human protein C inhibitor (PCI-B) mRNA, complete cds
929	10163	18320	0.59	5.0E-08	U35484.1	NT	Human protein C inhibitor (PCI-B) mRNA, complete cds
1804	11138	20334	1.39	5.0E-08	Y11365.1	NT	H. sapiens IMPA gene, exon 8
4562	13756	22854	1.41	5.0E-08	AF008680.1	NT	Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region
8637	17628		2.18	5.0E-08	BE890177.1	EST_HUMAN	601513157F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3914391 5'
6569	15785		8.7	3.0E-08	M85586.1	NT	Human E2AFHLA fusion protein (E2AFHLF) mRNA, complete cds
1248	10463		13.38	2.0E-08	AW274782.1	EST_HUMAN	xp09e08.x1 NCI_CGAP_HN9 Homo sapiens cDNA clone IMAGE:2739874 3' similar to gb:M31212 MYOSIN
3225	12468	21592	1.50	2.0E-08	M30838.1	NT	LIGHT CHAIN ALKALI, NON-MUSCLE ISOFORM (HUMAN);
4498	13688	22789	0.82	2.0E-08	BE612554.1	EST_HUMAN	Human Ku (p70/p80) subunit mRNA, complete cds
							Human Ku (p70/p80) subunit mRNA, complete cds
							601452087F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3855761 5'

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4498	13698	22790	0.82	2.0E-89	BE612554.1	EST_HUMAN	601452087F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3855791 5'
4540	13735	22833	2.2	2.0E-89	AF095703.1	NT	Homo sapiens short chain L-3-hydroxyacyl-CoA dehydrogenase precursor (HADHSC) gene, nuclear gene encoding mitochondrial protein, complete cds
6883	15878	25337	2.24	2.0E-88	W23507.1	EST_HUMAN	zb46408.r1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:308635 5' similar to gb:M15182 BETA-GLUCURONIDASE PRECURSOR (HUMAN);
7670	16866	26372	4.48	2.0E-88	AF247457.2	NT	Homo sapiens myosin X (MYO10) mRNA, complete cds
320	9591	18722	1.48	1.0E-89	AF114487.1	NT	Homo sapiens Intersectin long isoform (ITSN) mRNA, complete cds
384	9848	18783	0.88	1.0E-88	11528150	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (60kD) (GABPA), mRNA
1425	10638	18808	5	1.0E-88	M30938.1	NT	Homo sapiens Ku (p70/p80) subunit mRNA, complete cds
1541	10754	19277	1.5	1.0E-88	AF192523.1	NT	Homo sapiens truncated Niemann-Pick C3 protein (NPC3) mRNA, complete cds
1541	10754	19928	1.5	1.0E-88	AF192523.1	NT	Homo sapiens truncated Niemann-Pick C3 protein (NPC3) mRNA, complete cds
1895	11102	20283	1.21	1.0E-88	4503730	NT	Homo sapiens FK506-binding protein 6 (38kD) (FKBP6) mRNA, and translated products
1895	11102	20284	1.21	1.0E-88	4503730	NT	Homo sapiens FK506-binding protein 6 (38kD) (FKBP6) mRNA, and translated products
3050	12286	21412	1.22	1.0E-89	J03171.1	NT	Homo sapiens fatty acid amide hydrolase (FAAH) gene, exon 14
4374	13576	22872	2.53	1.0E-88	AF098018.1	NT	Homo sapiens fatty acid amide hydrolase (FAAH) gene, exon 14
4374	13576	22873	2.53	1.0E-88	AF098018.1	NT	Human interferon-alpha receptor (HuIFN-alpha-Rcc) mRNA, complete cds
6922	16115	25581	2.58	1.0E-99	AW340174.1	EST_HUMAN	Homo sapiens heat shock transcription factor 2 binding protein (HSF2BP), mRNA
7741	16837	26446	1.78	1.0E-88	6901979	NT	h002h02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2808371 3' similar to TR:002711
7916	17131	26681	2.7	1.0E-88	AB023222.1	NT	O02711 PRO-POL-OUTPASE POLYPROTEIN;
8268	17393	26923	1.78	1.0E-88	AF223391.1	NT	Homo sapiens heat shock transcription factor 2 binding protein (HSF2BP), mRNA
8387	17488						Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
1	9286	18401	4.43	1.0E-98	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
2	9299	18401	2.49	1.0E-100	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
68	9363	18487	4.78	1.0E-100	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
68	9363	18488	1.69	1.0E-100	11418230	NT	Homo sapiens Testis-specific XK-related protein on Y (XKRY), mRNA
86	9378	18510	1.69	1.0E-100	11418230	NT	Homo sapiens Testis-specific XK-related protein on Y (XKRY), mRNA
172	9453	18584	0.89	1.0E-100	AW275237.1	EST_HUMAN	sv78b11.x1 NCJ_CGAP_Brn53 Homo sapiens cDNA clone IMAGE:2824805 3'
322	9583	18724	0.83	1.0E-100	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C008
348	9616	18743	0.83	1.0E-100	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C049
443	9697		1.92	1.0E-100	AF003528.1	NT	Homo sapiens chromosome 21 segment HS21C049
						EST_HUMAN	EST02975 Fetal brain, Stralagene (cat#838206) Homo sapiens cDNA clone HFB0332
						EST_HUMAN	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
498	9749		6.33	1.0E-100	X89631.1	NT	G gorilla DNA for ZNF80 gene homolog
516	9767	18893	1.06	1.0E-100	BE180609.1	EST_HUMAN	RC3-HT0825-040500-022-509 HT0825 Homo sapiens cDNA
1028	10252	19402	2.26	1.0E-100	7681685	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
1028	10252	19403	2.26	1.0E-100	7681685	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
1532	10746		1.36	1.0E-100	AW207555.1	EST_HUMAN	UI-H-B11-eff-c-07-0-JL.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2722164 3'
1538	10749	18922	1.28	1.0E-100	AI200857.1	EST_HUMAN	qf62f09.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1754633 3' similar to SW:CYT_COTJA
2207	11404		1.09	1.0E-100	D83349.1	NT	P81081 CYSTATIN1
2401	11594	20812	0.98	1.0E-100	X62468.1	NT	Rat mRNA for short type PB-cadherin, complete cds
2667	11848	21063	1.09	1.0E-100	11418976	NT	H. sapiens mRNA for IFN-gamma (pKGC-0)
2683	12220		5.64	1.0E-100	D11078.1	NT	Homo sapiens KIAA0957 protein (KIAA0957), mRNA
4183	13397	22497	1.68	1.0E-100	AF057354.1	NT	Homo sapiens RGH2 gene, retrovirus-like element
4221	13424	22517	2.1	1.0E-100	4503793	NT	Homo sapiens myotubularin-related protein 1a mRNA, partial cds
5123	14302	23390	3.15	1.0E-100	5032104	NT	Homo sapiens follicle stimulating hormone receptor (FSHR) mRNA
5123	14302	23391	3.15	1.0E-100	5032104	NT	Homo sapiens small optic lobes (Drosophila) homolog (SOL) mRNA
5319	14551	23621	1.73	1.0E-100	BF244218.1	EST_HUMAN	Homo sapiens small optic lobes (Drosophila) homolog (SOL) mRNA
5536	14760	24127	1.88	1.0E-100	AU140214.1	EST_HUMAN	601863164F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4080899 5'
5875	15093	24506	5.22	1.0E-100	AU140214.1	EST_HUMAN	AU118182 HEMBA1 Homo sapiens cDNA clone HEMBA1003046 5'
6037	15245	24987	5.68	1.0E-100	X04571.1	NT	AU140214 PLACE2 Homo sapiens cDNA clone PLACE2000137 5'
6631	15827	25289	10.17	1.0E-100	BF103653.1	EST_HUMAN	Human mRNA for kidney epidermal growth factor (EGF) precursor
6643	15838		8.14	1.0E-100	AL163203.2	NT	601847357F1 NIH_MGC_61 Homo sapiens cDNA clone IMAGE:3931310 5'
6837	16031	25498	2.53	1.0E-100	AB040918.1	NT	Homo sapiens chromosome 21 segment HS21C003
6952	16130	25598	2.8	1.0E-100	AB046946.1	NT	Homo sapiens mRNA for KIAA1485 protein, partial cds
6952	16130	25599	2.8	1.0E-100	AB046946.1	NT	Homo sapiens mRNA for KIAA1826 protein, partial cds
7343	16559	26047	6.68	1.0E-100	BF327292.1	EST_HUMAN	Homo sapiens mRNA for KIAA1826 protein, partial cds
7834	17028	26542	3.59	1.0E-100	X04633.1	NT	MRO-BN0070-270300-008-h11 BN0070 Homo sapiens cDNA
7834	17028	26543	3.59	1.0E-100	X04633.1	NT	H. sapiens CD97 gene exon 4
7893	17109	26638	4.35	1.0E-100	AF111170.3	NT	H. sapiens CD97 gene exon 4
7893	17109	26639	4.35	1.0E-100	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
7922	9289	18401	2.41	1.0E-100	AL163247.2	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
8178	17311		2.07	1.0E-100	AF268285.1	NT	Homo sapiens chromosome 21 segment HS21C047
8309	17414	26936	8.55	1.0E-100	AF240786.1	NT	Homo sapiens golgin-like protein (GLP) gene, complete cds
							Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8439	18237		1.33	1.0E-100	BF448548.1	EST_HUMAN	7q88h03.x1 NCJ_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3' similar to TR:Q21897 Q21897 COSMID R151. [2] TR:Q8UA08;
8827	17620	23872	2.51	1.0E-100	11545732	NT	Homo sapiens SH3-domain binding protein 1 (SH3BP1), mRNA
8875	17772	23841	1.51	1.0E-100	11418123	NT	Homo sapiens KIAA0063 gene product (KIAA0063), mRNA
9282	18028	23854	4.18	1.0E-100	11417874	NT	Homo sapiens transcobalamin II: macrocytic anemia (TCN2), mRNA
77	9371	18500	0.89	1.0E-101	7110714	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
77	9371	18501	0.89	1.0E-101	7110714	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
683	9838	19068	1.7	1.0E-101	AB007915.2	NT	Homo sapiens mRNA for KIAA0448 protein, partial cds
711	9853	19092	5.91	1.0E-101	7110734	NT	Homo sapiens ventral anterior homeobox 2 (VAX2), mRNA
711	9853	19093	5.91	1.0E-101	7110734	NT	Homo sapiens ventral anterior homeobox 2 (VAX2), mRNA
760	10018	19188	2.81	1.0E-101	7657454	NT	Homo sapiens pascadillo (zabrafish) homolog 1, containing BRCT domain (PES1), mRNA
883	10099	19261	2.61	1.0E-101	4503914	NT	Homo sapiens phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylmethylidazole synthetase (GART) mRNA
834	10167	19324	1	1.0E-101	220858.1	NT	Homo sapiens of cardiac alpha-myosin heavy chain gene
882	10223	19380	8.49	1.0E-101	BF681218.1	EST_HUMAN	602158474F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4287281 5'
1059	10285	19435	1.88	1.0E-101	A1221878.1	EST_HUMAN	gg98a09.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:1843338 3'
1562	10776	19851	1.09	1.0E-101	5921460	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
1502	10776	19852	1.09	1.0E-101	5921460	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
1914	11119	20316	2.15	1.0E-101	4502898	NT	Homo sapiens carboxypeptidase A1 (pancreatic) (CPA1) mRNA
2023	11224	20432	6.82	1.0E-101	BE843070.1	EST_HUMAN	RC3-ST0281-160800-018-h09 ST0281 Homo sapiens cDNA
2318	12015	20732	1.12	1.0E-101	5728882	NT	Homo sapiens A kinase (PRKA) anchor protein 6 (AKAP6), mRNA
2577	11763	20884	6.88	1.0E-101	X72993.1	NT	H. sapiens EWS gene, exon 5
2700	11879	21064	12.23	1.0E-101	AJ237744.1	NT	Homo sapiens RIBIR gene (partial), exon 12
2700	11879	21065	12.23	1.0E-101	AJ237744.1	NT	Homo sapiens RIBIR gene (partial), exon 12
2808	12146		15.41	1.0E-101	AJ252312.1	NT	Homo sapiens genomic downstream Rhesus box
3167	12402	21537	2.87	1.0E-101	4885270	NT	Homo sapiens gamma-glutamyltransferase 1 (GGT1) mRNA
3207	12441		2.4	1.0E-101	BF035327.1	EST_HUMAN	601458531F1 NIH_MGC_86 Homo sapiens cDNA clone IMAGE:3862098 5'
3359	12887	21726	1.72	1.0E-101	AW965556.1	EST_HUMAN	EST377828 IMAGE resequences, MAGI Homo sapiens cDNA
3378	11879	21094	3.41	1.0E-101	AJ237744.1	NT	Homo sapiens RIBIR gene (partial), exon 12
3378	11879	21095	3.41	1.0E-101	AJ237744.1	NT	Homo sapiens RIBIR gene (partial), exon 12
3658	13074	22189	5.17	1.0E-101	AB022785.1	NT	Homo sapiens ASH2L gene, complete cds, similar to Drosophila ash2 gene
5058	14238	23327	1.2	1.0E-101	5921460	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
5058	14238	23328	1.2	1.0E-101	5921460	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
5170	14349	23437	0.73	1.0E-101	BE612554.1	EST_HUMAN	601452067F1 NIH_MGC_86 Homo sapiens cDNA clone IMAGE:3855761 5'

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5170	14349	23438	0.73	1.0E-101	BE612554.1	EST_HUMAN	601452087F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3856761 5'
5654	14877	24265	4.27	1.0E-101	7427512	NT	Homo sapiens cytoplasmic linker 2 (CYLN2), mRNA
5654	14877	24266	4.27	1.0E-101	7427512	NT	Homo sapiens cytoplasmic linker 2 (CYLN2), mRNA
6218	15389	24840	4.91	1.0E-101	AF208870.1	NT	Homo sapiens Kruppel-type zinc finger protein (PEG3) mRNA, alternative splice form 4, partial cds
6218	15389	24841	4.91	1.0E-101	AF208870.1	NT	Homo sapiens Kruppel-type zinc finger protein (PEG3) mRNA, alternative splice form 4, partial cds
6283	15484	24906	4.88	1.0E-101	AW008475.1	EST_HUMAN	hw55f12.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2533487 3'
6324	15505		1.73	1.0E-101	BE257384.1	EST_HUMAN	601109217F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3349801 5'
6385	15595	25022	6.59	1.0E-101	BF330759.1	EST_HUMAN	RC1-BT0313-220700-018-f12 BT0313 Homo sapiens cDNA
6483	15680	25149	4.94	1.0E-101	BF028174.1	EST_HUMAN	601764888F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3896837 5'
6899	15805	25070	25.34	1.0E-101	X60069.1	NT	Human mRNA for pancreatic gamma-glutamyltransferase
6899	15805	25071	25.34	1.0E-101	X60069.1	NT	Human mRNA for pancreatic gamma-glutamyltransferase
6904	16081	25328	16.67	1.0E-101	8845492	NT	Homo sapiens gamma-glutamyltransferase 1 (GGT1), transcript variant 3, mRNA
7003	16181	25653	4.96	1.0E-101	BE619687.1	EST_HUMAN	601472808T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875953 3'
7003	16181	25654	4.96	1.0E-101	BE619687.1	EST_HUMAN	601472808T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875953 3'
7188	16365	25845	2.7	1.0E-101	11428127	NT	Homo sapiens Janus kinase 2 (a protein tyrosine kinase) (JAK2), mRNA
7192	16369	25848	4.46	1.0E-101	AI570263.1	EST_HUMAN	1b77d11.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2184309 3' similar to gb:M26328
7192	16369	25849	4.46	1.0E-101	AI570263.1	EST_HUMAN	KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
8605	17766		5.23	1.0E-101	AW639051.1	EST_HUMAN	1b77d11.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2184309 3' similar to gb:M26328
41	8337	18444	0.9	1.0E-102	AF012672.1	NT	KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
349	8914	18740	3.75	1.0E-102	AL163303.2	NT	QV1-DT0068-240200-085-e01 DT0068 Homo sapiens cDNA
826	9871	18993	1.28	1.0E-102	BE252470.1	EST_HUMAN	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
784	10023	19173	1.51	1.0E-102	4557534	NT	Homo sapiens chromosome 21 segment HS21C103
1125	10349	19500	2.13	1.0E-102	M10876.1	NT	601108282F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3344328 5'
1275	10490	19848	1.28	1.0E-102	11437148	NT	Homo sapiens down-regulated in adenoma (DRA) mRNA
1275	10490	19849	1.28	1.0E-102	11437148	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
1423	10638	19805	387.84	1.0E-102	BE408447.1	EST_HUMAN	Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 9 (SLC2A9), mRNA
2275	11470	20691	4.52	1.0E-102	AI124669.1	EST_HUMAN	Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 9 (SLC2A9), mRNA
2275	11470	20692	4.52	1.0E-102	AI124669.1	EST_HUMAN	601288982F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3629801 5'
3028	12285	21393	1.55	1.0E-102	7881979	NT	am80c10.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1539854 3' similar to
3098	12334	21490	3.08	1.0E-102	AU141005.1	EST_HUMAN	SW:GG95_HUMAN Q08379 GOLGIN-95.;
							am80c10.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1539854 3' similar to
							SW:GG95_HUMAN Q08379 GOLGIN-95.;
							Homo sapiens KIAA0187 gene product (KIAA0187), mRNA
							AU141005 PLACE4 Homo sapiens cDNA clone PLACE400850 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3098	12334	21461	3.08	1.0E-102	AU141005.1	EST_HUMAN	AU141005 PLACE4 Homo sapiens cDNA clone PLACE4000850 5'
4217	13420	22515	1.84	1.0E-102	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
4408	13808	22705	1.98	1.0E-102	BE251310.1	EST_HUMAN	601107843F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3343882 5'
5145	14324	23415	0.97	1.0E-102	R68488.1	EST_HUMAN	y32c04.r1 Soares placenta NB2-HP Homo sapiens cDNA clone IMAGE:140634 5'
5550	14774		5.78	1.0E-102	AB034951.1	NT	Homo sapiens HSC54 mRNA for heat shock cognate protein 54, complete cds
5587	14782	24184	3.18	1.0E-102	7705398	NT	Homo sapiens histone deacetylase 7 (HDAC7), mRNA
5587	14792	24185	3.18	1.0E-102	7705398	NT	Homo sapiens histone deacetylase 7 (HDAC7), mRNA
5783	15001	24404	2.82	1.0E-102	AI459825.1	EST_HUMAN	ar92f09.x1 Barabead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2151785 3' similar to TR:Q13137
6233	15414	24855	8.1	1.0E-102	AJ238994.1	NT	Q13137 NDP52.1
6345	15528	24974	2.87	1.0E-102	AV710738.1	EST_HUMAN	Homo sapiens mRNA for Centaurin-alpha2 protein
6880	16050	25516	2.68	1.0E-102	AV710738.1	EST_HUMAN	AV710738 Cu Homo sapiens cDNA clone CuAAKD03 5'
6880	16050	25517	2.68	1.0E-102	AV710738.1	EST_HUMAN	ydl3d07.r1 Soares fetal liver spleen 1N1FLS Homo sapiens cDNA clone IMAGE:67021 5'
6882	16073	25542	3.85	1.0E-102	AV710738.1	EST_HUMAN	ydl3d07.r1 Soares fetal liver spleen 1N1FLS Homo sapiens cDNA clone IMAGE:67021 5'
7205	16382	25882	3.09	1.0E-102	AI905037.1	EST_HUMAN	AU124620 NT2RM4 Homo sapiens cDNA clone NT2RM4000309 5'
7205	16382	25883	3.09	1.0E-102	AI905037.1	EST_HUMAN	RC-BT074-260489-014 BT074 Homo sapiens cDNA
7840	16840	26337	2.15	1.0E-102	4507822	NT	RC-BT074-260489-014 BT074 Homo sapiens cDNA
7840	16840	26338	2.15	1.0E-102	4507822	NT	Homo sapiens UDP glycosyltransferase 2 family, polypeptide B11 (UGT2B11) mRNA
7842	17082	26810	3.51	1.0E-102	BF359243.1	EST_HUMAN	Homo sapiens UDP glycosyltransferase 2 family, polypeptide B11 (UGT2B11) mRNA
8200	17392	26875	4.71	1.0E-102	U41302.1	NT	RC8-ET0072-150600-011-F01 ET0072 Homo sapiens cDNA
8315	17418		3.74	1.0E-102	AL163280.2	NT	Human chromosome 16 creatine transporter (SLC6A8) and (CDM) paralogous genes, complete cds
8890	17785	23919	5.19	1.0E-102	AW300882.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C080
68	9384	18488	3.08	1.0E-103	BE908158.1	EST_HUMAN	xx07c12.x1 NCI_CGAP_Cc20 Homo sapiens cDNA clone IMAGE:2888038 3'
69	9384	18490	3.08	1.0E-103	BE908158.1	EST_HUMAN	601500405F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3902305 5'
100	9393	18522	9.97	1.0E-103	D87078.2	NT	601500405F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3902305 5'
213	9493	18825	3.06	1.0E-103	5453793	NT	Homo sapiens mRNA for KIAA0235 protein, partial cds
988	10218	19373	0.89	1.0E-103	AJ278348.1	NT	Homo sapiens nucleolar protein (KKE/D repeat) (NOP56) mRNA
1250	10468	19930	7.51	1.0E-103	BE77541.1	EST_HUMAN	Homo sapiens mRNA for pregnancy-associated plasma protein-E (PAPPE gene)
1578	10789	19985	2.39	1.0E-103	AF012872.1	NT	601485388F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3887876 5'
1879	11086	20276	1.08	1.0E-103	7657582	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
1944	11148	20348	1.12	1.0E-103	4502428	NT	Homo sapiens smg GDS-ASSOCIATED PROTEIN (SMAP), mRNA
1944	11148	20349	1.12	1.0E-103	4502428	NT	Homo sapiens bone morphogenetic protein 8 (osteogenic protein 2) (BMP8) mRNA
2270	11485	20886	2.28	1.0E-103	AU134991.1	EST_HUMAN	Homo sapiens bone morphogenetic protein 8 (osteogenic protein 2) (BMP8) mRNA
							AU134991 PLACE1 Homo sapiens cDNA clone PLACE1000985 5'

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2414	11805	20827	1.66	1.0E-103	AF060568.1	NT	Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds
2583	11769	20889	2.7	1.0E-103	N32770.1	EST_HUMAN	yw91408.s1 Soares_placenta_8to9weeks_2N1bHP8t5W Homo sapiens cDNA clone IMAGE:258569 3'
3033	12269		2.84	1.0E-103	BE74722.1	EST_HUMAN	601573113F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3834315 5'
3358	12586	21725	3.16	1.0E-103	AW288245.1	EST_HUMAN	UI-H-BW0-apt-h-11-Q-UI.s1 NCI CGAP_Sub56 Homo sapiens cDNA clone IMAGE:2733165 3'
3418	12843	21772	1.28	1.0E-103	AB040882.1	NT	Homo sapiens mRNA for KIAA1459 protein, partial cds
3737	12957		24.88	1.0E-103	AF023861.1	NT	Macaca mulatta cyclophilin A mRNA, complete cds
3778	12994	22110	1.05	1.0E-103	AA485683.1	EST_HUMAN	ab10412.s1 Striatogene lung (#837210) Homo sapiens cDNA clone IMAGE:840407 3' similar to contains element LTR10 repetitive element;
3980	13194	22302	2.68	1.0E-103	T23683.1	EST_HUMAN	603340 b4HB3MA-Cot109+10-Bio Homo sapiens cDNA clone b4HB3MA-Cot109+10-Bio-7 3'
4838	14025	23119	0.63	1.0E-103	BE000203.1	EST_HUMAN	601873135F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3955953 5'
5872	15188	24804	1.63	1.0E-103	AI590071.1	EST_HUMAN	tm58805.x1 NCI CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2182289 3' similar to TR:Q13769 Q13769 ANONYMOUS.;
5972	15188	24805	1.63	1.0E-103	AI590071.1	EST_HUMAN	tm58805.x1 NCI CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2182289 3' similar to TR:Q13769 Q13769 ANONYMOUS.;
6017	14507	23575	1.82	1.0E-103	6032282	NT	Homo sapiens dystrophin (muscular dystrophy, Duchenne and Becker types), includes DXS142, DXS164, DXS206, DXS230, DXS239, DXS268, DXS269, DXS270, DXS272 (DMD), transcript variant Dp427m, mRNA
6017	14507	23576	1.82	1.0E-103	6032282	NT	Homo sapiens dystrophin (muscular dystrophy, Duchenne and Becker types), includes DXS142, DXS164, DXS206, DXS230, DXS239, DXS268, DXS269, DXS270, DXS272 (DMD), transcript variant Dp427m, mRNA
6224	15405	24846	3.42	1.0E-103	BE748158.1	EST_HUMAN	601571537F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3838545 5'
6404	15585	25042	3.78	1.0E-103	AI590071.1	EST_HUMAN	tm58805.x1 NCI CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2182289 3' similar to TR:Q13769 Q13769 ANONYMOUS.;
6404	15585	25043	3.78	1.0E-103	AI590071.1	EST_HUMAN	tm58805.x1 NCI CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2182289 3' similar to TR:Q13769 Q13769 ANONYMOUS.;
6809	18004	25484	3.8	1.0E-103	6005921	NT	Homo sapiens triple functional domain (PTPRF Interacting) (TRIO), mRNA
6809	18004	25485	3.8	1.0E-103	6005921	NT	Homo sapiens triple functional domain (PTPRF Interacting) (TRIO), mRNA
7093	18270	25747	2.45	1.0E-103	Z37978.1	NT	H. sapiens mRNA for latent transforming growth factor-beta binding protein (LTBP-2)
7112	18289	25770	2.86	1.0E-103	AW983876.1	EST_HUMAN	EST375749 MAGE resequences, MAGH Homo sapiens cDNA
7148	18323	25805	14.27	1.0E-103	AI878956.1	EST_HUMAN	au51604.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2618326 5' similar to TR:Q16046 Q16046 KIAA0338;
7319	18538	28024	7.29	1.0E-103	AI792759.1	EST_HUMAN	0020408.y6 NCI CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1522283 5' similar to TR:Q62084 Q62084 PHOSPHOLIPASE C NEIGHBORING;

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7410	16822	28115	1.75	1.0E-103	11424061	NT	Homo sapiens AXL receptor tyrosine kinase (AXL), mRNA
7410	16822	28116	1.75	1.0E-103	11424061	NT	Homo sapiens AXL receptor tyrosine kinase (AXL), mRNA
7421	16832	28124	2.86	1.0E-103	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
7421	16832	28125	2.86	1.0E-103	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
7814	17128	28859	2.68	1.0E-103	AU136283.1	EST_HUMAN	AU136283 PLACE1 Homo sapiens cDNA clone PLACE1003923 5'
7882	16417	23904	5.33	1.0E-103	L43610.1	NT	Homo sapiens polycystic kidney disease (PKD1) gene, exons 27-30
8230	17359	28898	3.38	1.0E-103	BE844611.1	EST_HUMAN	768a10.x1 Soares_NSF_F8_GW_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3287610 3' similar to contains MER28.13 MER28 repetitive element
8310	17415		2.27	1.0E-103	AF224689.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
8340	17437		2.53	1.0E-103	11528281	NT	Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA
8548	17571	23992	2.58	1.0E-103	AB011399.1	NT	Homo sapiens gene for AF-8, complete cds
239	8518	18047	2.5	1.0E-104	AL037549.3	EST_HUMAN	DKFZp564H1072_r1 584 (synonym: hfr2) Homo sapiens cDNA clone DKFZp564H1072 5'
239	8518	18048	2.5	1.0E-104	AL037549.3	EST_HUMAN	DKFZp564H1072_r1 584 (synonym: hfr2) Homo sapiens cDNA clone DKFZp564H1072 5'
1853	11080	20251	1.92	1.0E-104	4502428	NT	Homo sapiens bone morphogenetic protein 8 (osteogenic protein 2) (BMP8) mRNA
2160	11358	20576	23.83	1.0E-104	AA132675.1	EST_HUMAN	z022006.s1 Strategene colon (#837204) Homo sapiens cDNA clone IMAGE:587626 3' similar to gb:Z14118_ma1 CD59 GLYCOPROTEIN PRECURSOR (HUMAN);
2170	11387	20588	10.72	1.0E-104	BE744828.1	EST_HUMAN	601577480F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3928438 5'
2337	11530	20752	10.57	1.0E-104	BF334221.1	EST_HUMAN	RC1-CT0249-110800-214-f12 CT0249 Homo sapiens cDNA
2337	11530	20753	10.57	1.0E-104	BF334221.1	EST_HUMAN	RC1-CT0249-110800-214-f12 CT0249 Homo sapiens cDNA
2400	11593	20811	7.19	1.0E-104	5031670	NT	Homo sapiens ARP2 (actin-related protein 2, yeast) homolog (ACTR2), mRNA
2487	11658	20878	4.12	1.0E-104	7682125	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
2487	11658	20879	4.12	1.0E-104	7682125	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
2823	12082	21185	13.3	1.0E-104	M34871.1	NT	Human lymphocytic antigen CD59/MEM43 mRNA, complete cds
2897	12105		2.26	1.0E-104	Y11151.1	NT	H. sapiens gene encoding phenylpyruvate tautomerase II
3230	12484	21596	1.01	1.0E-104	AU133828.1	EST_HUMAN	AU133828 OVARC1 Homo sapiens cDNA clone OVARC1000836 5'
3368	12508		2.12	1.0E-104	AA319438.1	EST_HUMAN	EST21858 Adrenal gland tumor Homo sapiens cDNA 5' end
3578	12801	21927	0.91	1.0E-104	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
3578	12801	21928	0.91	1.0E-104	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
3918	13134	22251	1.03	1.0E-104	AB032898.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
4112	13319	22419	0.85	1.0E-104	F11745.1	EST_HUMAN	HSC31A071 normalized infant brain cDNA Homo sapiens cDNA clone c-31a07
4371	13573	22688	4.33	1.0E-104	X02761.1	NT	Human mRNA for fibronectin (FN precursor)
4610	13804	22894	0.94	1.0E-104	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
4610	13804	22895	0.94	1.0E-104	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5855	15073	24484	8.42	1.0E-104	A1768787.1	EST_HUMAN	wf03b12x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2401727 3' similar to TR:Q14145 Q14145 KIAA0132 PROTEIN, contains element LTR7 repetitive element;
5855	15073	24485	8.42	1.0E-104	A1768787.1	EST_HUMAN	wf03b12x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2401727 3' similar to TR:Q14145 Q14145
5858	15281	24713	2.3	1.0E-104	BE314182.1	EST_HUMAN	KIAA0132 PROTEIN, contains element LTR7 repetitive element;
5858	15281	24714	2.3	1.0E-104	BE314182.1	EST_HUMAN	601150451F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3503220 5'
6178	15358	24798	1.82	1.0E-104	11425572	NT	601150451F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3503220 5'
6859	16048	25512	7.16	1.0E-104	AF091395.1	NT	Homo sapiens adaptor-related protein complex 2, beta 1 subunit (AP2B1), mRNA
6858	16048	25513	7.16	1.0E-104	AF091395.1	NT	Homo sapiens Trif isoform mRNA, complete cds
6880	15598	25059	5.48	1.0E-104	BF352841.1	EST_HUMAN	IL3-HT0819-080900-249-F07 HT0819 Homo sapiens cDNA
6880	15598	25060	5.48	1.0E-104	BF352841.1	EST_HUMAN	IL3-HT0819-080900-249-F07 HT0819 Homo sapiens cDNA
7108	16283	25783	5.13	1.0E-104	BE791713.1	EST_HUMAN	601581503F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3835977 5'
7108	16283	25784	5.13	1.0E-104	BE791713.1	EST_HUMAN	601581503F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3835977 5'
7193	16370	25850	4.72	1.0E-104	AU130765.1	EST_HUMAN	AU130765 NT2RP3 Homo sapiens cDNA clone NT2RP3001398 5'
7218	16395	25879	5.56	1.0E-104	U68535.1	NT	Human beta4-Integrin (ITGB4) gene, exons 18,20,21,22,23,24 and 25
7844	17036	26551	1.89	1.0E-104	BE720191.1	EST_HUMAN	RCO-HT0885-310700-021-509 HT0885 Homo sapiens cDNA
7844	17036	26552	1.89	1.0E-104	BE720191.1	EST_HUMAN	RCO-HT0885-310700-021-509 HT0885 Homo sapiens cDNA
7872	17081	26585	5.28	1.0E-104	BF684288.1	EST_HUMAN	602141215F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4302507 5'
9159	17858		1.43	1.0E-104	BE383882.1	EST_HUMAN	601312181F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3658876 5'
283	11837	18881	4.46	1.0E-105	4502188	NT	Homo sapiens amyloid beta (A4) precursor protein (protease headn-II, Alzheimer disease) (APP), mRNA
431	8288	18398	17.77	1.0E-105	4505150	NT	Homo sapiens Mals1 (mouse) homolog (MEIS1) mRNA
601	8848	18868	8.49	1.0E-105	AF032887.1	NT	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
601	8848	18867	8.49	1.0E-105	AF032887.1	NT	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
1654	10868		3.22	1.0E-105	AB020881.1	NT	Homo sapiens mRNA for cyclin B2, complete cds
1789	10869	20184	1.68	1.0E-105	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
1894	11101	20292	2.84	1.0E-105	D50918.1	NT	Human mRNA for KIAA0128 gene, partial cds
2156	11354	20572	5.87	1.0E-105	AA318389.1	EST_HUMAN	EST20809 Spleen 1 Homo sapiens cDNA 5' and similar to autoimmunogen antigen Ku, p70/p80 subunit
2280	11485		0.82	1.0E-105	BE581768.1	EST_HUMAN	601434491F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3818511 5'
2880	11862		0.89	1.0E-105	AA584808.1	EST_HUMAN	no10405.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100285 3'
2868	12204		3.44	1.0E-105	AJ228041.1	NT	Homo sapiens 659 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
3298	12530	21661	1.73	1.0E-105	BF347753.1	EST_HUMAN	602022585F1 NCI_CGAP_Bim87 Homo sapiens cDNA clone IMAGE:4158143 5'
3298	12530	21662	1.73	1.0E-105	BF347753.1	EST_HUMAN	602022585F1 NCI_CGAP_Bim87 Homo sapiens cDNA clone IMAGE:4158143 5'
3325	12554	21690	1.01	1.0E-105	7304922	NT	Homo sapiens bromodomain adjacent to zinc finger domain, 2B (BAZ2B), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3325	12554	21691	1.01	1.0E-105	7304922	NT	Homo sapiens bromodomain adjacent to zinc finger domain, 2B (BAZ2B), mRNA
4076	13285	22363	2.86	1.0E-105	AW981688.1	EST_HUMAN	EST373761 IMAGE:3850156 5'
4755	13946	23046	0.64	1.0E-105	BE888881.1	EST_HUMAN	601445623F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3850156 5'
4755	13946	23047	0.64	1.0E-105	BE888881.1	EST_HUMAN	601445623F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3850156 5'
4967	14144		5.22	1.0E-105	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C008
5137	14315	23406	0.96	1.0E-105	AB018339.1	NT	Homo sapiens mRNA for KIAA0798 protein, partial cds
5195	14371	23458	0.69	1.0E-105	AW986015.1	EST_HUMAN	EST378088 IMAGE:3850156 5'
6078	14526	23548	3.33	1.0E-105	11419196	NT	Homo sapiens GTPase activating protein-like (GAPL), mRNA
6078	14526	23547	3.33	1.0E-105	11419196	NT	Homo sapiens GTPase activating protein-like (GAPL), mRNA
6473	15670	25141	8.43	1.0E-105	T05087.1	EST_HUMAN	EST02875 Fetal brain, Striatum (cat336206) Homo sapiens cDNA clone HFBGR32
6785	15680	25440	3.95	1.0E-105	AW016879.1	EST_HUMAN	UIH-B10p-ab-b-12-0-UI.1 NCI CGAP Sub2 Homo sapiens cDNA clone IMAGE:2711782 3'
7508	16712	26200	6.62	1.0E-105	AF254822.1	NT	Homo sapiens SMARCA4 isoform (SMARCA4) gene, complete cds, alternatively spliced
7782	16977	26490	2.18	1.0E-105	D63548.1	NT	Homo sapiens COL4A6 gene for $\alpha 6(V)$ collagen, exon 31
7830	17022	26537	2.26	1.0E-105	77058936	NT	Homo sapiens Ran binding protein 11 (LOC51194), mRNA
8115	17249	26769	2.41	1.0E-105	AW027554.1	EST_HUMAN	w7407.x1 Soares_NHFT Homo sapiens cDNA clone IMAGE:2535301 3' similar to TR:P87892
154	8436		1.85	1.0E-108	AW503208.1	EST_HUMAN	P87892 PROTEASE:
210	8490	18623	1.58	1.0E-108	AI565086.1	EST_HUMAN	UI-HF-BND-akt-g-07-q-UI.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078348 5'
548	8756	18924	1.88	1.0E-106	AW965556.1	EST_HUMAN	iq78c01.x1 NCI CGAP_UH1 Homo sapiens cDNA clone IMAGE:2216008 3'
611	8858	18977	1.87	1.0E-108	J00148.1	NT	EST377629 IMAGE:3850156 5'
612	8868	18977	2.89	1.0E-108	J00148.1	NT	Human dihydrofolate reductase pseudogene (psl-hd1)
1511	10725	18987	1.01	1.0E-108	AF145712.1	NT	Human dihydrofolate reductase pseudogene (psl-hd1)
1676	10888	20074	4.47	1.0E-106	U48724.1	NT	Homo sapiens soluble neuropilin-1 mRNA, complete cds
1684	10908	20062	1.72	1.0E-106	U04510.1	NT	Human epidermal growth factor receptor (EGFR) precursor-mRNA, exon 4, partial cds
1772	10982	20172	5.79	1.0E-106	AA527448.1	EST_HUMAN	Homo sapiens type IV collagen alpha 6 chain (COL4A6) gene, exon 41
1772	10982	20173	5.79	1.0E-106	AA527448.1	EST_HUMAN	ng41c05.s1 NCI CGAP_Co3 Homo sapiens cDNA clone IMAGE:937352 3' similar to contains element
2263	11478	20700	7.27	1.0E-106	4504184	NT	LTR3 repetitive element;
2489	11680	20881	4.02	1.0E-106	AF003528.1	NT	LTR3 repetitive element;
2581	11747	20867	1.21	1.0E-106	U04075.2	NT	Homo sapiens glutathione S-transferase theta 1 (GSTT1), mRNA
2583	11749	20869	1.18	1.0E-106	BE260201.1	EST_HUMAN	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
2713	11892	21110	9.2	1.0E-106	AI276528.1	EST_HUMAN	Homo sapiens sperm membrane protein BS-63 mRNA, complete cds
							601148783F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3502481 5'
							q178h10.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1878307 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2777	10648	19821	2.45	1.0E-106	4504184	NT	Homo sapiens glutathione S-transferase theta 1 (GSTT1), mRNA
2777	10648	19822	2.45	1.0E-106	4504184	NT	Homo sapiens glutathione S-transferase theta 1 (GSTT1), mRNA
2828	12067	21188	2.2	1.0E-106	BE384296.1	EST_HUMAN	601272875F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3613818 5'
2892	12129	21263	6.26	1.0E-106	AB037747.1	NT	Homo sapiens mRNA for KIAA1326 protein, partial cds
2892	12129	21264	6.26	1.0E-106	AB037747.1	NT	Homo sapiens mRNA for KIAA1326 protein, partial cds
3145	12380	21511	2.8	1.0E-106	8922965	NT	Homo sapiens hypothetical protein FLJ11273 (FLJ11273), mRNA
3145	12380	21512	2.8	1.0E-106	8922965	NT	Homo sapiens hypothetical protein FLJ11273 (FLJ11273), mRNA
3352	12580	21720	0.65	1.0E-106	AB008681.1	NT	Homo sapiens gene for activin receptor type IIB, complete cds
3790	13008	22123	0.99	1.0E-106	AF001445.1	NT	Homo sapiens core binding factor alpha1 subunit (CBFA1) gene, exon 2
4015	13227	22328	10.33	1.0E-106	AW974650.1	EST_HUMAN	EST386875 MAGC resequences, MAGN Homo sapiens cDNA
4015	13227	22329	10.33	1.0E-106	AW974650.1	EST_HUMAN	EST386875 MAGC resequences, MAGN Homo sapiens cDNA
4034	13244	22347	1.34	1.0E-106	5729729	NT	Homo sapiens API5-like 1 (API5L1), mRNA
4601	13785	22885	0.73	1.0E-106	BE144286.1	EST_HUMAN	MRO-HT0165-140200-008-d10 HT0165 Homo sapiens cDNA
4918	14106	23200	1.48	1.0E-106	U31520.1	NT	Human alpha mannosidase II mRNA, complete cds
5381	14610	23722	2.35	1.0E-106	AA781155.1	EST_HUMAN	aj24609.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391225 3' similar to gb:X12433 PROTEIN
5708	14927	24322	14.75	1.0E-106	BF679574.1	EST_HUMAN	PHPSP1-2 (HUMAN);
5836	15053	24460	18.72	1.0E-106	11545913	NT	602154012F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4285067 5'
5836	15053	24461	18.72	1.0E-106	11545913	NT	Homo sapiens xylosyltransferase II (XT2), mRNA
6243	15424	24885	4.9	1.0E-106	AA663779.1	EST_HUMAN	Homo sapiens xylosyltransferase II (XT2), mRNA
6261	15442	24881	4.59	1.0E-106	11429617	NT	ae72e07.s1 Strabagene schizo brain S11 Homo sapiens cDNA clone IMAGE:969732 3' similar to gb:X65873
8341	15521	24968	8.36	1.0E-106	11425503	NT	KINESIN HEAVY CHAIN (HUMAN);
8341	15521	24969	8.36	1.0E-106	11425503	NT	Homo sapiens XPMC2 protein (LOC57109), mRNA
6458	15655	25125	6.43	1.0E-106	BE741408.1	EST_HUMAN	Homo sapiens sorting nexin 11 (SNX11), mRNA
6458	15655	25126	6.43	1.0E-106	BE741408.1	EST_HUMAN	Homo sapiens sorting nexin 11 (SNX11), mRNA
6517	15713	25178	2.23	1.0E-106	AI523066.1	EST_HUMAN	601594333F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948483 5'
6682	15877	25336	2.64	1.0E-106	AI654123.1	EST_HUMAN	601594333F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948483 5'
6816	16011	25474	2.41	1.0E-106	AA825307.1	EST_HUMAN	ar68ae07.x1 Barstead aorta HPLR86 Homo sapiens cDNA clone IMAGE:2127732 3' similar to gb:X06233
6816	16011	25475	2.41	1.0E-106	AA825307.1	EST_HUMAN	CALGRANULIN B (HUMAN);
7148	16325	25808	6.74	1.0E-106	AA604417.1	EST_HUMAN	iy62a05.x1 NCI_CGAP_Kd11 Homo sapiens cDNA clone IMAGE:2283632 3' similar to SW:ICA6_HUMAN
7148	16325	25809	6.74	1.0E-106	AA604417.1	EST_HUMAN	Q05084 69 KD ISLET CELL AUTOANTIGEN ;
							oc67e08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1354790 3'
							oc67e08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1354790 3'
							np57b10.s1 NCI_CGAP_B12 Homo sapiens cDNA clone IMAGE:1130395 3'
							np57b10.s1 NCI_CGAP_B12 Homo sapiens cDNA clone IMAGE:1130395 3'

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7165	16342	25821	2.68	1.0E-108	AW363298.1	EST_HUMAN	RC0-CT0318-201199-031-11 CT0318 Homo sapiens cDNA
7221	16398	25882	2.78	1.0E-108	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
7472	16880	26182	6.77	1.0E-108	BF032755.1	EST_HUMAN	601453481F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3857368 5'
7472	16880	26183	6.77	1.0E-108	BF032755.1	EST_HUMAN	601453481F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3857368 5'
7629	16830	26327	2.56	1.0E-108	J05200.1	NT	Human ryanodine receptor mRNA, complete cds
7629	16830	26328	2.56	1.0E-108	J05200.1	NT	Human ryanodine receptor mRNA, complete cds
7948	17088	26815	2.41	1.0E-108	BE257385.1	EST_HUMAN	601109219F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3349897 5'
8077	17212	26743	1.82	1.0E-108	BE010882.1	EST_HUMAN	RC5-BN0192-100500-021-B02 BN0192 Homo sapiens cDNA
8077	17212	26744	1.82	1.0E-108	BE010882.1	EST_HUMAN	RC5-BN0192-100500-021-B02 BN0192 Homo sapiens cDNA
8384	18161		4.43	1.0E-108	AW410405.1	EST_HUMAN	h05h11.1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2861644 5'
8618	17616	23968	2.49	1.0E-108	BE894488.1	EST_HUMAN	601433087F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918524 5'
8618	17616	23968	2.49	1.0E-108	BE894488.1	EST_HUMAN	601433087F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918524 5'
8843	17762		5.27	1.0E-108	BE695905.1	EST_HUMAN	RC1-CT0249-080800-024-005 CT0249 Homo sapiens cDNA
240	9518		3.88	1.0E-107	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
269	9544		1.37	1.0E-107	X00459.1	NT	Human IFNAR gene for interferon alpha/beta receptor
638	9881	19005	1.89	1.0E-107	AF155103.1	NT	Homo sapiens NY-REN-25 antigen mRNA, partial cds
823	10061	19213	1.08	1.0E-107	X00459.1	NT	Human IFNAR gene for interferon alpha/beta receptor
898	10131	19283	1.89	1.0E-107	X00459.1	NT	Human IFNAR gene for interferon alpha/beta receptor
976	10208	19363	11.69	1.0E-107	AF154121.1	NT	Homo sapiens sodium-dependent high-affinity dicarboxylate transporter (NADC3) mRNA, complete cds
1285	10500	19861	1.31	1.0E-107	AB032253.1	NT	Homo sapiens BAZ1B mRNA for bromodomain adjacent to zinc finger domain 1B, complete cds
1550	10764	19938	4.8	1.0E-107	BF087405.1	EST_HUMAN	QV2-HT0540-120800-358-e05 HT0540 Homo sapiens cDNA
1724	10936	20110	5.69	1.0E-107	AF138275.1	NT	Homo sapiens cathepsin Z precursor (CTSZ) gene, exon 3
2175	11372	20594	1.07	1.0E-107	U13728.1	NT	Human dipeptidyl peptidase IV (CD26) gene, exon 20
2330	11523	20745	10.58	1.0E-107	AW842451.1	EST_HUMAN	PM1-CN0031-190100-001-403 CN0031 Homo sapiens cDNA
2330	11523	20746	10.58	1.0E-107	AW842451.1	EST_HUMAN	PM1-CN0031-190100-001-403 CN0031 Homo sapiens cDNA
2500	11689	20908	2.58	1.0E-107	BE732460.1	EST_HUMAN	601567618F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842308 5'
2500	11689	20910	2.56	1.0E-107	BE732460.1	EST_HUMAN	601567618F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842308 5'
2987	12205	21340	3.76	1.0E-107	AW842451.1	EST_HUMAN	PM1-CN0031-190100-001-403 CN0031 Homo sapiens cDNA
2987	12205	21341	3.76	1.0E-107	AW842451.1	EST_HUMAN	PM1-CN0031-190100-001-403 CN0031 Homo sapiens cDNA
3065	12301	21425	3.94	1.0E-107	5802087	NT	Homo sapiens SMT3 (suppressor of mit two 3, yeast) homolog 2 (SMT3H2), mRNA
3816	13034	22145	4.53	1.0E-107	AF020671.1	NT	Homo sapiens myotubularin (MTM1) gene, exon 9
5587	14821	24188	2.68	1.0E-107	BE687469.1	EST_HUMAN	601442568F1 NIH_MGC_85 Homo sapiens cDNA clone IMAGE:3846494 5'
6239	16420	24860	1.82	1.0E-107	AW503913.1	EST_HUMAN	UIHF-BN0-alf-c-08-0-UI.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3076310 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6239	16420	24861	1.82	1.0E-107	AW503913.1	EST_HUMAN	UI-HF-BNO-af-c-08-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3076310 5'
7263	16512	26004	3.78	1.0E-107	AI392850.1	EST_HUMAN	U10406.x1 NCL_CGAP_GLL1 Homo sapiens cDNA clone IMAGE:2108363 3' similar to SW:AACT_DICD1
7520	16725	26216	1.91	1.0E-107	L49141.1	NT	P05085 ALPHA-ACTININ 3, NON MUSCULAR;
7531	16736	26226	2.86	1.0E-107	BF666511.1	EST_HUMAN	Homo sapiens neuroendocrine-specific protein (NSP) gene, exon 4
7688	17058	26579	4.19	1.0E-107	BE540550.1	EST_HUMAN	602123963F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:4281039 5'
7931	16407	25891	4.65	1.0E-107	11419701	NT	601066681F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3452829 5'
7931	16407	25892	4.65	1.0E-107	11419701	NT	Homo sapiens HSPC049 protein (HSPC049), mRNA
8450	18293		5.84	1.0E-107	AA001415.1	EST_HUMAN	Homo sapiens HSPC049 protein (HSPC049), mRNA
8476	18147		1.52	1.0E-107	11418318	NT	z645601.s1 Soares retina N2b-4HR Homo sapiens cDNA clone IMAGE:361944 3' similar to contains THR.b1
181	9461		1.35	1.0E-108	AA341834.1	EST_HUMAN	THR repetitive element;
962	10195	16950	1.46	1.0E-108	BE266042.1	EST_HUMAN	Homo sapiens G-2 and S-phase expressed 1 (GTSE1), mRNA
1272	10487	19845	3.63	1.0E-108	Y18000.1	NT	EST47363 Fetal muscle Homo sapiens cDNA 5' end
2046	11247	20457	2.49	1.0E-108	BF026728.1	EST_HUMAN	601177018F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532348 5'
							Homo sapiens NF2 gene
							601671914F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954839 5'
2391	11584	20802	107.38	1.0E-108	BE206894.1	EST_HUMAN	b25b10.x1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2963898 3' similar to gb:X63777 60S
3323	12552	21686	0.71	1.0E-108	AF032897.1	NT	RIBOSOMAL PROTEIN L23 (HUMAN); gb:J05277 Mouse hexokinase mRNA, complete cds (MOUSE);
3323	12552	21687	0.71	1.0E-108	AF032897.1	NT	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
3802	13020	22132	1.04	1.0E-108	5453855	NT	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
4139	13345	22445	1.37	1.0E-108	AW684438.1	EST_HUMAN	Homo sapiens pericentriolar material 1 (PCM1) mRNA
4525	13721	22818	6.72	1.0E-108	U72861.1	NT	h12a11.x1 NCL_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2972060 3' similar to SW:3BP1_MOUSE
4525	13721	22817	6.72	1.0E-108	U72861.1	NT	P55194 SH3-BINDING PROTEIN 3BP-1;
4818	14007	23107	3.11	1.0E-108	7681979	NT	Human hepatocyte nuclear factor 4-alpha gene, exon 2
4939	14128	23222	0.77	1.0E-108	AW504798.1	EST_HUMAN	Human hepatocyte nuclear factor 4-alpha gene, exon 2
4939	14128	23222	0.77	1.0E-108	AW504798.1	EST_HUMAN	Homo sapiens KIAA0187 gene product (KIAA0187), mRNA
4939	14128	23222	0.77	1.0E-108	AW504798.1	EST_HUMAN	UI-HF-BNO-af-c-04-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3080168 5'
5165	14344	23433	0.99	1.0E-108	5031624	NT	Homo sapiens PSN1 gene, alternative transcript
5197	14373	23460	1.06	1.0E-108	Y12490.1	NT	Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA
5454	14680	23840	3.03	1.0E-108	BE669016.1	EST_HUMAN	Homo sapiens mRNA for Golgi-associated microtubule-binding protein (GMAP-210)
5454	14680	23841	3.03	1.0E-108	BE669016.1	EST_HUMAN	601444922F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3848980 5'
5729	14948	24346	5.76	1.0E-108	AF264717.1	NT	601444922F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3848980 5'
							Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP2 mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5729	14948	24347	5.76	1.0E-108	AF264717.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP2 mRNA, complete cds
6148	15330	24788	5.4	1.0E-108	11431857	NT	Homo sapiens G protein-coupled receptor, family C, group 5, member B (GPCR5B), mRNA
6269	15449	24888	2.13	1.0E-108	4758333	NT	Homo sapiens delta-6 fatty acid desaturase (FADS6), mRNA
6485	15882		2.74	1.0E-108	AF083500.1	NT	Homo sapiens connective tissue growth factor-like protein precursor, mRNA, complete cds
7260	15591	25052	2.23	1.0E-108	BE535227.1	EST_HUMAN	601058769F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3445361 5'
7404	14373	23460	1.9	1.0E-108	Y12490.1	NT	Homo sapiens mRNA for Golgi-associated microtubule-binding protein (GMAP-210)
7832	16833	26330	1.84	1.0E-108	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
7820	17013	26527	5.69	1.0E-108	AW068185.1	EST_HUMAN	EST378258 MAGE resequences, MAGI Homo sapiens cDNA
7810	17125		2.41	1.0E-108	11441465	NT	Homo sapiens G protein-coupled receptor 48 (GPR48), mRNA
7868	17145	26879	1.7	1.0E-108	D93539.1	NT	Homo sapiens COL4A8 gene for alpha(V) collagen, exon 23
8633	17623	23973	3.18	1.0E-108	AK024447.1	NT	Homo sapiens mRNA for FLJ00337 protein, partial cds
8040	17882		6.89	1.0E-108	BF346358.1	EST_HUMAN	602018571F1 NCI CGAP_Bim67 Homo sapiens cDNA clone IMAGE:4154297 5'
44	9340	19447	1.37	1.0E-109	AW803116.1	EST_HUMAN	IL2-JM0077-260400-079-D08 UM0077 Homo sapiens cDNA
67	9382	19486	2.74	1.0E-109	D68974.1	NT	Human mRNA for KIAA0220 gene, partial cds
223	9502	19833	0.83	1.0E-109	11422488	NT	Homo sapiens hypothetical protein FLJ11316 (FLJ11316), mRNA
232	9510	19838	6.14	1.0E-109	11438391	NT	Homo sapiens reticulocalbin 1, EF-hand calcium binding domain (RCN1), mRNA
473	9728	19858	3.14	1.0E-109	4507712	NT	Homo sapiens tetratricopeptide repeat domain 2 (TTC2) mRNA
605	9852	19871	16.2	1.0E-109	AB023216.1	NT	Homo sapiens mRNA for KIAA0999 protein, partial cds
605	9852	19872	16.2	1.0E-109	AB023216.1	NT	Homo sapiens mRNA for KIAA0999 protein, partial cds
1210	10429	19585	41.98	1.0E-109	M28698.1	NT	Homo sapiens mRNA for KIAA0999 protein, partial cds
1211	10429	19585	22.4	1.0E-109	M28698.1	NT	Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds
1528	10742	19914	1.35	1.0E-109	BE283673.1	EST_HUMAN	Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds
1528	10742	19915	1.35	1.0E-109	BE283673.1	EST_HUMAN	601186922F2 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2669638 5'
1840	11048	20238	5.02	1.0E-109	D13843.2	NT	601186922F2 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2669638 5'
2206	11403	20628	4.37	1.0E-109	AL163284.2	NT	Homo sapiens mRNA for KIAA0018 protein, partial cds
2215	11412	20638	2.87	1.0E-109	Y17123.1	NT	Homo sapiens chromosome 21 segment HS21C084
2585	11771	20891	3.63	1.0E-109	AI022328.1	EST_HUMAN	Homo sapiens SNF5/INI1 gene, exon 8
2585	11771	20892	3.53	1.0E-109	AI022328.1	EST_HUMAN	ow85a01.x1 Soares fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1654536 3' similar to TR:002197 002197 CIRCULATING CATHODIC ANTIGEN. ;
2588	11772	20893	2.15	1.0E-109	4504208	NT	ow85a01.x1 Soares fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1654536 3' similar to TR:002197 002197 CIRCULATING CATHODIC ANTIGEN. ; Homo sapiens guanylate cyclase activator 1A (retina) (GUCA1A) mRNA

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
							J21816F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J21816 5' similar to ZINC
3023	12559	21387	1.32	1.0E-109	N85190.1	EST_HUMAN	CHN3-NN0009-180400-150-110 NN0009 Homo sapiens cDNA
3366	12594	21733	1.33	1.0E-109	AW893192.1	EST_HUMAN	CHN3-NN0009-180400-150-110 NN0009 Homo sapiens cDNA
3368	12594	21734	1.33	1.0E-109	AW893192.1	EST_HUMAN	CHN3-NN0009-180400-150-110 NN0009 Homo sapiens cDNA
3491	12715	21851	1.1	1.0E-109	AF240698.1	NT	Homo sapiens retinol dehydrogenase homodog isoform-1 (RDH) mRNA, complete cds
3828	13048		1.43	1.0E-109	BE148144.1	EST_HUMAN	MRO-HT0209-110400-108-a04 HT0209 Homo sapiens cDNA
							ts98c08.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2239330 3' similar to WP:F53A2.8
4129	13335	22434	4.35	1.0E-109	AI655417.1	EST_HUMAN	CE16100 ;
							nu83c12.s1 NCI_CGAP_P122 Homo sapiens cDNA clone IMAGE:1218262 3' similar to SW:GTT2_HUMAN
4144	13350	22450	1.02	1.0E-109	AA682274.1	EST_HUMAN	P30712 GLUTATHIONE S-TRANSFERASE THETA 2 ;
							nu83c12.s1 NCI_CGAP_P122 Homo sapiens cDNA clone IMAGE:1218262 3' similar to SW:GTT2_HUMAN
4144	13350	22451	1.02	1.0E-109	AA682274.1	EST_HUMAN	P30712 GLUTATHIONE S-TRANSFERASE THETA 2 ;
4368	13598	22700	2.55	1.0E-109	4504208	NT	Homo sapiens guanylate cyclase activator 1A (retina) (GUCA1A) mRNA
4800	13794	22884	1.28	1.0E-109	7682083	NT	Homo sapiens KIAA0377 gene product (KIAA0377), mRNA
5084	14284	23350	0.72	1.0E-109	BE283973.1	EST_HUMAN	6011186922F2 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2859838 5'
5084	14284	23351	0.72	1.0E-109	BE283973.1	EST_HUMAN	6011186922F2 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2859838 5'
5340	14570	23845	3.5	1.0E-109	5174822	NT	Homo sapiens placental protein 11 (serine proteinase) (P11) mRNA
6319	15501	24948	3.53	1.0E-109	11432574	NT	Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA
6320	15502	24947	5.4	1.0E-109	BF182707.1	EST_HUMAN	601809495F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040279 5'
6320	15502	24948	5.4	1.0E-109	BF182707.1	EST_HUMAN	601809495F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040279 5'
6882	15887	25348	12.39	1.0E-109	BE787540.1	EST_HUMAN	601479417F1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:3882124 5'
6882	15887	25347	12.39	1.0E-109	BE787540.1	EST_HUMAN	601479417F1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:3882124 5'
7385	16598	26087	25.47	1.0E-109	BF684831.1	EST_HUMAN	601479417F1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:3882124 5'
7638	16744	26237	2.35	1.0E-109	7662279	NT	602080724F2 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4245341 5'
7638	16744	26238	2.35	1.0E-109	7662279	NT	602080724F2 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4245341 5'
7685	16884	26392	1.87	1.0E-109	AU121370.1	EST_HUMAN	Homo sapiens KIAA0744 gene product: histone deacetylase 7 (KIAA0744), mRNA
7909	17124	26955	2.23	1.0E-109	4502838	NT	Homo sapiens KIAA0744 gene product: histone deacetylase 7 (KIAA0744), mRNA
							AU121370 HEMBB1 Homo sapiens cDNA clone HEMBB1002890 5'
							Homo sapiens Chediak-Higashi syndrome 1 (CHS1) mRNA
7945	17085	26814	6.23	1.0E-109	W18510.1	EST_HUMAN	z08b12.r1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:301439 5' similar to
8628	11412	20636	2.3	1.0E-109	Y17123.1	NT	PIR:S43968 S43968.p54-beta stress-activated protein kinases - rat ;
8761	11412	20636	1.98	1.0E-109	Y17123.1	NT	Homo sapiens SNF5/INI1 gene, exon 6
8883	17778	23944	3.23	1.0E-109	AB011399.1	NT	Homo sapiens SNF5/INI1 gene, exon 6
3	9300	18402	1.41	1.0E-110	7549804	NT	Homo sapiens gene for AF-6, complete cds
39	9335	18441	4.02	1.0E-110	5803073	NT	Homo sapiens delodinease, iodothyronine, type II (DIO2), transcript variant 2, mRNA
							Homo sapiens leucine-zipper-like transcriptional regulator, 1 (LZTR1), mRNA

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Table 4
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
39	9335	18442	4.02	1.0E-110	5803073	NT	Homo sapiens leucine-zipper-like transcriptional regulator, 1 (LZTR1), mRNA
109	9300	18402	1.41	1.0E-110	7549804	NT	Homo sapiens deiodinase, iodothyronine, type II (DIO2), transcript variant 2, mRNA
299	9572	18705	0.65	1.0E-110	D87291.1	NT	Human mRNA for inward rectifier potassium channel, complete cds
533	9784	18907	0.95	1.0E-110	U84550.1	NT	Human dystrobrevin (DTN) gene, exon 20
1188	10409	19563	0.8	1.0E-110	5031620	NT	Homo sapiens calcitonin receptor-like (CALCRL) mRNA
1286	10501	19662	2.39	1.0E-110	AB032253.1	NT	Homo sapiens BAZ1B mRNA for bromodomain adjacent to zinc finger domain 1B, complete cds
1889	11096	20287	1.11	1.0E-110	BE379477.1	EST_HUMAN	601237545F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609683 5'
2025	11226		1.68	1.0E-110	BF50896.1	EST_HUMAN	U1-H-B14-aos-b-05-0-U1.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085784 3'
2783	12033		0.97	1.0E-110	4503098	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
2996	10501	19682	1.14	1.0E-110	AB032253.1	NT	Homo sapiens BAZ1B mRNA for bromodomain adjacent to zinc finger domain 1B, complete cds
3052	12288		1.19	1.0E-110	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
3158	12383	21527	2.68	1.0E-110	11438041	NT	Homo sapiens pregnancy-zone protein (PZP), mRNA
3158	12393	21528	2.68	1.0E-110	11436041	NT	Homo sapiens pregnancy-zone protein (PZP), mRNA
4185	13389	22488	2.18	1.0E-110	M15918.1	NT	Human autoimmunity antigen small nuclear ribonucleoprotein E pseudogene
4836	13830	22917	2.23	1.0E-110	A1017213.1	EST_HUMAN	ou32b10.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:1627963 3' similar to
4856	13850	22945	2.83	1.0E-110	AU117812.1	EST_HUMAN	SW/N121_RAT_P52591 NUCLEAR ENVELOPE PORE MEMBRANE PROTEIN POM 121 ;
4993	14180		1.54	1.0E-110	7662441	NT	Homo sapiens KIAA1002 protein (KIAA1002), mRNA
5324	14558	23828	2.32	1.0E-110	BE299406.1	EST_HUMAN	601118710F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028538 5'
5548	14772	24139	7.74	1.0E-110	11419323	NT	Homo sapiens hypothetical protein FLJ10300 (FLJ10300), mRNA
5548	14772	24140	7.74	1.0E-110	11419323	NT	Homo sapiens hypothetical protein FLJ10300 (FLJ10300), mRNA
5971	18068	24803	4.49	1.0E-110	M55112.1	NT	Human cystic fibrosis transmembrane conductance regulator (CFTR) gene, exon 7
6262	15443	24882	9.01	1.0E-110	AV714276.1	EST_HUMAN	AV714276 DCB Homo sapiens cDNA clone DCBCGE01 5'
6262	15443	24883	9.01	1.0E-110	AV714276.1	EST_HUMAN	AV714276 DCB Homo sapiens cDNA clone DCBCGE01 5'
6278	15458	24899	2.8	1.0E-110	AB020875.1	NT	Homo sapiens mRNA for KIAA0868 protein, partial cds
6949	16127	25595	3.81	1.0E-110	AW838394.1	EST_HUMAN	GV2-LT0053-020400-119-e04 LT0053 Homo sapiens cDNA
7178	16353	25831	4.68	1.0E-110	11432732	NT	Homo sapiens galactokinase 2 (GALK2), mRNA
7333	16549	26039	4.23	1.0E-110	Y12337.1	NT	H.sapiens mRNA for myotonic dystrophy protein kinase like protein
7538	16743	26235	4.26	1.0E-110	BE734357.1	EST_HUMAN	601565604F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3840433 5'
7538	16743	26236	4.26	1.0E-110	BE734357.1	EST_HUMAN	601565604F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3840433 5'
7979	18414	25901	2.82	1.0E-110	AA446529.1	EST_HUMAN	zw67g02.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:781298 5' similar to TR:G1145816
8342	17439		3.73	1.0E-110	BE897218.1	EST_HUMAN	G1145816 FKBP54 ;
							601439784F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924548 5'

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8469	17522		8.8	1.0E-110	AW082258.1	EST_HUMAN	IL0-BT0163-040899-094-g10 BT0163 Homo sapiens cDNA
8725	17677		2.84	1.0E-110	AB011389.1	NT	Homo sapiens gene for AF-6, complete cds
8898	18305		3.72	1.0E-110	BF384548.1	EST_HUMAN	PM3-NN1082-140800-006-f12 NN1082 Homo sapiens cDNA
9158	11228		1.83	1.0E-110	BF508898.1	EST_HUMAN	UJ-H-B14-act-g-04-0-UJ.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085784 3'
178	9458		27.48	1.0E-111	U43701.1	NT	Human ribosomal protein L23a mRNA, complete cds
201	9481	18814	0.76	1.0E-111	4758807	NT	Homo sapiens ras GTPase activating protein-like (NGAP) mRNA
742	9883		2.18	1.0E-111	BF035327.1	EST_HUMAN	801458531F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3882086 5'
751	9882	18136	4.09	1.0E-111	8383092	NT	Homo sapiens cat eye syndrome critical region gene 1 (CECR1), mRNA
935	10168	18325	3.26	1.0E-111	M25142.1	NT	Human cardiac alpha-myosin heavy chain (MYH8) gene, exons 32 to 34
3878	12899	22019	0.93	1.0E-111	6912841	NT	Homo sapiens sex comb on midleg homolog 1 (SCMH1), mRNA
3878	12899	22020	0.93	1.0E-111	6912841	NT	Homo sapiens sex comb on midleg homolog 1 (SCMH1), mRNA
4153	13359	22460	1.86	1.0E-111	7081569	NT	Homo sapiens DKFZP434D156 protein (DKFZP434D156), mRNA
4321	13522	22817	4.54	1.0E-111	K02288.1	NT	Human enkephalin B (enkeB) gene, exon 4 and 3' flank and complete cds
4752	13943	23045	1.01	1.0E-111	4506778	NT	Homo sapiens phosphotyrosine kinase, alpha 1 (muscle) (PHKA1), mRNA
6271	15451	24890	2.93	1.0E-111	BF386228.1	EST_HUMAN	IL2-NT0101-280700-114-E03 NT0101 Homo sapiens cDNA
6338	15734	25188	3.4	1.0E-111	U88533.1	NT	Human beta4-integrin (ITGB4) gene, exon 13
6720	15915		6.95	1.0E-111	BF214902.1	EST_HUMAN	Human beta4-integrin (ITGB4) gene, exon 13
6740	15935	25395	18.91	1.0E-111	X17033.1	NT	Human mRNA for Integrin alpha-2 subunit
6740	15935	25398	18.91	1.0E-111	X17033.1	NT	Human mRNA for Integrin alpha-2 subunit
6800	15995	28453	4.59	1.0E-111	AF091395.1	NT	Homo sapiens Tric isoform mRNA, complete cds
7124	18301	25782	2.58	1.0E-111	AA504180.1	EST_HUMAN	aa58g02.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:825170 3' similar to gb:L09235
7158	18335	25818	7.75	1.0E-111	AA131248.1	EST_HUMAN	VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A, UBIQUITOUS (HUMAN);
7613	18816	26312	5.35	1.0E-111	U88159.1	NT	z31601.r1 Soares_pregnant_uterus_NHPU Homo sapiens cDNA clone IMAGE:503545 5'
8299	17407	26832	4.66	1.0E-111	11417901	NT	Human thrombopoietin receptor (MPL) gene, exons 1,2,3,4,5 and 6
8880	17783	23938	1.5	1.0E-111	AV708482.1	EST_HUMAN	Homo sapiens meningioma (disrupted in balanced translocation) 1 (MN1), mRNA
8882	18098	23804	2.08	1.0E-111	W25882.1	EST_HUMAN	AV708482 ADC Homo sapiens cDNA clone ADCAOB08 5'
9128	14505	23589	1.53	1.0E-111	AB035358.1	NT	72C9 Human retina cDNA Tsp5091-cleaved sublibrary Homo sapiens cDNA not directional
614	9859	18878	0.98	1.0E-112	4501854	NT	Homo sapiens mRNA for neuradin-like protein, complete cds
616	9861	18880	6.43	1.0E-112	U28103.1	NT	Homo sapiens acyl-Coenzyme A carboxylase beta (ACACB), mRNA
616	9861	18881	6.43	1.0E-112	U28103.1	NT	Homo sapiens sterologenic acute regulatory protein (SAR) gene, exon 6
638	9883	19007	1.7	1.0E-112	BF509039.1	EST_HUMAN	Human sterologenic acute regulatory protein (SAR) gene, exon 5
638	9883	19008	1.7	1.0E-112	BF509039.1	EST_HUMAN	UJ-H-B14-act-g-04-0-UJ.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3086023 3'
1009	10240	19392	3.97	1.0E-112	AF157623.1	NT	UJ-H-B14-act-g-04-0-UJ.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3086023 3'
							Homo sapiens HTRA serine protease (PRSS11) gene, complete cds

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1089	10295	19444	1.67	1.0E-112	P52742	SWISSPROT	ZINC FINGER PROTEIN 135
1659	10872	20054	4.44	1.0E-112	7862126	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
1659	10872	20055	4.44	1.0E-112	7862125	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
2473	11684	20883	3.23	1.0E-112	BE868659.1	EST_HUMAN	601442874F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3846858 5'
3043	12280		0.82	1.0E-112	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
3211	12445	21577	1.35	1.0E-112	BE083092.1	EST_HUMAN	RC2-BT0842-030400-021-009 BT0842 Homo sapiens cDNA
3211	12445	21578	1.35	1.0E-112	BE083092.1	EST_HUMAN	RC2-BT0842-030400-021-009 BT0842 Homo sapiens cDNA
3338	12565	21703	0.61	1.0E-112	AI828511.1	EST_HUMAN	wk46512.x1 NCI_CGAP_P122 Homo sapiens cDNA clone IMAGE:2418335 3' similar to gb:M81650_ma1
3863	13078	22185	0.78	1.0E-112	BE076073.1	EST_HUMAN	SEMNOGELIN 1 PROTEIN PRECURSOR (HUMAN);
4604	13768	22888	0.62	1.0E-112	4504116	NT	MIR2-BT0590-090300-113-009 BT0590 Homo sapiens cDNA
4763	13953	23053	5	1.0E-112	AB037632.1	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
4763	13953	23054	5	1.0E-112	AB037632.1	NT	Homo sapiens mRNA for KIAA1411 protein, partial cds
5521	14746	24114	37.86	1.0E-112	NA6046.1	EST_HUMAN	Homo sapiens mRNA for KIAA1411 protein, partial cds
6526	16722	25187	3.4	1.0E-112	AU118051.1	EST_HUMAN	y35d07.1 Soares melanocyte 2Nblm Homo sapiens cDNA clone IMAGE:273229 5'
6766	16951	26408	3.08	1.0E-112	BE867635.1	EST_HUMAN	AU118051 HEMBA1 Homo sapiens cDNA clone HEMBA1002773 5'
6766	16951	26409	3.08	1.0E-112	BE867635.1	EST_HUMAN	601443151F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847285 5'
7359	16575	26087	2.68	1.0E-112	AW863327.1	EST_HUMAN	601443151F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847285 5'
7522	16727	26218	5.43	1.0E-112	AJ249900.1	NT	MIR3-SN0009-100400-106-512 SN0009 Homo sapiens cDNA
7682	16862	26384	1.98	1.0E-112	BE280479.1	EST_HUMAN	Homo sapiens mRNA for secreted modular calcium-binding protein (smoc1 gene)
7739	16835	26443	4.65	1.0E-112	AW377670.1	EST_HUMAN	601155323F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138989 5'
8850	17757		1.37	1.0E-112	AF106656.1	NT	PIM0-CT0237-141089-001-002 CT0237 Homo sapiens cDNA
760	8891	19134	5.03	1.0E-113	AI365586.1	EST_HUMAN	Homo sapiens adenylosuccinate lyase gene, complete cds
760	8891	19135	5.03	1.0E-113	AI365586.1	EST_HUMAN	ac95f01.x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1953825 3'
850	10183	19339	17.13	1.0E-113	M11865.1	NT	ac95f01.x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1953825 3'
1527	10741	19913	3.46	1.0E-113	AI365586.1	EST_HUMAN	Human X-linked phosphoglycerate kinase gene, exon 8
1908	11948	20309	1.11	1.0E-113	AF240775.1	NT	ac95f01.x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1953825 3'
2064	11265	20478	0.88	1.0E-113	BF515218.1	EST_HUMAN	Homo sapiens eIF4E-transporter mRNA, complete cds
3094	12330	21456	1.75	1.0E-113	AJ223948.1	NT	U1H-BW1-ant4-03-0-U1.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3082876 3'
6301	18134		3.33	1.0E-113	BE780858.1	EST_HUMAN	Homo sapiens mRNA for putative RNA helicase, 3' end
5439	14666	23819	6.09	1.0E-113	AU127214.1	EST_HUMAN	601469465F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3872538 5'
5675	14848	24231	4.08	1.0E-113	AU127214.1	EST_HUMAN	AU127214 NT2RP2 Homo sapiens cDNA clone NT2RP2000807 5'
5698	14918	24312	2.38	1.0E-113	11525737	NT	AU140291 PLACE2 Homo sapiens cDNA clone PLACE2000274 5'
							Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetyl-galactosaminyltransferase 8 (GalNAc-T8) (GALNT8), mRNA

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6803	15998	25456	3.64	1.0E-113	BE382842.1	EST_HUMAN	601267709F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3827554 5'
6803	15998	25457	3.64	1.0E-113	BE382842.1	EST_HUMAN	601267709F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3827554 5'
7683	16882	26390	1.75	1.0E-113	AW500518.1	EST_HUMAN	U1-HF-BN0-ak-b-12-Q-U1.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077328 5'
7691	16890	26397	3.01	1.0E-113	AW630291.1	EST_HUMAN	hh81a09.y1 NCL CGAP_GU1 Homo sapiens cDNA clone IMAGE:2669176 5' similar to TR:O60327 O60327 KIAA0584 PROTEIN;
7691	16890	26398	3.01	1.0E-113	AW630291.1	EST_HUMAN	hh81a09.y1 NCL CGAP_GU1 Homo sapiens cDNA clone IMAGE:2669176 5' similar to TR:O60327 O60327 KIAA0584 PROTEIN;
7812	17005	26518	3.8	1.0E-113	BE282868.1	EST_HUMAN	601105528F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2688368 5'
8031	17168	26708	3.34	1.0E-113	AA580720.1	EST_HUMAN	nc80b03.r1 NCL CGAP_GC1 Homo sapiens cDNA clone IMAGE:797069 5' similar to SW:FEN1_HUMAN P39748 FLAP ENDONUCLEASE-1;
8031	17168	26707	3.34	1.0E-113	AA580720.1	EST_HUMAN	nc80b03.r1 NCL CGAP_GC1 Homo sapiens cDNA clone IMAGE:797069 5' similar to SW:FEN1_HUMAN P39748 FLAP ENDONUCLEASE-1;
60	9356	18474	1.21	1.0E-114	Y17151.2	NT	Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3)
60	9358	18475	1.21	1.0E-114	Y17151.2	NT	Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3)
60	9358	18476	1.21	1.0E-114	Y17151.2	NT	Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3)
661	9897	19023	8.43	1.0E-114	T70551.1	EST_HUMAN	yd15cd1.s1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:108288 3' similar to gb:A21187 ALPHA-2-MACROGLOBULIN PRECURSOR (HUMAN); contains Alu repetitive element;
1078	10303	19454	1.39	1.0E-114	8923087	NT	Homo sapiens hypothetical protein FLJ20080 (FLJ20080), mRNA
1320	10535	19698	4.23	1.0E-114	7657529	NT	Homo sapiens ribodoid tumor deletion region protein 1 (RTDR1), mRNA
1619	10832	20007	4.87	1.0E-114	6631094	NT	Homo sapiens minichromosome maintenance deficient (S. cerevisiae) 3 (MCM3), mRNA
1647	10861	20042	8.45	1.0E-114	6876079	NT	Homo sapiens nucleoporin-like protein 1 (NLP_1), mRNA
2220	11417	20842	1.28	1.0E-114	AB002374.1	NT	Human mRNA for KIAA0376 gene, partial cds
2766	9342	18460	1.22	1.0E-114	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
2758	9342	18451	1.22	1.0E-114	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
3095	12331	21457	2.27	1.0E-114	X04086.1	NT	Human gene for catalase (EC 1.11.1.6) exon 2 mapping to chromosome 11, band p13
3138	12371	21602	1.28	1.0E-114	BF06374.1	EST_HUMAN	601869632F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4100214 5'
3982	13206	22312	1.54	1.0E-114	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
4385	13586	22888	0.77	1.0E-114	J03171.1	NT	Human interferon-alpha receptor (HuIFN-alpha-Rcc) mRNA, complete cds
5168	14347	23435	1.03	1.0E-114	BE275324.1	EST_HUMAN	601122173F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3346068 5'
5206	14391	23467	0.94	1.0E-114	AF004849.1	NT	Homo sapiens PKY protein kinase mRNA, complete cds
6201	15382	24823	9.02	1.0E-114	Y18000.1	NT	Homo sapiens NF2 gene
6201	15382	24824	9.02	1.0E-114	Y18000.1	NT	Homo sapiens NF2 gene
6425	15822	25086	2.57	1.0E-114	4557800	NT	Homo sapiens gamma-aminobutyric acid (GABA) A receptor, alpha 2 (GABRA2) mRNA

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Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6680	15875	25334	4.26	1.0E-114	U63041.1	NT	Human neural cell adhesion molecule CD56 mRNA, complete cds
6706	15901	25362	7.86	1.0E-114	AB011133.1	NT	Homo sapiens mRNA for KIAA0561 protein, partial cds
6706	15901	25363	7.86	1.0E-114	AB011133.1	NT	Homo sapiens mRNA for KIAA0561 protein, partial cds
6884	16075		10.62	1.0E-114	AW327455.1	EST_HUMAN	dq0305.x1 NIH_MGC_2 Homo sapiens cDNA clone IMAGE:2846744 5'
6900	15606	25072	4.01	1.0E-114	AF077754.1	NT	Homo sapiens tyrosine kinase pp60c-src (SRC) gene, exon 12 and partial cds
7368	16584		15.17	1.0E-114	BE302666.1	EST_HUMAN	ba73g12.y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2906086 5' similar to gb:X17206 40S RIBOSOMAL PROTEIN S4 (HUMAN); gb:M20632 Mouse LLRep3 protein mRNA from a repetitive element, complete (MOUSE);
7745	16941	26452	3.76	1.0E-114	AV733454.1	EST_HUMAN	AV733454 cda Homo sapiens cDNA clone cdABA08 5'
7745	16941	26453	3.76	1.0E-114	AV733454.1	EST_HUMAN	AV733454 cda Homo sapiens cDNA clone cdABA08 5'
8767	18368		2.74	1.0E-114	11418041	NT	Homo sapiens TNF-Inducible protein CG12-1 (CG12-1), mRNA
9033	17878	23891	3.22	1.0E-114	11034850	NT	Homo sapiens hypothetical protein (DJ1042K10.2), mRNA
9033	17878	23892	3.22	1.0E-114	11034850	NT	Homo sapiens hypothetical protein (DJ1042K10.2), mRNA
23	9319	18423	5.81	1.0E-115	4758111	NT	Homo sapiens HLA-B associated transcript-1 (D6S81E) mRNA
127	9410	18544	2.6	1.0E-115	4505938	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide A (220kD) (POLR2A) mRNA
131	9414		16.52	1.0E-115	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
297	9570	18702	2.23	1.0E-115	AW804759.1	EST_HUMAN	QV4-UM0094-300300-156-508 UM0094 Homo sapiens cDNA
542	9793	18916	0.6	1.0E-115	AI339206.1	EST_HUMAN	q106f01.x1 NCL_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1946809 3' similar to TR:O00536 O00536 TTF-1 INTERACTING PEPTIDE 5;
542	9793	18917	0.6	1.0E-115	AI339206.1	EST_HUMAN	q106f01.x1 NCL_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1946809 3' similar to TR:O00536 O00536 TTF-1 INTERACTING PEPTIDE 5;
796	10035	19185	1.09	1.0E-115	5174702	NT	Homo sapiens transforming growth factor beta-activated kinase-binding protein 1 (TAB1), mRNA
796	10035	19186	1.09	1.0E-115	5174702	NT	Homo sapiens transforming growth factor beta-activated kinase-binding protein 1 (TAB1), mRNA
798	10037	19188	349.13	1.0E-115	4503794	NT	Homo sapiens ferritin, heavy polypeptide 1 (FTH1) mRNA
1808	11017	20210	1.36	1.0E-115	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
2048	11249	20459	1.05	1.0E-115	BE745469.1	EST_HUMAN	601579838F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3928832 5'
2048	11249	20460	1.05	1.0E-115	BE745469.1	EST_HUMAN	601579838F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3928832 5'
2054	11255	20468	0.94	1.0E-115	AB007902.1	NT	Homo sapiens KIAA0442 mRNA, partial cds
2264	11459	20678	1.92	1.0E-115	AF231124.1	NT	Homo sapiens testican-1 mRNA, complete cds
3079	12315	21437	5.51	1.0E-115	AJ245922.1	NT	Homo sapiens mRNA for alpha-tubulin 8 (TUBA8 gene)
3079	12315	21438	5.51	1.0E-115	AJ245922.1	NT	Homo sapiens mRNA for alpha-tubulin 8 (TUBA8 gene)
3449	12674	21809	2.12	1.0E-115	AJ277892.1	NT	Homo sapiens partial TTN gene for titin
4019	13231	22334	3.93	1.0E-115	AB002348.2	NT	Homo sapiens mRNA for KIAA0350 protein, partial cds

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Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4253	13456	22548	1.31	1.0E-115	AL137163.1	NT	Novel human gene mapping to chromosome X
4395	13566	22697	3.42	1.0E-115	6912659	NT	Homo sapiens si2-like 3 (SIRT3), mRNA
4428	13628	22722	4.3	1.0E-115	4758278	NT	Homo sapiens EphA4 (EPHA4) mRNA
4591	13785	22876	1.84	1.0E-115	8922435	NT	Homo sapiens hypothetical protein FLJ10488 (FLJ10488), mRNA
4591	13785	22877	1.84	1.0E-115	8922435	NT	Homo sapiens hypothetical protein FLJ10488 (FLJ10488), mRNA
4679	13872	22871	2.8	1.0E-115	AL098857.1	NT	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes
4679	13872	22872	2.9	1.0E-115	AL098857.1	NT	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes
4927	14115	23210	3.92	1.0E-115	AL163288.2	NT	Homo sapiens chromosome 21 segment HS21C088
4927	14115	23211	3.92	1.0E-115	AL163288.2	NT	Homo sapiens chromosome 21 segment HS21C088
5363	14593	23670	1.74	1.0E-115	AW970335.1	EST_HUMAN	EST382416 IMAGE sequences, MAGK Homo sapiens cDNA
5463	14689	24040	1.79	1.0E-115	11425128	NT	Homo sapiens similar to ER to nucleus signalling 1 (H. sapiens) (LOC83433), mRNA
5463	14689	24041	1.79	1.0E-115	11425128	NT	Homo sapiens similar to ER to nucleus signalling 1 (H. sapiens) (LOC83433), mRNA
5828	15045	24448	14.79	1.0E-115	11426038	NT	Homo sapiens similar to ribosomal protein S26 (H. sapiens) (LOC83436), mRNA
5890	15107	24517	1.88	1.0E-115	7681883	NT	Homo sapiens KIAA0054 gene product; Helicase (KIAA0054), mRNA
5890	15107	24518	1.88	1.0E-115	7681883	NT	Homo sapiens KIAA0054 gene product; Helicase (KIAA0054), mRNA
6255	15430	24875	7.4	1.0E-115	AB023212.1	NT	Homo sapiens mRNA for KIAA0985 protein, partial cds
6511	15707	25172	6.99	1.0E-115	BE830187.1	EST_HUMAN	RC8-ET0081-130700-011-G01 ET0081 Homo sapiens cDNA
6511	15707	25173	6.99	1.0E-115	BE830187.1	EST_HUMAN	RC8-ET0081-130700-011-G01 ET0081 Homo sapiens cDNA
6722	15917	25376	9.46	1.0E-115	11434772	NT	Homo sapiens eukaryotic translation initiation factor 4B (EIF4B), mRNA
7305	16523	26014	3.52	1.0E-115	AW571544.1	EST_HUMAN	xc2f08.x1 NCL_OGAP_U1 Homo sapiens cDNA clone IMAGE:2839239 3' similar to SW:CAYP_CANFA
7898	17076	26804	2.84	1.0E-115	4502528	NT	P10483 CALCYPHOSINE;
8252	17380	26914	4.28	1.0E-115	BF361984.1	EST_HUMAN	Homo sapiens calcium channel, voltage-dependent, alpha 1E subunit (CACNA1E) mRNA
8324	17425		1.78	1.0E-115	AF240786.1	NT	QV2-NN0044-210800-308-610 NN0044 Homo sapiens cDNA
579	9828	18947	0.93	1.0E-116	BE275502.1	EST_HUMAN	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
810	10049	19200	1.33	1.0E-116	4507334	NT	601121347F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2888875 5'
869	10105		0.8	1.0E-116	4507334	NT	Homo sapiens synaptobrevin 1 (SYNJ1), mRNA
1866	11170	20375	2.57	1.0E-116	5174478	NT	Homo sapiens synaptobrevin 1 (SYNJ1), mRNA
1988	11170	20378	2.57	1.0E-116	5174478	NT	Homo sapiens pericentrin (PCNT) mRNA
1985	11188	20408	1.19	1.0E-116	AU133080.1	EST_HUMAN	Homo sapiens pericentrin (PCNT) mRNA
2067	12008	20480	1	1.0E-116	M19824.1	NT	AU133080 NT2RP4 Homo sapiens cDNA clone NT2RP4001228 5'
2087	12009	20481	1	1.0E-116	M19824.1	NT	Human apolipoprotein B-100 (apoB) gene, exons 17 and 18
2273	11488	20889	1.85	1.0E-116	5453941	NT	Human apolipoprotein B-100 (apoB) gene, exons 17 and 18
							Homo sapiens protein phosphatase, EF hand calcium-binding domain 1 (PPEF1) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2309	11503		4.25	1.0E-116	U78308.1	NT	Human olfactory receptor olfr17-201-1 (OR17-201-1) gene, olfactory receptor olfr17-32 (OR17-32) gene and olfactory receptor pseudo olfr17-01 (OR17-01) pseudogene, complete cds
2419	11610	20832	2.52	1.0E-116	AB018333.1	NT	Homo sapiens mRNA for KIAA0780 protein, partial cds
2891	11958	21088	8.81	1.0E-116	BE889256.1	EST_HUMAN	601513337F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3914600 5'
3130	12385		8.84	1.0E-116	T07515.1	EST_HUMAN	EST T05405 Fetal brain, Striatum (cat836208) Homo sapiens cDNA clone HFBEK28 similar to EST containing L1 repeat
3139	12374	21504	6.18	1.0E-116	L77570.1	NT	Homo sapiens DiGeorge syndrome critical region, centromeric end
3139	12374	21505	6.18	1.0E-116	L77570.1	NT	Homo sapiens DiGeorge syndrome critical region, centromeric end
4372	13574	22870	2.17	1.0E-116	5031854	NT	Homo sapiens sodium phosphate transporter 3 (NPT3) mRNA
4470	13668	22759	1.39	1.0E-116	AB026808.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
4872	14080	23154	1.55	1.0E-116	AI807096.1	EST_HUMAN	PM-BT135-070499-018 BT135 Homo sapiens cDNA
5844	14887	24252	2.81	1.0E-116	W42822.1	EST_HUMAN	zc24d07.1 Soares, senescent fibroblasts, NBHSF Homo sapiens cDNA clone IMAGE:323245 5' similar to SW:MDHM_MOUSE P08249 MALATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR;
5757	14976	24374	1.97	1.0E-116	AB048856.1	NT	Homo sapiens mRNA for KIAA1638 protein, partial cds
5757	14976	24375	1.87	1.0E-116	AB048856.1	NT	Homo sapiens mRNA for KIAA1638 protein, partial cds
5881	15098		2.13	1.0E-116	BE158133.1	EST_HUMAN	Homo sapiens mRNA for KIAA1638 protein, partial cds
6060	15250	24672	1.77	1.0E-116	C02844.1	EST_HUMAN	MR2-HT0379-210200-102-b04 HT0379 Homo sapiens cDNA
6167	15349	24787	8.61	1.0E-116	AV716314.1	EST_HUMAN	G02844 Human heart cDNA (YNakamura) Homo sapiens cDNA clone 3NH00587
6588	15782	25242	2.68	1.0E-116	AA354258.1	EST_HUMAN	AV716314 DCB Homo sapiens cDNA clone DCBCCG08 5'
6588	15782	25243	2.68	1.0E-116	AA354258.1	EST_HUMAN	EST02685 Jurkat T-cells V Homo sapiens cDNA 5' end similar to similar to keratin 2
6905	16000	25459	8.64	1.0E-116	AI216352.1	EST_HUMAN	q08c05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1844188 3' similar to gb:X53741_mai1 FIBULIN-1, ISOFORM A PRECURSOR (HUMAN);
7279	18498	25990	4.18	1.0E-116	BF335849.1	EST_HUMAN	CM2-CT0482-300800-349-a08 CT0482 Homo sapiens cDNA
7695	18894	26403	3.79	1.0E-116	AI367140.1	EST_HUMAN	q41e04.x1 Soares_NhrMPu_S1 Homo sapiens cDNA clone IMAGE:1835102 3' similar to WP:B0495.7 CE01765;
8253	17381	26915	3.84	1.0E-116	D44816.1	EST_HUMAN	HUMSUPY287 Human brain cDNA Homo sapiens cDNA clone NF187-S
8880	18361		1.69	1.0E-116	BE258569.1	EST_HUMAN	601108350F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3344590 5'
9081	18225		2.02	1.0E-116	AL134889.1	EST_HUMAN	DKFZp782L1110.1 782 (synonym: hmel2) Homo sapiens cDNA clone DKFZp782L1110 5'
565	9816	18937	1.67	1.0E-117	4828636	NT	Homo sapiens acetyl-Coenzyme A carboxylase alpha (ACACA), mRNA
1085	11985	19462	2.51	1.0E-117	AF124393.1	NT	Mus musculus fragile-X-related protein 1 (Fxr1h) gene, exons 13a through 15
1725	10637	20120	1.74	1.0E-117	AF123320.1	NT	Homo sapiens lymphocyte activation-associated protein mRNA, complete cds
1796	11008	20201	2.17	1.0E-117	MI9816.1	NT	Human apolipoprotein B-100 (apoB) gene, exon 10

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2178	11375	20587	3.14	1.0E-117	AW957699.1	EST_HUMAN	EST369769 MAGe resequences, MAGe Homo sapiens cDNA
2672	11767	20977	4.99	1.0E-117	M63468.1	NT	Human alpha-5 collagen type IV gene, exon 5
3235	12469	21901	2.35	1.0E-117	AA978114.1	EST_HUMAN	op32c11.s1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1578548 3'
3988	13183	22283	10.3	1.0E-117	AA316723.1	EST_HUMAN	EST188414 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to ribosomal protein L29
4000	13213	22317	0.68	1.0E-117	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
4337	13538	22629	3.11	1.0E-117	8659564	NT	Homo sapiens collagen, type IV, alpha 5 (Alport syndrome) (COL4A5), mRNA
4576	13769	22684	2.19	1.0E-117	AL042120.1	EST_HUMAN	DKFZp434C1120_1 434 (synonym: fites3) Homo sapiens cDNA clone DKFZp434C1120 5'
4736	13927	23030	0.89	1.0E-117	X89870.1	NT	H. sapiens mRNA for TPCR16 protein
4736	13927	23031	0.89	1.0E-117	X89870.1	NT	H. sapiens mRNA for TPCR16 protein
4824	14013	23112	10.37	1.0E-117	AF134304.2	NT	Homo sapiens Scar2 (SCAR2) gene, partial cds
4824	14013	23113	10.37	1.0E-117	AF134304.2	NT	Homo sapiens Scar2 (SCAR2) gene, partial cds
4885	14073	23170	1.62	1.0E-117	U59109.1	NT	Mus musculus nebulin mRNA, partial cds
4885	14073	23171	1.62	1.0E-117	U59109.1	NT	Mus musculus nebulin mRNA, partial cds
4858	14145	23237	3.13	1.0E-117	AB020673.1	NT	Homo sapiens mRNA for KIAA0869 protein, complete cds
5274	14448	23518	0.81	1.0E-117	6912481	NT	Homo sapiens atrophin-1 interacting protein 1; activin receptor interacting protein 1 (KIAA0705), mRNA
5285	14458	23525	15.42	1.0E-117	6987248	NT	Homo sapiens sal (Drosophila)-like 1 (SALL1), mRNA
6384	14594	23671	3.1	1.0E-117	BE730508.1	EST_HUMAN	601562657F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3832214 5'
6273	15453	24893	5.21	1.0E-117	L76571.1	NT	Homo sapiens nuclear hormone receptor (shp) gene, 3' end of cds
6273	15453	24894	5.21	1.0E-117	L76571.1	NT	Homo sapiens nuclear hormone receptor (shp) gene, 3' end of cds
6311	15482	24937	4.74	1.0E-117	AV171788.1	EST_HUMAN	AV171788 DCB Homo sapiens cDNA clone DCBBAE01 5'
6311	15482	24938	4.74	1.0E-117	AV171788.1	EST_HUMAN	AV171788 DCB Homo sapiens cDNA clone DCBBAE01 5'
6454	15651	25119	6.33	1.0E-117	AI650145.1	EST_HUMAN	wp88b07.x1 NCI_CGAP_Bn25 Homo sapiens cDNA clone IMAGE:2468629 3' similar to TR:O75085
7434	16643	26135	1.68	1.0E-117	D83776.1	NT	Human mRNA for KIAA0191 gene, partial cds
7822	17014	26528	2.73	1.0E-117	AB011541.1	NT	Homo sapiens mRNA for MEGF8, partial cds
7822	17014	26529	2.73	1.0E-117	AB011541.1	NT	Homo sapiens mRNA for MEGF8, partial cds
7932	17072	26797	32.7	1.0E-117	BE269856.1	EST_HUMAN	601186203F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3544286 5'
8121	17255	26798	2.27	1.0E-117	4501848	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
8121	17255	26797	2.27	1.0E-117	4501848	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
8587	18304		1.98	1.0E-117	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
8277	11885	18482	1.98	1.0E-117	AF124393.1	NT	Mus musculus fragile-X-related protein 1 (Fxrh) gene, exons 13a through 15

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
70	8365	18491	3.8	1.0E-118	AF161500.1	NT	Homo sapiens HSPC151 mRNA, complete cds
85	8389	18517	0.88	1.0E-118	AL045854.1	EST_HUMAN	DKFZp434i056_r1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434i056 5'
523	9774	18899	7.45	1.0E-118	7857018	NT	Homo sapiens hypothetical protein (DJ328E19.C1.1), mRNA
924	11981	19316	0.92	1.0E-118	5174890	NT	Homo sapiens sine oculis homeobox (Drosophila) homolog 1 (SIX1) mRNA
2199	11396	20618	4.13	1.0E-118	BE389705.1	EST_HUMAN	601281947F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3804019 5'
2199	11396	20619	4.13	1.0E-118	BE389705.1	EST_HUMAN	601281947F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3804019 5'
2199	11396	20620	4.13	1.0E-118	BE389705.1	EST_HUMAN	601281947F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3804019 5'
2288	11493		12.88	1.0E-118	AW851729.1	EST_HUMAN	EST3683789 MAGE resequences, MAGB Homo sapiens cDNA
2897	11877	21091	4.25	1.0E-118	U07000.1	NT	Human breakpoint cluster region (BCR) gene, complete cds
2897	11877	21092	4.25	1.0E-118	U07000.1	NT	Human breakpoint cluster region (BCR) gene, complete cds
3068	12304		4.88	1.0E-118	Y13832.1	NT	Homo sapiens PRKY exon 7
3159	12394	21529	5.35	1.0E-118	A1347894.1	EST_HUMAN	qp01105.x1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1916789 3'
3159	12394	21530	5.35	1.0E-118	A1347894.1	EST_HUMAN	qp01105.x1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1916789 3'
3926	13141	22268	1.12	1.0E-118	AB024469.1	NT	Pongo pygmaeus DNA, similar to pol gene of HIRV-W and MSRV, isolate:ORW3-3
4064	13274	22374	7.45	1.0E-118	D23660.1	NT	Human mRNA for ribosomal protein, complete cds
4718	13909	23011	1.8	1.0E-118	11425763	NT	Homo sapiens KIAA0478 gene product (KIAA0478), mRNA
5405	14633	23744	1.89	1.0E-118	AF142624.1	NT	Homo sapiens calcium channel gamma 4 subunit (CACNG4) gene, exon 3
5405	14633	23745	1.89	1.0E-118	AF142624.1	NT	Homo sapiens calcium channel gamma 4 subunit (CACNG4) gene, exon 3
5634	14958	24241	1.85	1.0E-118	11420764	NT	Homo sapiens transient receptor potential channel 5 (TRPC5), mRNA
6333	15814	24981	4.89	1.0E-118	11431060	NT	Homo sapiens chromosome 2 open reading frame 3 (C2ORF3), mRNA
6592	15788	25247	7.57	1.0E-118	BE082855.1	EST_HUMAN	QV0-BT0263-080200-097-h03 BT0263 Homo sapiens cDNA
6592	15788	25248	7.57	1.0E-118	BE082855.1	EST_HUMAN	QV0-BT0263-080200-097-h03 BT0263 Homo sapiens cDNA
6595	15791	25249	3.03	1.0E-118	AA443024.1	EST_HUMAN	z098d07.r1 Soarea_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:811789 5'
6595	15791	25250	3.03	1.0E-118	AA443024.1	EST_HUMAN	z098d07.r1 Soarea_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:811789 5'
6775	15970	25426	3.19	1.0E-118	BE263134.1	EST_HUMAN	601144983F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3180502 5'
7828	17018	28534	5.5	1.0E-118	AA315007.1	EST_HUMAN	EST168814 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to dynein, light chain 1, cytoplasmic
8098	17230	28768	1.71	1.0E-118	BF093687.1	EST_HUMAN	QV0-UJM0091-120900-385-b12 UJM0091 Homo sapiens cDNA
8098	17230	28768	1.71	1.0E-118	BF093687.1	EST_HUMAN	QV0-UJM0091-120900-385-b12 UJM0091 Homo sapiens cDNA
8218	17349		1.97	1.0E-118	6325465	NT	Homo sapiens flap structure-specific endonuclease 1 (FEN1), mRNA
765	10005	19154	0.77	1.0E-118	AF170492.1	NT	Homo sapiens chloride channel CLC4 (CLC4) mRNA, complete cds
1044	11984	19420	1.99	1.0E-118	7705607	NT	Homo sapiens CGI-105 protein (LOC51011), mRNA
1902	11108	20301	2.49	1.0E-118	AB023147.1	NT	Homo sapiens mRNA for KIAA0930 protein, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3206	12440		0.74	1.0E-119	AA916760.1	EST_HUMAN	on10b05.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1556241 3' similar to WP:E04F8.2
3928	13145	22262	0.87	1.0E-119	4504118	NT	CE01214 :
6367	14587	23664	2.81	1.0E-119	AU133398.1	EST_HUMAN	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
5365	14595	23872	10.86	1.0E-119	M88914.1	NT	AU133398 NT2RP4 Homo sapiens cDNA clone NT2RP4001891 5'
5368	14598	23678	3.48	1.0E-119	BE936121.1	EST_HUMAN	Human neurofibromin (NF1) gene, complete cds
5409	14637	23765	1.8	1.0E-119	AV693731.1	EST_HUMAN	RC1-NN0073-260800-018-g08 NN0073 Homo sapiens cDNA
							AV693731 GKCG Homo sapiens cDNA clone GKCDHB03 5'
5723	14941	24337	6.95	1.0E-119	AI150703.1	EST_HUMAN	qb77c08.x1 Soares_fetal_hear NIH-H19W Homo sapiens cDNA clone IMAGE:1706128 3' similar to
5852	15070	24480	2.4	1.0E-119	X06292.1	NT	SW:K1CJ_MOUSE P02535 KERATIN, TYPE I CYTOSKELETAL 10 ;
5858	15076	24489	4.25	1.0E-119	AW974183.1	EST_HUMAN	Human c-fos/prob-1 oncogene
7150	16327	23810	3.05	1.0E-119	AA485124.1	EST_HUMAN	EST1386298 MAGE resequences, MAGM Homo sapiens cDNA
7225	16402	25887	5.18	1.0E-119	AB032281.1	NT	aa32105.1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:814977 5'
7755	16951		11.06	1.0E-119	BF568571.1	EST_HUMAN	Homo sapiens Sec mRNA for stearyl-CoA desaturase, complete cds
8024	18291		7.48	1.0E-119	AW847519.1	EST_HUMAN	602186072F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310633 5'
308	9579	18711	0.7	1.0E-120	4507334	NT	RC3-CT0212-240998-011-103 CT0212 Homo sapiens cDNA
1048	10274	19426	5.48	1.0E-120	AF248540.1	NT	Homo sapiens synaptobrevin 1 (SYNJ1), mRNA
1048	10274	19427	5.48	1.0E-120	AF248540.1	NT	Homo sapiens Intersectin 2 (SH3D1B) mRNA, complete cds
1429	10842	19813	3.03	1.0E-120	N44873.1	EST_HUMAN	Homo sapiens Intersectin 2 (SH3D1B) mRNA, complete cds
1561	10794	19971	4.28	1.0E-120	AF167706.1	NT	W40g12.1 Soares melanocyte 2N18HM Homo sapiens cDNA clone IMAGE:273766 5'
1778	10895	20177	1.78	1.0E-120	4537250	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds
2077	11277	20493	1.44	1.0E-120	AB011399.1	NT	Homo sapiens disintegrin and metalloprotease domain 10 (ADAM10) mRNA
2077	11277	20494	1.44	1.0E-120	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
3278	9578	18711	0.65	1.0E-120	4507334	NT	Homo sapiens gene for AF-6, complete cds
4351	13553	22648	1.8	1.0E-120	AF058490.1	NT	Homo sapiens synaptobrevin 1 (SYNJ1), mRNA
4351	13553	22649	1.8	1.0E-120	AF058490.1	NT	Homo sapiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds
4668	13680	22660	1.74	1.0E-120	AF098463.1	NT	Homo sapiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds
4668	13680	22661	1.74	1.0E-120	AF098463.1	NT	Homo sapiens stannocalcin (STC) gene, partial cds
5179	14358		0.69	1.0E-120	BE289720.1	EST_HUMAN	Homo sapiens stannocalcin (STC) gene, partial cds
5200	14378	23463	1.38	1.0E-120	A1904151.1	EST_HUMAN	600944362F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2860414 5'
5545	14768	24135	13.47	1.0E-120	BF568222.1	EST_HUMAN	CM-BT043-080289-075 BT043 Homo sapiens cDNA
5545	14769	24136	13.47	1.0E-120	BF568222.1	EST_HUMAN	602183994F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300174 5'
6426	15623	25087	2.58	1.0E-120	Y00067.1	NT	602183994F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300174 5'
6426	15623	25088	2.58	1.0E-120	Y00067.1	NT	Human gene for neurofilament subunit M (NF-M)
							Human gene for neurofilament subunit M (NF-M)

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Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6573	15769	25232	2.76	1.0E-120	BF337598.1	EST_HUMAN	602035352F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4183333 5'
6803	15789	25256	2.72	1.0E-120	AB007894.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0495
6803	15789	25257	2.72	1.0E-120	AB007894.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0495
6911	16089	25506	6.03	1.0E-120	BE382102.1	EST_HUMAN	601307739F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3625344 5'
6911	16089	25508	6.03	1.0E-120	BE382102.1	EST_HUMAN	601307739F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3625344 5'
7000	16178	25649	3.58	1.0E-120	BF308541.1	EST_HUMAN	601888959F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4122876 5'
7004	16182	25655	12.1	1.0E-120	AU133205.1	EST_HUMAN	AU133205 NT2RP4 Homo sapiens cDNA clone NT2RP4001541 5'
7098	16276	25756	2.58	1.0E-120	AB028000.1	NT	Homo sapiens mRNA for KIAA1077 protein, partial cds
7680	16865	26393	10.02	1.0E-120	BE288387.1	EST_HUMAN	601176727F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532015 5'
7684	17100	26630	1.7	1.0E-120	BE667619.1	EST_HUMAN	601443135F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847281 5'
7884	17100	26631	1.7	1.0E-120	BE667619.1	EST_HUMAN	601443135F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847281 5'
8782	17711	23957	1.24	1.0E-120	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
73	9387	18495	1.62	1.0E-121	Y18000.1	NT	Homo sapiens NF2 gene
363	8647	18782	1.32	1.0E-121	AU134683.1	EST_HUMAN	AU134683 PLACE1 Homo sapiens cDNA clone PLACE1000889 5'
731	11975	19111	1.23	1.0E-121	5032182	NT	Homo sapiens TNF receptor-associated factor 1 (TRAF1) mRNA
1935	11139	20335	0.96	1.0E-121	4755139	NT	Homo sapiens inositol polyphosphate-4-phosphatase, type I, 107KD (INPP4A), splice variant a, mRNA
1935	11139	20336	0.96	1.0E-121	4755139	NT	Homo sapiens inositol polyphosphate-4-phosphatase, type I, 107KD (INPP4A), splice variant a, mRNA
2072	11272	20487	1.12	1.0E-121	L76831.1	NT	Homo sapiens metabotropic glutamate receptor 1 beta (mGluR1beta) mRNA, complete cds
2540	11728	20945	1.42	1.0E-121	BF344378.1	EST_HUMAN	602014759F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4150286 5'
2540	11728	20946	1.42	1.0E-121	BF344378.1	EST_HUMAN	602014759F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4150286 5'
3046	12282	21409	4.5	1.0E-121	Y19208.1	NT	Homo sapiens hHb3 gene for hair keratin, exons 1 to 9
3046	12282	21410	4.5	1.0E-121	Y19208.1	NT	Homo sapiens hHb3 gene for hair keratin, exons 1 to 9
3510	12734	21872	1	1.0E-121	AB037758.1	NT	Homo sapiens mRNA for KIAA1337 protein, partial cds
3510	12734	21873	1	1.0E-121	AB037758.1	NT	Homo sapiens mRNA for KIAA1337 protein, partial cds
3657	12878	21868	8.82	1.0E-121	AF155156.2	NT	Homo sapiens adaptor-related protein complex AP-4 epsilon subunit mRNA, complete cds
3704	12924	22043	0.74	1.0E-121	AI804151.1	EST_HUMAN	CM-BT043-090289-075 BT043 Homo sapiens cDNA
4322	13523	22618	15.63	1.0E-121	AI263294.1	EST_HUMAN	q67b01.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2005417 3'
4986	14183	23271	3.41	1.0E-121	X91937.1	NT	H. sapiens ECE-1 gene (exon 17)
5139	14318	23408	1.19	1.0E-121	AI804151.1	EST_HUMAN	CM-BT043-090289-075 BT043 Homo sapiens cDNA
6437	15634	25069	2.45	1.0E-121	11438217	NT	H. sapiens ECE-1 gene (exon 17)
6438	15635	25100	2.34	1.0E-121	D84122.1	NT	Homo sapiens gamma-aminobutyric acid (GABA) A receptor, alpha 2 (GABRA2), mRNA
6438	15635	25101	2.34	1.0E-121	D84122.1	NT	Homo sapiens DNA for prostacyclin synthase, exon 8

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Table 4
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7357	16573	26065	3.21	1.0E-121	11427788	NT	Homo sapiens COX11 (yeast) homolog, cytochrome c oxidase assembly protein (COX11), mRNA
7384	16580	26071	2.22	1.0E-121	AF084200.1	NT	Homo sapiens UDP-glucuronosyltransferase 2B4 precursor (UGT2B4) mRNA, UGT2B4*E458 allele, complete cds
7640	16745	26239	4.58	1.0E-121	7330334	NT	Homo sapiens chloride intracellular channel 4-like (CLIC4L), mRNA
7567	16772	26264	1.92	1.0E-121	N59824.1	EST_HUMAN	y74c01.s1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:248448 3'
272	9547	19678	1.18	1.0E-122	11526176	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
341	9809	18736	3.68	1.0E-122	AF114488.1	NT	Homo sapiens Intersectin short isoform (ITSN) mRNA, complete cds
363	9629	18781	1.23	1.0E-122	11526176	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
892	10127	18290	3.5	1.0E-122	AF114488.1	NT	Homo sapiens Intersectin short isoform (ITSN) mRNA, complete cds
1227	10445	18601	4.46	1.0E-122	M20707.1	NT	Human kappa-immunoglobulin germline pseudogene (Chr22.4) variable region (subgroup V kappa II)
1688	10881	20065	3.77	1.0E-122	AF18708.1	NT	Homo sapiens cytochrome-rich repeat-containing protein S52 precursor, mRNA, complete cds
1687	10869	20087	2.46	1.0E-122	11418424	NT	Homo sapiens collagen, type XII, alpha 1 (COL12A1), mRNA
1687	10869	20088	2.46	1.0E-122	11418424	NT	Homo sapiens collagen, type XII, alpha 1 (COL12A1), mRNA
1783	10863	20198	6.26	1.0E-122	BE906024.1	EST_HUMAN	601497032F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3899368 5'
2454	11845	20865	22.46	1.0E-122	BF316170.1	EST_HUMAN	601806173F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125234 5'
2454	11845	20866	22.45	1.0E-122	BF316170.1	EST_HUMAN	601806173F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125234 5'
2782	12032	21157	1.26	1.0E-122	AF264717.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP2 mRNA, complete cds
4863	14051	23145	3.37	1.0E-122	4502186	NT	Homo sapiens amyloid beta (A4) precursor protein (protease resistant, Alzheimer disease) (APP), mRNA
5011	14198		1.3	1.0E-122	AW504845.1	EST_HUMAN	UI-HF-BNO-01-03-0-U1.1 NIH_MGC_60 Homo sapiens cDNA clone IMAGE:3078848 5'
5982	14700	24064	6.1	1.0E-122	BE256039.1	EST_HUMAN	601113587F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3354232 5'
6362	17453		3.75	1.0E-122	11418187	NT	Homo sapiens phosphomannomutase 1 (PMM1), mRNA
777	10018	19164	1.53	1.0E-123	BF345274.1	EST_HUMAN	602018058F1 NCI_CGAP_Bim67 Homo sapiens cDNA clone IMAGE:4153870 5'
777	10018	19165	1.53	1.0E-123	BF345274.1	EST_HUMAN	602018058F1 NCI_CGAP_Bim67 Homo sapiens cDNA clone IMAGE:4153870 5'
1020	10248	18399	6.17	1.0E-123	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C049
1028	10255	19408	3.73	1.0E-123	5903114	NT	Homo sapiens inner membrane protein, mitochondrial (mitofilin) (MIMT), mRNA
1245	10461	19621	4.94	1.0E-123	4505818	NT	Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type II, beta (PIP5K2B) mRNA, and translated products
1245	10461	19622	4.94	1.0E-123	4505818	NT	Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type II, beta (PIP5K2B) mRNA, and translated products
2069	11269	20483	2.18	1.0E-123	M55419.1	NT	Human amelogenin (AMELY) gene, 3' end of cds
2069	11269	20484	2.18	1.0E-123	M55419.1	NT	Human amelogenin (AMELY) gene, 3' end of cds

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2069	11269	20485	2.18	1.0E-123	M55419.1	NT	Human amelogenin (AMELY) gene, 3' end of cds
2281	11478		3.68	1.0E-123	7705982	NT	Homo sapiens RAB9-like protein (LOC51209), mRNA
5417	14845	23777	1.83	1.0E-123	L34219.1	NT	Homo sapiens retinaldehyde-binding protein (CRALBP) gene, complete cds
5417	14845	23778	1.83	1.0E-123	L34219.1	NT	Homo sapiens retinaldehyde-binding protein (CRALBP) gene, complete cds
5857	15076	24488	1.97	1.0E-123	AU118435.1	EST_HUMAN	AU118435 HEMBA1 Homo sapiens cDNA clone HEMBA1003591 5'
6357	15537	24991	1.92	1.0E-123	BE283001.1	EST_HUMAN	601152815F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3509162 5'
6870	16082	26560	3.52	1.0E-123	AB007823.1	NT	Homo sapiens mRNA for KIAA0454 protein, partial cds
6812	16100	25587	31.08	1.0E-123	U09823.1	NT	Oryctolagus cuniculus New Zealand white elongation factor 1 alpha (Rabefla2) mRNA, complete cds
8211	17342	26881	5.75	1.0E-123	BF677292.1	EST_HUMAN	602086781F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4250879 5'
8211	17342	26882	5.75	1.0E-123	BF677292.1	EST_HUMAN	602086781F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4250879 5'
273	9548	18677	1.3	1.0E-124	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
273	9548	18678	1.3	1.0E-124	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
278	9554		1.47	1.0E-124	D97675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
492	9746	18878	2.98	1.0E-124	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21G048
698	9840	19073	4.88	1.0E-124	AA397551.1	EST_HUMAN	z81b04.r1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR:G300482
698	9840	19074	4.88	1.0E-124	AA397551.1	EST_HUMAN	G300482 POL=REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT);
788	10008	19155	8.95	1.0E-124	AF155654.1	NT	z81b04.r1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR:G300482
818	10058	19209	1.35	1.0E-124	4507500	NT	G300482 POL=REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT);
914	10149	19309	1.78	1.0E-124	7705446	NT	Human putative ribosomal protein S1 mRNA
1354	10569	19733	7.35	1.0E-124	AF274892.1	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
1354	10569	19734	7.35	1.0E-124	AF274892.1	NT	Homo sapiens glucose transporter 3 gene, exons 9, 10, and complete cds
1784	10894	20190	4.41	1.0E-124	AJ131712.1	NT	Homo sapiens glucose transporter 3 gene, exons 9, 10, and complete cds
2028	11230	20439	1.29	1.0E-124	BE879524.1	EST_HUMAN	Homo sapiens mRNA for nucleolar RNA-helicase (noH81 gene)
2420	11611	20833	2.16	1.0E-124	AB024069.1	NT	601491715F1 NIH_MGC_89 Homo sapiens cDNA clone IMAGE:3883954 5'
3341	12570	21709	0.8	1.0E-124	4504118	NT	Homo sapiens gene for B120, exon 11
3495	12890	21828	0.73	1.0E-124	S78684.1	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
3495	12890	21827	0.73	1.0E-124	S78684.1	NT	Homo sapiens ATP-sensitive inwardly rectifying K-channel subunit (KCNJ8/BIR1) gene, exon
3628	12849	21988	3.42	1.0E-124	X13784.1	NT	Homo sapiens ATP-sensitive inwardly rectifying K-channel subunit (KCNJ8/BIR1) gene, exon
3878	13092	22208	0.7	1.0E-124	4507500	NT	H. sapiens lactate dehydrogenase B gene exon 1 and 2 (EC 1.1.27) (and joined CDS)
4044	13254	22356	0.6	1.0E-124	4504118	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
4053	13263	22366	0.99	1.0E-124	4504118	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA

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Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4757	13948	23049	1.91	1.0E-124	AB024069.1	NT	Homo sapiens gene for B120, exon 11
5327	14559	23631	9.25	1.0E-124	8922337	NT	Homo sapiens hypothetical protein FLJ10300 (FLJ10300), mRNA
5609	14833	24208	6.87	1.0E-124	BF696135.1	EST_HUMAN	602124644F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4281635 5'
6094	15294	24727	3.05	1.0E-124	Y11717.1	NT	M.musculus mRNA for hoxa3 gene
6545	15741	25202	12.36	1.0E-124	4506654	NT	Homo sapiens ribosomal protein L5 (RPL5) mRNA
6909	16097	25563	2.65	1.0E-124	AV645633.1	EST_HUMAN	AV645633 GLC Homo sapiens cDNA clone GLCACE04 3'
6909	16097	25564	2.65	1.0E-124	AV645633.1	EST_HUMAN	AV645633 GLC Homo sapiens cDNA clone GLCACE04 3'
6967	16145	25615	9.53	1.0E-124	AI767133.1	EST_HUMAN	W93102.x1 NCI_CGAP_Kd12 Homo sapiens cDNA clone IMAGE:2400891 3'
6967	16145	25616	9.53	1.0E-124	AI767133.1	EST_HUMAN	W93102.x1 NCI_CGAP_Kd12 Homo sapiens cDNA clone IMAGE:2400891 3'
7877	17065	26589	3.49	1.0E-124	AW665663.1	EST_HUMAN	HJ05c06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2980906 3'
8008	16443	25932	3.27	1.0E-124	AI446455.1	EST_HUMAN	YKRS PROTEIN.;
8008	16443	25933	3.27	1.0E-124	AI446455.1	EST_HUMAN	YKRS PROTEIN.;
8437	9940	19073	5.82	1.0E-124	AA397551.1	EST_HUMAN	z181b04.r1 Stralagene schizo brain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR:G300482 (RETROVIRAL ELEMENT);
8437	9940	19074	5.82	1.0E-124	AA397551.1	EST_HUMAN	z181b04.r1 Stralagene schizo brain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR:G300482 (RETROVIRAL ELEMENT);
8895	17789	23922	1.72	1.0E-124	AB029016.1	NT	Homo sapiens mRNA for KIAA1093 protein, partial cds
9164	18238	23704	1.62	1.0E-124	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
9164	18238	23705	1.62	1.0E-124	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
153	9435	18569	3.63	1.0E-125	BE219510.1	EST_HUMAN	hV59a08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3177686 3' similar to TR:Q25058 Q25058 FIBROPELLEIN IA;
153	9435	18570	3.63	1.0E-125	BE219510.1	EST_HUMAN	hV59a08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3177686 3' similar to TR:Q25058 Q25058 FIBROPELLEIN IA;
324	9595		9.19	1.0E-125	AB032998.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
432	9297	18399	5.95	1.0E-125	BE743922.1	EST_HUMAN	601577981F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3926685 5'
650	9386	19021	4.06	1.0E-125	AI110656.1	EST_HUMAN	HA0086 Human fetal liver cDNA library Homo sapiens cDNA
650	9396	19022	4.06	1.0E-125	AI110656.1	EST_HUMAN	HA0086 Human fetal liver cDNA library Homo sapiens cDNA
735	9978	19115	1.92	1.0E-125	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
870	10106	19268	1.99	1.0E-125	AA042813.1	EST_HUMAN	z153c07.s1 Soares_pregnant_uterus NbHPU Homo sapiens cDNA clone IMAGE:486540 3' similar to gb:X65857_cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E (HUMAN);
1006	10237	19389	1.04	1.0E-125	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1162	10384	19534	1.97	1.0E-125	7662279	NT	Homo sapiens KIAA0744 gene product; histone deacetylase 7 (KIAA0744), mRNA

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1780	10990	20185	2.74	1.0E-125	AF015450.1	NT	Homo sapiens Usurpin-alpha mRNA, complete cds
1780	10990	20186	2.74	1.0E-125	AF015450.1	NT	Homo sapiens Usurpin-alpha mRNA, complete cds
2326	11519	20739	4.04	1.0E-125	AA011278.1	EST_HUMAN	z01g09.r1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:429568 5'
2488	11659	20880	3.16	1.0E-125	AA042813.1	EST_HUMAN	z01g09.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:486540 3' similar to
2556	11743	20961	2.42	1.0E-125	4504696	NT	gb:X65857_cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E (HUMAN);
2556	11743	20962	2.42	1.0E-125	4504696	NT	Homo sapiens inhibin, alpha (INH) mRNA
2971	14484	21345	1.26	1.0E-125	BE018009.1	EST_HUMAN	Homo sapiens inhibin, alpha (INH) mRNA
3841	13058	22173	1.21	1.0E-125	AA042813.1	EST_HUMAN	bb74f06.y1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3048131 5' similar to TR:Q95604 Q95604
4547	13742	22842	2.2	1.0E-125	11425114	NT	ZINC FINGER PROTEIN ;
4547	13742	22843	2.2	1.0E-125	11425114	NT	z01g09.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:486540 3' similar to
4619	13813	22903	1.18	1.0E-125	BE315412.1	EST_HUMAN	gb:X65857_cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E (HUMAN);
5056	9435	18569	1.71	1.0E-125	BE219510.1	EST_HUMAN	Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA
5056	9435	18570	1.71	1.0E-125	BE219510.1	EST_HUMAN	Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA
5629	14853	24236	3.41	1.0E-125	BE892660.1	EST_HUMAN	601141152F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3140796 5'
5919	15136	24546	4.5	1.0E-125	BE562526.1	EST_HUMAN	hV59a08.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3177886 3' similar to TR:Q25058 Q25058
5919	15136	24547	4.5	1.0E-125	BE562526.1	EST_HUMAN	FIBROPELLEIN IA ;
6109	15203	24621	4.08	1.0E-125	X03427.1	NT	hV59a08.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3177886 3' similar to TR:Q25058 Q25058
6109	15203	24622	4.08	1.0E-125	X03427.1	NT	FIBROPELLEIN IA ;
6812	16007	25468	12.48	1.0E-125	BE181640.1	EST_HUMAN	601433472F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918952 5'
6812	16007	25469	12.48	1.0E-125	BE181640.1	EST_HUMAN	601335826F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3689790 5'
7274	16493	25985	3.47	1.0E-125	AF043458.1	NT	601335826F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3689790 5'
7696	16895	26404	4.49	1.0E-125	AB014587.1	NT	Homo sapiens GF-II gene, exon 5
7696	16895	26404	4.49	1.0E-125	AB014587.1	NT	Homo sapiens GF-II gene, exon 5
7837	17028	26545	1.76	1.0E-125	7669505	NT	Homo sapiens GF-II gene, exon 5
7842	17034	26550	5.99	1.0E-125	AF026029.1	NT	Homo sapiens GF-II gene, exon 5
7939	17079	26607	3.23	1.0E-125	AW812899.1	EST_HUMAN	Homo sapiens mRNA for KIAA0687 protein, partial cds
8035	17171	26709	5.52	1.0E-125	BE074267.1	EST_HUMAN	Homo sapiens myosin, heavy polypeptide 1, skeletal muscle, adult (MYH1), mRNA
8035	17171	26710	5.52	1.0E-125	BE074267.1	EST_HUMAN	Homo sapiens poly(A) binding protein II (PABP2) gene, complete cds
783	10022	19172	1.06	1.0E-126	4758007	NT	RC3-ST0186-250200-018-c11 ST0186 Homo sapiens cDNA
786	10025	19175	1.61	1.0E-126	M61936.1	NT	QV3-BT0569-020200-075-g09 BT0569 Homo sapiens cDNA
							QV3-BT0569-020200-075-g09 BT0569 Homo sapiens cDNA
							Homo sapiens CDC-like kinase (CLK) mRNA
							Human laminin B1 chain gene, exon 20

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2313	11507	20728	1.65	1.0E-126	8923056	NT	Homo sapiens hypothetical protein FLJ20048 (FLJ20048), mRNA
2313	11507	20728	1.65	1.0E-126	8923056	NT	Homo sapiens hypothetical protein FLJ20048 (FLJ20048), mRNA
2557	11744	20863	6.17	1.0E-126	6382078	NT	Homo sapiens RAN binding protein 2 (RANBP2), mRNA
3037	12274	21403	11.07	1.0E-126	AA160709.1	EST_HUMAN	z072c03.11 Stratagene pancreas (#637208) Homo sapiens cDNA clone IMAGE:592420 5'
3037	12274	21404	11.07	1.0E-126	AA160709.1	EST_HUMAN	z072c03.11 Stratagene pancreas (#637208) Homo sapiens cDNA clone IMAGE:592420 5'
3607	12828	21948	0.94	1.0E-126	X53941.1	NT	H. sapiens DNA for liver cytochrome b5 pseudogene
3635	12858	21975	1.42	1.0E-126	7857038	NT	Homo sapiens death receptor 8 (DR6), mRNA
4787	13988	23081	1.09	1.0E-126	AF101108.1	NT	Homo sapiens collagen type XI alpha-1 (COL11A1) gene, exon 63
4787	13988	23082	1.09	1.0E-126	AF101108.1	NT	Homo sapiens collagen type XI alpha-1 (COL11A1) gene, exon 63
4851	14040	23133	1.81	1.0E-126	N34078.1	EST_HUMAN	y078c06.1 Soares melanocyte 2NblHM Homo sapiens cDNA clone IMAGE:287850 5'
5184	14360	23448	0.61	1.0E-126	BE743922.1	EST_HUMAN	601577981F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3926885 5'
5767	14988	24388	4.09	1.0E-126	AA460075.1	EST_HUMAN	z086c03.1 Soares total_fetus_Nb2HF9_9w Homo sapiens cDNA clone IMAGE:798444 5' similar to TR:G1145980 G1145980 TITIN;
5781	14988	24401	3.92	1.0E-126	AB040958.1	NT	Homo sapiens mRNA for KIAA1525 protein, partial cds
5781	14988	24402	3.92	1.0E-126	AB040958.1	NT	Homo sapiens mRNA for KIAA1525 protein, partial cds
6459	15656	25127	3.09	1.0E-126	X18608.1	NT	Human mRNA for ankryrin (variant 2.1)
7435	16844	26136	3.63	1.0E-126	BF883175.1	EST_HUMAN	602139138F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4298240 5'
8049	17185	28724	2.23	1.0E-126	BE281660.1	EST_HUMAN	601149404F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3502129 5'
8933	14360	23449	5.06	1.0E-126	BE743922.1	EST_HUMAN	601577981F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3926885 5'
175	9456	18588	7.09	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
175	9456	18589	7.09	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
178	9456	18588	6.74	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
178	9456	18589	6.74	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
278	9553	18685	1.51	1.0E-127	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
278	9553	18688	1.51	1.0E-127	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
891	10126	19289	0.9	1.0E-127	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
928	10160	18318	1.07	1.0E-127	U72621.2	NT	Homo sapiens lost on transformation LOTT1 mRNA, complete cds
1866	10878	20063	2.02	1.0E-127	4827053	NT	Homo sapiens ubiquitin specific protease 8 (USP8) mRNA
2033	11234	20441	2.82	1.0E-127	5803085	NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 1 (LILRA1), mRNA
2033	11234	20442	2.82	1.0E-127	5803085	NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 1 (LILRA1), mRNA
2168	11364	20563	85.3	1.0E-127	4506820	NT	Homo sapiens ribosomal protein L26 (RPL26) mRNA
2310	11504	20725	2.49	1.0E-127	AF245505.1	NT	Homo sapiens adipican mRNA, complete cds

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2568	11754	20874	40.25	1.0E-127	X12881.1	NT	Human mRNA for cytokeratin 18
3870	12891	22012	0.83	1.0E-127	AF114488.1	NT	Homo sapiens interacin short isoform (ITSN) mRNA, complete cds
3788	13017	22130	1.23	1.0E-127	AW161287.1	EST_HUMAN	au80e06.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782594 5' similar to TR:Q15170 Q15170 TRANSCRIPTION FACTOR S-II-RELATED PROTEIN ;contains element MER22 repetitive element ;
4084	13302	22402	0.80	1.0E-127	AF135188.1	NT	Homo sapiens delayed rectifier potassium channel subunit (SK mRNA, complete cds
4241	13444	22534	22.24	1.0E-127	7708239	NT	Homo sapiens neuroblastoma-amplified protein (LOC51584), mRNA
4241	13444	22535	22.24	1.0E-127	7708239	NT	Homo sapiens neuroblastoma-amplified protein (LOC51584), mRNA
4498	13697	22791	0.82	1.0E-127	AF232297.1	NT	Homo sapiens cytochrome P450 retinoid metabolizing protein P450RAI-2 mRNA, complete cds
4603	13797	22887	4.81	1.0E-127	4508384	NT	Homo sapiens RAD1 (S. pombe) homolog (RAD1) mRNA, and translated products
4635	13829		2.81	1.0E-127	AL163288.2	NT	Homo sapiens chromosome 21 segment HS21C088
4678	13870	22868	0.96	1.0E-127	6912839	NT	Homo sapiens Ring1 and YY1 binding protein (RYBP), mRNA
5188	14382	23447	0.88	1.0E-127	AF105988.1	NT	Homo sapiens acetylcholine receptor epsilon subunit (CHRNAE) gene, complete cds
5188	14382	23448	0.88	1.0E-127	AF105989.1	NT	Homo sapiens acetylcholine receptor epsilon subunit (CHRNAE) gene, complete cds
5188	14382	23449	0.88	1.0E-127	AF105989.1	NT	Homo sapiens acetylcholine receptor epsilon subunit (CHRNAE) gene, complete cds
							z801a10.r1 Soares melanocyte 2N10HM Homo sapiens cDNA clone IMAGE:281258 5' similar to SW:PIP8 RAT P10688 1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 ;
5539	14783	24130	2.03	1.0E-127	W03547.1	EST_HUMAN	
5573	14797	24171	4.34	1.0E-127	X85784.1	NT	H. sapiens NOS2 gene, exon 6
5737	14956	24355	2.24	1.0E-127	X84080.1	NT	H. sapiens TCF11 gene, exon 3-6
5788	15015	24418	6.1	1.0E-127	4504778	NT	Homo sapiens Integrin, beta 8 (ITGB8) mRNA
6978	16156	25627	4.37	1.0E-127	AF274883.1	NT	Homo sapiens secretory pathway component Sec31B-1 mRNA, alternatively spliced, complete cds
6978	16156	25628	4.37	1.0E-127	AF274883.1	NT	Homo sapiens secretory pathway component Sec31B-1 mRNA, alternatively spliced, complete cds
7178	16356	25834	3.58	1.0E-127	11427235	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA
7718	16917	28424	6.61	1.0E-127	11417339	NT	Homo sapiens similar to heat shock 70kD protein 9B (mortalin-2) (H. sapiens) (LOC83184), mRNA
7718	16917	28425	6.61	1.0E-127	11417339	NT	Homo sapiens similar to heat shock 70kD protein 9B (mortalin-2) (H. sapiens) (LOC83184), mRNA
8148	17278	28822	1.83	1.0E-127	BE885415.1	EST_HUMAN	601434784F1 NIH_MGC 72 Homo sapiens cDNA clone IMAGE:3918917 5'
8148	17278	28823	1.83	1.0E-127	BE885415.1	EST_HUMAN	601434784F1 NIH_MGC 72 Homo sapiens cDNA clone IMAGE:3918917 5'
8674	9456	18588	3.11	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
8674	9456	18589	3.11	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
8884	17779	23945	1.58	1.0E-127	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
468	9719	18851	3.7	1.0E-128	BE385617.1	EST_HUMAN	601278127F1 NIH_MGC 20 Homo sapiens cDNA clone IMAGE:3618922 5'

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Table 4
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2038	11239	20448	30.04	1.0E-128	U02523.1	NT	Human FAU1P pseudogene, trinucleotide repeat regions
2038	11239	20447	30.04	1.0E-128	U02523.1	NT	Human FAU1P pseudogene, trinucleotide repeat regions
2178	11373	20595	153.58	1.0E-128	4508718	NT	Homo sapiens ribosomal protein S2 (RPS2) mRNA
2408	11800		6.88	1.0E-128	11437455	NT	Homo sapiens chromatin-specific transcription elongation factor, 140 kDa subunit (FACTP140), mRNA
3371	12688	21735	1.23	1.0E-128	AB033073.1	NT	Homo sapiens mRNA for KIAA1247 protein, partial cds
4887	13881	22882	4.92	1.0E-128	11428873	NT	Homo sapiens prospero-related homeobox 1 (PROX1), mRNA
5835	15052	24459	1.84	1.0E-128	11420985	NT	Homo sapiens phosphodiesterase 1C, calmodulin-dependent (70kD) (PDE1C), mRNA
6056	15225	24644	6.7	1.0E-128	BF224345.1	EST_HUMAN	7q86b10.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE: 3'
7120	16297	25779	3.35	1.0E-128	AA639188.1	EST_HUMAN	ns04a11.1 NCI CGAP Ew1 Homo sapiens cDNA clone IMAGE:1182820 similar to TR:G951338 G951338 CHROMOSOME SEGREGATION GENE HOMOLOG CAS.:
7288	16517	26008	5.1	1.0E-128	11425254	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2D (GRIN2D), mRNA
7308	16524	28015	8.5	1.0E-128	AA928958.1	EST_HUMAN	cm88h08.s1 NCI CGAP_G04 Homo sapiens cDNA clone IMAGE:1552383 3' similar to gb:X54941 CYCLIN-DEPENDENT KINASES REGULATORY SUBUNIT 1 (HUMAN);
8533	17559		5.07	1.0E-128	AW955290.1	EST_HUMAN	EST397360 MAGE resequences, MAGC Homo sapiens cDNA
419	9672	18814	0.87	1.0E-128	S37722.1	NT	Insulin-like growth factor binding protein-2 [human, placenta, Genomic, 1019 nt, segment 2 of 4]
1693	10905	20091	3.35	1.0E-128	AL098880.1	NT	Novel human mRNA containing Zinc finger C2H2 type domains
1698	10910	20098	1.46	1.0E-128	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
1698	10910	20097	1.46	1.0E-128	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
1613	11021	20214	2.87	1.0E-128	11418522	NT	Homo sapiens zinc finger protein 78 (expressed in testis) (ZNF78), mRNA
3082	12328	21451	1.51	1.0E-128	Q14585	SWISSPROT	ZINC FINGER PROTEIN HZF10
3082	12328	21482	1.51	1.0E-128	Q14585	SWISSPROT	ZINC FINGER PROTEIN HZF10
3082	12328	21453	1.51	1.0E-128	Q14585	SWISSPROT	ZINC FINGER PROTEIN HZF10
4148	13352	22454	2.08	1.0E-128	AB040882.1	NT	Homo sapiens mRNA for KIAA1459 protein, partial cds
4285	13488	22559	2.19	1.0E-128	AW755254.1	EST_HUMAN	CMYA5 Human cardiac muscle expression library Homo sapiens cDNA clone 4151835 similar to CMYA5 Cardiomyopathy associated gene 5
4285	13488	22560	2.19	1.0E-128	AW755254.1	EST_HUMAN	CMYA5 Human cardiac muscle expression library Homo sapiens cDNA clone 4151835 similar to CMYA5 Cardiomyopathy associated gene 5
5704	14823	24316	4.43	1.0E-128	AJ006345.1	NT	Homo sapiens KVLQ11 gene
6130	15314	24748	4.22	1.0E-128	AJ006345.1	NT	Homo sapiens KVLQ11 gene
6161	15344	24781	9.49	1.0E-128	11420850	NT	Homo sapiens similar to ribosomal protein S28 (H. sapiens) (LOC83684), mRNA
6587	15783		8.3	1.0E-128	AB014534.1	NT	Homo sapiens mRNA for KIAA0634 protein, partial cds

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7776	16971	26484	3.53	1.0E-129	AA62528.1	EST_HUMAN	af7207.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1047689 5'
7845	15344	24781	10.01	1.0E-129	11420850	NT	Homo sapiens similar to ribosomal protein S28 (H. sapiens) (LOC63694), mRNA
8520	17551		4.44	1.0E-129	HB3155.1	EST_HUMAN	y448c05.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:198112 5' similar to
8925	17808		1.73	1.0E-129	AL120739.1	EST_HUMAN	SP:B48150 B48150 HP-25-HIBERNATION-RELATED PROTEIN - TAMIAS ASIATICUS-ASIAN ;
76	9370	18499	3.47	1.0E-130	7705530	NT	DKFZp762K171_r1 762 (synonym: hmel2) Homo sapiens cDNA clone DKFZp762K171 5'
1178	10399	18552	0.7	1.0E-130	AB037835.1	NT	Homo sapiens hypothetical protein (HSPC242), mRNA
1642	10556	20037	36.76	1.0E-130	BE275192.1	EST_HUMAN	Homo sapiens mRNA for KIAA1414 protein, partial cds
1642	10556	20038	36.76	1.0E-130	BE275192.1	EST_HUMAN	601121995F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3346368 5'
1852	11168		1.9	1.0E-130	X04092.1	NT	601121995F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3346368 5'
2726	11905		8.45	1.0E-130	AJ010230.1	NT	Human gene for catelase (EC 1.11.1.6) exon 8 mapping to chromosome 11, band p13
2832	12071	21192	1.26	1.0E-130	BE564219.1	EST_HUMAN	Homo sapiens RET finger protein-like 1 antisense transcript, partial
2832	12071	21193	1.26	1.0E-130	BE564219.1	EST_HUMAN	601343016F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685468 5'
3553	12776	21905	1.13	1.0E-130	AF240898.1	NT	601343016F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685468 5'
3750	12071	21192	5.98	1.0E-130	BE564219.1	EST_HUMAN	Homo sapiens retinal dehydrogenase homolog isoform-1 (RDH) mRNA, complete cds
3750	12071	21193	5.98	1.0E-130	BE564219.1	EST_HUMAN	601343016F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685468 5'
3910	13128	22243	1.57	1.0E-130	AW503580.1	EST_HUMAN	601343016F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685468 5'
4049	13269	22361	0.97	1.0E-130	M87710.1	NT	UHF-BND-eky-g-06-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078731 5'
4535	13731	22828	8.08	1.0E-130	AW843983.1	EST_HUMAN	Human T-cell receptor (V alpha 22.1, J alpha RPM14265-variant, C alpha 1) mRNA
5127	14306	23398	1.16	1.0E-130	AW363299.1	EST_HUMAN	GM4-CN0045-180200-511-f02 CN0045 Homo sapiens cDNA
5127	14306	23397	1.16	1.0E-130	AW363299.1	EST_HUMAN	RCO-CT0318-201189-031-a11 CT0318 Homo sapiens cDNA
6187	15369	24809	2.09	1.0E-130	11416777	NT	RCO-CT0318-201189-031-a11 CT0318 Homo sapiens cDNA
6832	16026	25492	2.38	1.0E-130	AB037758.1	NT	Homo sapiens solute carrier family 8 (neurotransmitter transporter, L-proline), member 7 (SLC8A7), mRNA
4	8301	18403	2.48	0.0E+00	AA228128.1	EST_HUMAN	Homo sapiens mRNA for KIAA1335 protein, partial cds
4	8301	18404	2.48	0.0E+00	AA228128.1	EST_HUMAN	z58c04.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:667590 5' similar to TR:G222811
7	8303	18407	1.29	0.0E+00	4885136	NT	G222811 ALPHA 1 CHAIN OF TYPE XII COLLAGEN. ;
15	8311	18413	0.72	0.0E+00	8923349	NT	z58c04.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:667590 5' similar to TR:G222811
15	8311	18414	0.72	0.0E+00	8923349	NT	G222811 ALPHA 1 CHAIN OF TYPE XII COLLAGEN. ;
22	8318	18421	3.45	0.0E+00	D83327.1	NT	Homo sapiens checkpoint suppressor 1 (CHEST), mRNA
22	8318	18422	3.45	0.0E+00	D83327.1	NT	Homo sapiens hypothetical protein FLJ20371 (FLJ20371), mRNA
28	8324	18427	23.31	0.0E+00	AF141349.1	NT	Homo sapiens hypothetical protein FLJ20371 (FLJ20371), mRNA

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
38	9332	18437	2.44	0.0E+00	5802987	NT	Homo sapiens Cdc42 effector protein 2 (CEP2), mRNA
38	9334	18440	0.84	0.0E+00	M58800.1	NT	Human heparin cofactor II (HCF2) gene, exons 1 through 5
42	9338	18445	5.84	0.0E+00	6857825	NT	Homo sapiens RNA-binding protein S1, serine-rich domain (RNPS1), mRNA
58	9355	18472	2.5	0.0E+00	Y17151.2	NT	Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3)
68	9356	18473	2.5	0.0E+00	Y17151.2	NT	Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3)
61	9357	18477	1.28	0.0E+00	D78804.1	EST_HUMAN	HUM516H08B Human placenta polyA+ (TFujwara) Homo sapiens cDNA clone GEN-516H08 5'
61	9357	18478	1.28	0.0E+00	D78804.1	EST_HUMAN	HUM516H08B Human placenta polyA+ (TFujwara) Homo sapiens cDNA clone GEN-516H08 5'
62	9358	18479	27.84	0.0E+00	L16558.1	NT	Human ribosomal protein L7 (RPL7) mRNA, complete cds
64	9360	18482	8.6	0.0E+00	AW069534.1	EST_HUMAN	cr48e07.x1 Jia bone marrow stroma Homo sapiens cDNA clone HBMSC_cr48e07 3'
64	9360	18483	8.6	0.0E+00	AW069534.1	EST_HUMAN	cr48e07.x1 Jia bone marrow stroma Homo sapiens cDNA clone HBMSC_cr48e07 3'
78	9369	18487	0.73	0.0E+00	4758977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
75	9369	18488	0.73	0.0E+00	4758977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
78	9369	18497	0.82	0.0E+00	4758977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
78	9369	18498	0.82	0.0E+00	4758977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
81	9374	18504	0.87	0.0E+00	4501850	NT	Homo sapiens amiloride binding protein 1 (amiline oxidase (copper-containing)) (ABP1), nuclear gene encoding mitochondrial protein, mRNA
82	9375	18504	33.19	0.0E+00	4504444	NT	Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1) mRNA
91	9384	18513	39.94	0.0E+00	5016088	NT	Homo sapiens actin, beta (ACTB) mRNA
94	9387	18516	25.33	0.0E+00	U89277.1	NT	Homo sapiens actin, beta (ACTB) mRNA
101	9394	18523	1.41	0.0E+00	A1114743.1	EST_HUMAN	Human polyhomeotic 1 homolog (HPH1) mRNA, partial cds
102	9395	18524	1.65	0.0E+00	AB037784.1	NT	HA1347 Human fetal liver cDNA library Homo sapiens cDNA
107	9397	18527	0.68	0.0E+00	X91213.1	NT	Homo sapiens mRNA for KIAA1363 protein, partial cds
116	9404	18533	2.12	0.0E+00	A1623701.1	EST_HUMAN	H. sapiens ncl1 gene (exon 2)
117	9404	18533	1.15	0.0E+00	A1623701.1	EST_HUMAN	ts38b05.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2230833 3' similar to TR:Q99551 Q98551 MITOCHONDRIAL TRANSCRIPTION TERMINATION FACTOR PRECURSOR.;
118	11836	18534	2.65	0.0E+00	N36040.1	EST_HUMAN	ts38b05.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2230833 3' similar to TR:Q99551 Q98551 MITOCHONDRIAL TRANSCRIPTION TERMINATION FACTOR PRECURSOR.;
118	11838	18535	2.65	0.0E+00	N36040.1	EST_HUMAN	ts38b05.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2230833 3' similar to TR:Q99551 Q98551 MITOCHONDRIAL TRANSCRIPTION TERMINATION FACTOR PRECURSOR.;
128	9411	18545	4.14	0.0E+00	4505938	NT	Y01h08.r1 Soares melanocyte 2NbhM Homo sapiens cDNA clone IMAGE:270017 5'
128	9411	18546	4.14	0.0E+00	4505938	NT	Y01h08.r1 Soares melanocyte 2NbhM Homo sapiens cDNA clone IMAGE:270017 5'
137	9419	18553	1.13	0.0E+00	T56945.1	EST_HUMAN	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide A (220kD) (POLR2A) mRNA
137	9419	18554	1.13	0.0E+00	T56945.1	EST_HUMAN	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide A (220kD) (POLR2A) mRNA
158	9438	18575	34.89	0.0E+00	4504444	NT	ye83g04.r2 Stratigene fetal spleen (#837205) Homo sapiens cDNA clone IMAGE:88310 5'
160	9442	18575	2.05	0.0E+00	BF038881.1	EST_HUMAN	ye83g04.r2 Stratigene fetal spleen (#837205) Homo sapiens cDNA clone IMAGE:88310 5'
							Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1) mRNA
							601460375F1 NIH_MGC_86 Homo sapiens cDNA clone IMAGE:3863803 5'

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Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
736	9877	19116	4.24	0.0E+00	AF284750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
736	9877	19117	4.24	0.0E+00	AF284750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
738	9878	19120	13.52	0.0E+00	11545800	NT	Homo sapiens hypothetical protein FLJ21834 (FLJ21834), mRNA
744	9885	19128	2.08	0.0E+00	BE241577.1	EST_HUMAN	TCAAP1D0779 Pediatric acute myelogenous leukemia cell (FAB M1) Bay/for-HGSC project=TCAA Homo sapiens cDNA clone TCAAP0779
764	10004	19152	1.52	0.0E+00	AF226890.2	NT	Homo sapiens MHC class I antigen (HLA-G) mRNA, HLA-G1 allele, complete cds
764	10004	19153	1.52	0.0E+00	AF226890.2	NT	Homo sapiens MHC class I antigen (HLA-G) mRNA, HLA-G1 allele, complete cds
767	10007	19156	1.76	0.0E+00	J03784.1	NT	Human, plasminogen activator inhibitor-1 gene, exons 2 to 9
767	10007	19157	1.76	0.0E+00	J03784.1	NT	Human, plasminogen activator inhibitor-1 gene, exons 2 to 9
770	10010	19168	1.02	0.0E+00	AB037760.1	NT	Homo sapiens mRNA for KIAA1339 protein, partial cds
771	10011	19159	2.04	0.0E+00	6912749	NT	Homo sapiens zinc finger protein 212 (ZNF212), mRNA
773	11877	19161	2.38	0.0E+00	D30612.1	NT	Homo sapiens mRNA for repressor protein, partial cds
774	10013	19162	2.78	0.0E+00	BE868735.1	EST_HUMAN	601445947F1 NIH_MGC 95 Homo sapiens cDNA clone IMAGE:3949803 5'
778	10017	19168	3.28	0.0E+00	R48915.1	EST_HUMAN	y68908.r1 Soares breast ZNF181 Homo sapiens cDNA clone IMAGE:154048 5'
778	10018	19167	3	0.0E+00	5032088	NT	Homo sapiens splicing factor 3a, subunit 1, 120kD (SF3A1), mRNA
788	10027	19178	1.78	0.0E+00	AB011398.1	NT	Homo sapiens gene for AF-6, complete cds
791	10031	19180	3.24	0.0E+00	7681985	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
802	10041	19182	0.95	0.0E+00	D80008.1	NT	Human mRNA for KIAA0184 gene, partial cds
802	10041	19183	0.95	0.0E+00	D80008.1	NT	Human mRNA for KIAA0184 gene, partial cds
807	10046	19197	2.72	0.0E+00	X89772.1	NT	H. sapiens mRNA for interferon alpha/beta receptor (long form)
811	10050	19201	3.81	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
811	10050	19202	3.81	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
816	10054	19208	12.64	0.0E+00	5174478	NT	Homo sapiens pericentrin (PCNT) mRNA
817	10055	19228	10.04	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
834	10072	19228	1.58	0.0E+00	7857213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
835	10073	19230	2.71	0.0E+00	7857213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
837	10075	19232	2.56	0.0E+00	4557688	NT	Homo sapiens potassium voltage-gated channel, Isk-related family, member 1 (KCNE1) mRNA
843	10080	19238	1.38	0.0E+00	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MN1BH) mRNA, complete cds
843	10080	19239	1.38	0.0E+00	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MN1BH) mRNA, complete cds
844	10081	19240	0.85	0.0E+00	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MN1BH) mRNA, complete cds
849	10088	19245	1.3	0.0E+00	4503854	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (GABPA), mRNA
853	10089	19250	2.28	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
853	10089	19251	2.28	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
860	10098		1.51	0.0E+00	AF027153.1	NT	Homo sapiens sodium/myo-inositol cotransporter (SLC5A3) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
884	10100	19282	6.12	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
884	10100	19283	6.12	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
885	10101	19284	8.12	0.0E+00	4507152	NT	Homo sapiens SON DNA binding protein (SON) mRNA
886	10102	19285	3.01	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
887	10103	19286	9.08	0.0E+00	4508728	NT	Homo sapiens ribosomal protein S5 (RPS5) mRNA
871	10107	19288	1.67	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
871	10107	19270	1.67	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
872	10108	19271	2.32	0.0E+00	AA53272.1	EST_HUMAN	U68d07.s1 NCI_CGAP_P10 Homo sapiens cDNA clone IMAGE:597453
872	10108	19272	2.32	0.0E+00	AA53272.1	EST_HUMAN	U68d07.s1 NCI_CGAP_P10 Homo sapiens cDNA clone IMAGE:597453
873	10109		8.85	0.0E+00	BF677694.1	EST_HUMAN	802085578F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4246815 5'
877	10113	19273	1.37	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
877	10113	19274	1.37	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
878	10114	19275	2.16	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
878	10114	19276	2.16	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
801	10136	19289	1.84	0.0E+00	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
908	10143	19304	1.71	0.0E+00	BE089592.1	EST_HUMAN	QV0-BT0703-280400-211-g11 BT0703 Homo sapiens cDNA
908	10143	19305	1.71	0.0E+00	BE089592.1	EST_HUMAN	QV0-BT0703-280400-211-g11 BT0703 Homo sapiens cDNA
918	10153	19314	2.88	0.0E+00	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
928	10162		38.57	0.0E+00	4504958	NT	Homo sapiens laminin receptor 1 (67kD, ribosomal protein SA) (LAMR1), mRNA
930	10162		32.73	0.0E+00	4504958	NT	Homo sapiens laminin receptor 1 (67kD, ribosomal protein SA) (LAMR1), mRNA
931	10164	19321	0.76	0.0E+00	AF088747.1	NT	Homo sapiens alpha-1-antichymotrypsin precursor, mRNA, partial cds
932	10165	19322	1.87	0.0E+00	L28101.1	NT	Homo sapiens kallistatin (Pl4) gene, exons 1-4, complete cds
988	10191	19345	1.41	0.0E+00	M37190.1	NT	Human ras inhibitor mRNA, 3' end
959	10192	19346	8.37	0.0E+00	M37190.1	NT	Human ras inhibitor mRNA, 3' end
980	10193	19347	0.83	0.0E+00	M37190.1	NT	Human ras inhibitor mRNA, 3' end
961	10194	19348	1.68	0.0E+00	4507430	NT	Homo sapiens thymotropic embryonic factor (TEF), mRNA
961	10194	19349	1.68	0.0E+00	4507430	NT	Homo sapiens thymotropic embryonic factor (TEF), mRNA
969	11982	19356	2.74	0.0E+00	A001948.1	EST_HUMAN	cs98e03.s1 NCI_CGAP_GC3 Homo sapiens cDNA clone IMAGE:1613404 3'
969	11982	19357	2.74	0.0E+00	A001948.1	EST_HUMAN	cs98e03.s1 NCI_CGAP_GC3 Homo sapiens cDNA clone IMAGE:1613404 3'
971	10203	19359	7.12	0.0E+00	7657288	NT	Homo sapiens KIAA0929 protein Max2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
982	10213	19369	2.97	0.0E+00	AB030566.1	NT	Homo sapiens mRNA for PSP24, complete cds
980	10221	19375	1.29	0.0E+00	BF366974.1	EST_HUMAN	PM2-GN0014-050900-001-f02 GN0014 Homo sapiens cDNA
980	10221	19376	1.29	0.0E+00	BF366974.1	EST_HUMAN	PM2-GN0014-050900-001-f02 GN0014 Homo sapiens cDNA

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
980	10221	18377	1.29	0.0E+00	BF368974.1	EST_HUMAN	PM2-GN0014-050800-001-f02 GN0014 Homo sapiens cDNA
981	10222	18378	2.96	0.0E+00	X52207.1	NT	Homo sapiens partial c-fgr gene, exons 2 and 3
991	10222	18379	2.96	0.0E+00	X52207.1	NT	Homo sapiens partial c-fgr gene, exons 2 and 3
1000	10231	18386	2.42	0.0E+00	4757868	NT	Homo sapiens chromodomain protein, Y chromosome-like (CDYL) mRNA
1012	10242	18394	2.4	0.0E+00	U83688.1	NT	Human beta-tubulin (TUB44) gene, complete cds
1013	10243	18395	37.53	0.0E+00	U83688.1	NT	Human beta-tubulin (TUB44) gene, complete cds
1014	10243	18395	9.7	0.0E+00	U83688.1	NT	Human beta-tubulin (TUB44) gene, complete cds
1017	10246		13.45	0.0E+00	AF188490.1	NT	Homo sapiens 8q22.1 region and MTG8 (CBFA2T1) gene, partial cds
1018	10246		12.78	0.0E+00	AF188490.1	NT	Homo sapiens 8q22.1 region and MTG8 (CBFA2T1) gene, partial cds
1021	10249	19400	2.19	0.0E+00	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
1022	10249	19400	2.09	0.0E+00	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
1023	10249	19400	1.72	0.0E+00	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
1024	10250	19401	2.61	0.0E+00	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
1027	10253	19404	3.31	0.0E+00	7661685	NT	Homo sapiens DKFZ586M0122 protein (DKFZ586M0122), mRNA
1031	10267	19408	4.14	0.0E+00	5803114	NT	Homo sapiens inner membrane protein, mitochondrial (IMMT), mRNA
1033	10259		4.94	0.0E+00	AA456880.1	EST_HUMAN	aa8607.e1 Stratiogene fetal retina 937202 Homo sapiens cDNA clone IMAGE:838236 3' similar to SW:PRS8_HUMAN P47210 26S PROTEASE REGULATORY SUBUNIT 8 ;
1038	10262	19413	0.95	0.0E+00	N43182.1	EST_HUMAN	EST5124 WATM1 Homo sapiens cDNA clone 5124 similar to DNA-DIRECTED RNA POLYMERASE II (alignment Ser and Pro with BLASTx or p)
1038	10262	19414	0.95	0.0E+00	N43182.1	EST_HUMAN	EST5124 WATM1 Homo sapiens cDNA clone 5124 similar to DNA-DIRECTED RNA POLYMERASE II (alignment Ser and Pro with BLASTx or p)
1037	10263	19415	2.08	0.0E+00	4759249	NT	Homo sapiens TRAF family member-associated NFKB activator (TANK) mRNA
1037	10263	19416	2.06	0.0E+00	4759249	NT	Homo sapiens TRAF family member-associated NFKB activator (TANK) mRNA
1040	10266		6.28	0.0E+00	8923833	NT	Homo sapiens hypothetical protein FLJ11198 (FLJ11198), mRNA
1054	10260	19431	9.68	0.0E+00	4759569	NT	Homo sapiens heat shock 70kD protein 98 (hsc70) (HSPA98) mRNA
1072	10297	19448	2.84	0.0E+00	4826872	NT	Homo sapiens cadherin 6, K-cadherin (fetal kidney) (CDH6) mRNA
1072	10297	19447	2.84	0.0E+00	4826872	NT	Homo sapiens cadherin 6, K-cadherin (fetal kidney) (CDH6) mRNA
1078	10301	19451	7.53	0.0E+00	8923824	NT	Homo sapiens hypothetical protein FLJ20685 (FLJ20685), mRNA
1078	10301	19452	7.53	0.0E+00	8923824	NT	Homo sapiens hypothetical protein FLJ20685 (FLJ20685), mRNA
1077	10302	19453	88.63	0.0E+00	AJ245922.1	NT	Homo sapiens mRNA for alpha-tubulin 8 (TUBA8 gene)
1079	10304		0.78	0.0E+00	8923087	NT	Homo sapiens hypothetical protein FLJ20080 (FLJ20080), mRNA
1081	10306	19457	3.29	0.0E+00	5174384	NT	Homo sapiens alkylation repair; alkB homolog (ABH), mRNA
1080	10314	19468	10.32	0.0E+00	4756117	NT	Homo sapiens Death associated protein 3 (DAP3) mRNA
1104	10328	19478	2.49	0.0E+00	BE005208.1	EST_HUMAN	MRO-BN0115-200300-003-h08 BN0115 Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1127	10351	19502	4.27	0.0E+00	7706134	NT	Homo sapiens potassium channel, subfamily K, member 9 (KCNK9), mRNA
1127	10351	19503	4.27	0.0E+00	7706134	NT	Homo sapiens potassium channel, subfamily K, member 9 (KCNK9), mRNA
1140	10363	19513	1.08	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
1140	10363	19514	1.08	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
1141	10384	19515	18.48	0.0E+00	4508712	NT	Homo sapiens ribosomal protein S27a (RPS27A) mRNA
1143	10388	19517	0.74	0.0E+00	8923290	NT	Homo sapiens hypothetical protein FLJ20309 (FLJ20309), mRNA
1148	10369	19520	8.75	0.0E+00	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
1148	10371	19521	27.94	0.0E+00	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
1149	10372	19522	3.79	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
1149	10372	19523	3.79	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
1153	10376	19528	1.82	0.0E+00	7706500	NT	Homo sapiens Npw38-binding protein NpwBP (LOC51728), mRNA
1154	10378	19527	0.63	0.0E+00	X95826.1	NT	H. sapiens ART4 gene
1154	10378	19528	0.63	0.0E+00	X95826.1	NT	H. sapiens ART4 gene
1155	10377	19529	0.79	0.0E+00	A1147850.1	EST_HUMAN	gb22d10.x1 Scores_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:1697011 3'
1167	10379	19531	1.09	0.0E+00	AB020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
1164	10388	19537	2.81	0.0E+00	8906844	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
1176	10397	19548	2.31	0.0E+00	7305078	NT	Homo sapiens glutamate decarboxylase 1 (brain, 67kD) (GAD1), transcript variant GAD25, mRNA
1176	10397	19550	2.31	0.0E+00	7305078	NT	Homo sapiens glutamate decarboxylase 1 (brain, 67kD) (GAD1), transcript variant GAD25, mRNA
1179	10400	19553	0.8	0.0E+00	AB037835.1	NT	Homo sapiens mRNA for KIAA1414 protein, partial cds
1186	10407	19562	34.92	0.0E+00	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
1217	10435		1.33	0.0E+00	7667338	NT	Homo sapiens mult. (E. coli) homolog 3 (MLH3), mRNA
1230	10448	19604	1.02	0.0E+00	8922593	NT	Homo sapiens hypothetical protein FLJ10697 (FLJ10697), mRNA
1233	10451	19607	1.44	0.0E+00	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1234	10451	19608	1.44	0.0E+00	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1234	10452	19609	1.02	0.0E+00	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1235	11968	19610	1.63	0.0E+00	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1253	10469	19633	5.36	0.0E+00	AF106718.1	NT	Homo sapiens chromosome 3 subtelomeric region
1254	10470	19634	1.58	0.0E+00	4503098	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
1284	10479	19640	1.08	0.0E+00	4505740	NT	Homo sapiens prefoldin 4 (PFDN4) mRNA
1273	10488		2.95	0.0E+00	Y18000.1	NT	Homo sapiens NIF2 gene
1281	10496	19655	97.05	0.0E+00	4506718	NT	Homo sapiens ribosomal protein S2 (RPS2) mRNA
1288	10503	19684	3.99	0.0E+00	AF084478.1	NT	Homo sapiens Williams-Beuren syndrome deletion transcript 8 (WBSOR8) mRNA, complete cds
1294	10509	19698	3.05	0.0E+00	AB040940.1	NT	Homo sapiens mRNA for KIAA1507 protein, partial cds
1284	10508	19669	3.05	0.0E+00	AB040940.1	NT	Homo sapiens mRNA for KIAA1507 protein, partial cds

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
162	9444		61.78	0.0E+00	4504444	NT	Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1) mRNA
165	9447	18578	0.97	0.0E+00	AF111188.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
167	9449	18579	0.94	0.0E+00	BE285973.1	EST_HUMAN	601174270F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3528884 5'
168	9449	18579	0.76	0.0E+00	BE285973.1	EST_HUMAN	601174270F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3528884 5'
169	9450	18580	3.85	0.0E+00	W73973.1	EST_HUMAN	zid6205.1 Soares_fetal_Heart_NbHH19W Homo sapiens cDNA clone IMAGE:345201 5' similar to
170	9451	18581	0.69	0.0E+00	BE162832.1	EST_HUMAN	QV3-HT0457-140200-088-d04 HT0457 Homo sapiens cDNA
170	9451	18582	0.89	0.0E+00	BE162832.1	EST_HUMAN	QV3-HT0457-140200-088-d04 HT0457 Homo sapiens cDNA
171	9452	18583	2.33	0.0E+00	AF244088.1	NT	Homo sapiens zinc finger protein mRNA, complete cds
174	9455	18586	7.31	0.0E+00	AL183202.2	NT	Homo sapiens chromosome 21 segment HS21C002
174	9455	18587	7.31	0.0E+00	AL183202.2	NT	Homo sapiens chromosome 21 segment HS21C002
185	9484	18594	4.28	0.0E+00	BE018970.1	EST_HUMAN	bb24e12.y1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2863854 5' similar to WP:Y67A10A.Z
185	9484	18595	4.28	0.0E+00	BE018970.1	EST_HUMAN	bb24e12.y1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2863854 5' similar to WP:Y67A10A.Z
180	9489	18598	2.81	0.0E+00	AB018327.1	NT	Homo sapiens mRNA for KIAA0784 protein, partial cds
190	9490	18599	2.81	0.0E+00	AB018327.1	NT	Homo sapiens mRNA for KIAA0784 protein, partial cds
191	9470	18600	1.3	0.0E+00	AB018327.1	NT	Homo sapiens mRNA for KIAA0784 protein, partial cds
191	9470	18601	1.3	0.0E+00	AB018327.1	NT	Homo sapiens mRNA for KIAA0784 protein, partial cds
199	9479	18612	122.25	0.0E+00	D50659.1	NT	Human gamma-cytoplasmic actin (ACTG38) pseudogene
204	9484	18617	4.3	0.0E+00	AF273045.1	NT	Homo sapiens CTCL tumor antigen se14-3 mRNA, complete cds
204	9484	18618	4.3	0.0E+00	AF273045.1	NT	Homo sapiens CTCL tumor antigen se14-3 mRNA, complete cds
208	9488	18620	12.98	0.0E+00	AF167174.1	NT	Homo sapiens chromosome X MSL3-2 protein mRNA, complete cds
208	9488	18621	12.98	0.0E+00	AF167174.1	NT	Homo sapiens chromosome X MSL3-2 protein mRNA, complete cds
215	11862	18627	28.1	0.0E+00	AI587308.1	EST_HUMAN	tp04f08.x1 NCI_CGAP_U13 Homo sapiens cDNA clone IMAGE:2207847 3' similar to gb:J03181 PROFILIN1 (HUMAN);
215	11862	18628	28.1	0.0E+00	AI587308.1	EST_HUMAN	tp04f08.x1 NCI_CGAP_U13 Homo sapiens cDNA clone IMAGE:2207847 3' similar to gb:J03181 PROFILIN1 (HUMAN);
217	9496	18630	2	0.0E+00	AF195658.1	NT	Homo sapiens DNA mismatch repair protein (MLH3) gene, complete cds
219	9498		39.28	0.0E+00	4508632	NT	Homo sapiens ribosomal protein L31 (RPL31) mRNA
220	9499		11.09	0.0E+00	AF132000.1	NT	Homo sapiens TADA1 protein mRNA, complete cds
226	9505	18635	1.91	0.0E+00	AB018284.1	NT	Homo sapiens mRNA for KIAA0721 protein, partial cds
227	9505	18635	1.98	0.0E+00	AB018284.1	NT	Homo sapiens mRNA for KIAA0721 protein, partial cds
228	9508	18636	2.02	0.0E+00	6878444	NT	Mus musculus testis-specific protein, Y-encoded-like (TespY), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
242	9520	18651	6.91	0.0E+00	5453805	NT	Homo sapiens NS1-associated protein 1 (NSAP1) mRNA
244	9522		10.25	0.0E+00	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
251	9527	18657	4.08	0.0E+00	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
253	9529	18660	1.76	0.0E+00	X89772.1	NT	H. sapiens mRNA for Interferon alpha/beta receptor (long form)
261	9537		9.15	0.0E+00	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
274	9549	18679	1.3	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
274	9549	18680	1.3	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
276	9551	18682	2.35	0.0E+00	7706028	NT	Homo sapiens hypothetical protein (LOC51250), mRNA
287	9561		1.27	0.0E+00	D83327.1	NT	Homo sapiens DCRR1 mRNA, partial cds
288	9562	18695	3.32	0.0E+00	D83327.1	NT	Homo sapiens DCRR1 mRNA, partial cds
288	9562	18698	3.32	0.0E+00	D83327.1	NT	Homo sapiens DCRR1 mRNA, partial cds
288	9563		0.81	0.0E+00	AW845293.1	EST_HUMAN	IL2-CT0031-181199-020-B03 CT0031 Homo sapiens cDNA
298	9571	18703	8.24	0.0E+00	4557028	NT	Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 15 (KCNJ15) mRNA
298	9571	18704	8.24	0.0E+00	4557028	NT	Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 15 (KCNJ15) mRNA
309	9582	18714	3.6	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
310	9583	18715	3.82	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
311	11905		14.42	0.0E+00	4508728	NT	Homo sapiens ribosomal protein S5 (RPS5) mRNA
312	9594	18716	0.88	0.0E+00	4503914	NT	Homo sapiens phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase,
313	9595		4.5	0.0E+00	AA480002.1	EST_HUMAN	phosphoribosylmethylimidazole synthetase (GART) mRNA
314	9598	18717	21.53	0.0E+00	4507152	NT	zv18c08.r1 Soares_NIHMPy_S1 Homo sapiens cDNA clone IMAGE:753994 5'
315	9599	18717	17.61	0.0E+00	4507152	NT	Homo sapiens SON DNA binding protein (SON) mRNA
319	9599	18721	1.63	0.0E+00	AF114488.1	NT	Homo sapiens SON DNA binding protein (SON) mRNA
332	9602	18730	1.09	0.0E+00	O14867	SWISSPROT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
332	9602	18731	1.09	0.0E+00	O14867	SWISSPROT	TRANSCRIPTION REGULATOR PROTEIN BACH1 (BTB AND CNC HOMOLOG 1) (HA2303)
333	9603	18732	3.8	0.0E+00	7657213	NT	Homo sapiens homonally upregulated neu tumor-associated kinase (HUNK), mRNA
334	9603	18732	2.51	0.0E+00	7657213	NT	Homo sapiens homonally upregulated neu tumor-associated kinase (HUNK), mRNA
349	9617	18744	1.86	0.0E+00	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4
350	9618	18745	1.11	0.0E+00	4505256	NT	(MLLT4) mRNA
353	9621	18749	22.13	0.0E+00	4827057	NT	Homo sapiens moesin (MSN), mRNA
356	9624	18754	1.89	0.0E+00	U71600.1	NT	Homo sapiens X-box binding protein 1 (XBP1) mRNA
361	9628	18758	2.64	0.0E+00	AF231918.1	NT	Human zinc finger protein zfp31 (zfp31) mRNA, partial cds
361	9628	18758	2.54	0.0E+00	AF231918.1	NT	Homo sapiens chromosome 21 unknown mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
362	11968	18760	4.02	0.0E+00	AF231819.1	NT	Homo sapiens chromosome 21 unknown mRNA
364	9630	18762	0.8	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
366	9633	18766	1.94	0.0E+00	4503854	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (GABPA), mRNA
367	9634	18767	1.2	0.0E+00	D80008.1	NT	Human mRNA for KIAA0184 gene, partial cds
368	9634	18767	1	0.0E+00	D80008.1	NT	Human mRNA for KIAA0184 gene, partial cds
370	9638	18769	0.89	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
381	9645	18780	2.68	0.0E+00	AU134863.1	EST_HUMAN	AU134863 PLACE1 Homo sapiens cDNA clone PLACE1000889 5'
392	9686	18824	7.13	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
393	9687	18825	2.48	0.0E+00	AJ363014.1	EST_HUMAN	q61H05.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2018457 3' similar to gb:X54189
397	9652	18787	2.84	0.0E+00	AW764180.1	EST_HUMAN	PHOSPHORIBOSYLAMINE--GLYCINE LIGASE (HUMAN);
400	9654	18790	12.1	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
401	9655	18791	2.32	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
401	9655	18792	2.32	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
402	9658	18793	1.17	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
403	9657	18794	1.6	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
403	9657	18795	1.6	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
404	9658	18796	0.59	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
405	9659	18797	3.48	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
406	9660	18798	0.61	0.0E+00	4503680	NT	Homo sapiens gene for RNA pol II largest subunit, exons 23-29
407	9661	18799	1.85	0.0E+00	X74870.1	NT	H. sapiens gene for RNA pol II largest subunit, exons 23-29
408	9661	18799	1.89	0.0E+00	X74870.1	NT	H. sapiens gene for RNA pol II largest subunit, exons 23-29
408	9661	18800	1.89	0.0E+00	X74870.1	NT	H. sapiens gene for RNA pol II largest subunit, exons 23-29
412	9665		51.35	0.0E+00	4506608	NT	Homo sapiens ribosomal protein L19 (RPL19) mRNA
426	9291	18993	1.21	0.0E+00	R17765.1	EST_HUMAN	yg09a02.1 Soares Infant brain T1B1 Homo sapiens cDNA clone IMAGE:31652 5'
434	9668	18826	1.24	0.0E+00	4503914	NT	Homo sapiens phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase,
435	9669		18.94	0.0E+00	4506728	NT	phosphoribosylaminimidazole synthetase (GART) mRNA
436	9690	18827	7.31	0.0E+00	AB028942.1	NT	Homo sapiens ribosomal protein S5 (RPS5) mRNA
437	9691	18828	4.64	0.0E+00	4507152	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
437	9691	18829	4.64	0.0E+00	4507152	NT	Homo sapiens SON DNA binding protein (SON) mRNA
438	9692	18830	3.52	0.0E+00	AF193607.1	NT	Homo sapiens SON DNA binding protein (SON) mRNA
450	9703		0.92	0.0E+00	AL163201.2	NT	Mus musculus truncated SON protein (Son) mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
452	9705	18843	1.29	0.0E+00	4557879	NT	Homo sapiens Interferon gamma receptor 1 (IFNGR1) mRNA
457	9710		1.48	0.0E+00	AA324262.1	EST_HUMAN	EST27054 Carabellum II Homo sapiens cDNA 5' end
458	9711		2.64	0.0E+00	BE254447.1	EST_HUMAN	601111520F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352348 5'
474	9727	18857	6.06	0.0E+00	4504532	NT	Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1B (HTR1B) mRNA
474	9727	18858	6.06	0.0E+00	4504532	NT	Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1B (HTR1B) mRNA
480	9732	18866	15.14	0.0E+00	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
480	9732	18867	15.14	0.0E+00	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
490	9743	18873	3.04	0.0E+00	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
491	9744	18874	7.23	0.0E+00	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
491	9744	18875	7.23	0.0E+00	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
500	9752	18880	2.83	0.0E+00	AB033035.1	NT	Homo sapiens mRNA for KIAA1209 protein, partial cds
502	9754	18882	1.88	0.0E+00	AU132898	EST_HUMAN	AU132898 NT2RP4 Homo sapiens cDNA clone NT2RP4000837 5'
510	9762	18888	3.47	0.0E+00	AU132898.1	EST_HUMAN	601274951F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3615756 5'
511	11969	18889	1.89	0.0E+00	BE385144.1	EST_HUMAN	PMO-D10065-130400-002-c08 DT0065 Homo sapiens cDNA
514	9765	18891	1.14	0.0E+00	AL117233.1	NT	Novel human gene mapping to chromosome 1
515	9766	18892	1.09	0.0E+00	8923955	NT	Homo sapiens PC328 protein (PC328), mRNA
518	9769		0.75	0.0E+00	BF373403.1	EST_HUMAN	IL2-F10159-070800-120-F07 F10159 Homo sapiens cDNA
525	9776	18901	8.28	0.0E+00	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
532	11970	18905	1.5	0.0E+00	BE081527.1	EST_HUMAN	QV2-BT0635-160400-142-R05 BT0635 Homo sapiens cDNA
537	9788	18911	1.08	0.0E+00	BF028005.1	EST_HUMAN	601764658F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3896898 5'
543	9784	18918	1.13	0.0E+00	AB040809.1	NT	Homo sapiens mRNA for KIAA1478 protein, partial cds
546	9787	18921	9.28	0.0E+00	6006030	NT	Homo sapiens transcription elongation factor B (SIII), polypeptide 1-like (TCEB1L) mRNA
547	9788	18922	4.75	0.0E+00	4504036	NT	Homo sapiens guanine nucleotide binding protein (G protein), alpha 11 (Gq class) (GNA11) mRNA
547	9788	18923	4.75	0.0E+00	4504036	NT	Homo sapiens guanine nucleotide binding protein (G protein), alpha 11 (Gq class) (GNA11) mRNA
549	9800	18925	1.77	0.0E+00	8923831	NT	Homo sapiens anillin (LOC54443), mRNA
550	9801	18926	1.44	0.0E+00	8923831	NT	Homo sapiens anillin (LOC54443), mRNA
550	9801	18927	1.44	0.0E+00	8923831	NT	Homo sapiens anillin (LOC54443), mRNA
555	9805		5.12	0.0E+00	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
563	9813	18936	1.42	0.0E+00	AW135324.1	EST_HUMAN	UH-H-BJ1-acb-h-04-0-UJ.e1 NCJ_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2713951 3'
573	9823		7.59	0.0E+00	D10083.1	NT	Homo sapiens RGH1 gene, retrovirus-like element
593	9841	18961	3.94	0.0E+00	5174742	NT	Homo sapiens ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1 (UQCRCF1), nuclear gene encoding mitochondrial protein, mRNA
606	9853		5.9	0.0E+00	J04086.1	NT	Human apolipoprotein A-I (ApoA-I) gene, exon 1

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
609	9858	18875	3.34	0.0E+00	BF104898.1	EST_HUMAN	601822827F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4045447 5'
615	9860	18879	1.28	0.0E+00	4501854	NT	Homo sapiens acetyl-Coenzyme A carboxylase beta (ACACB), mRNA
620	9865	18885	0.9	0.0E+00	AF221712.1	NT	Homo sapiens Smad- and Olf-interacting zinc finger protein mRNA, partial cds
620	9865	18886	0.9	0.0E+00	AF221712.1	NT	Homo sapiens Smad- and Olf-interacting zinc finger protein mRNA, partial cds
628	9873	18894	2.58	0.0E+00	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
630	9875	18897	0.93	0.0E+00	AB037807.1	NT	Homo sapiens mRNA for KIAA1388 protein, partial cds
632	9877	18898	1.89	0.0E+00	6806818	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
633	9878	18899	2.11	0.0E+00	6806818	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
633	9878	19000	2.11	0.0E+00	6806818	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
634	9879	19001	0.94	0.0E+00	6806818	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
634	9879	19002	0.94	0.0E+00	6806818	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
641	9887	19012	1.32	0.0E+00	AA396486.1	EST_HUMAN	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
645	9891	19016	12.08	0.0E+00	D11078.1	NT	Homo sapiens RGH2 gene, retrovirus-like element
649	9895	19019	3.5	0.0E+00	W78811.1	EST_HUMAN	zh51b04.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:415587 5' similar to gb:A21187 ALPHA-2-MACROGLOBULIN PRECURSOR (HUMAN);
649	9895	19020	3.5	0.0E+00	W78811.1	EST_HUMAN	zh51b04.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:415587 5' similar to gb:A21187 ALPHA-2-MACROGLOBULIN PRECURSOR (HUMAN);
652	9896		3.55	0.0E+00	4885526	NT	Homo sapiens novel SH2-containing protein 3 (NSP3) mRNA
659	9905	19032	2.48	0.0E+00	6006003	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2B (GRIN2B) mRNA
661	9907	19035	1.98	0.0E+00	5031624	NT	Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA
664	9910	19039	1.49	0.0E+00	U05235.1	NT	Human neutral amino acid transporter (ASCT1) gene, exon 8
668	9914	19042	0.87	0.0E+00	AF108389.1	NT	Homo sapiens sodium/calcium exchanger isoform NaCa3 (NCX1) mRNA, complete cds
668	9914	19043	0.87	0.0E+00	AF108389.1	NT	Homo sapiens sodium/calcium exchanger isoform NaCa3 (NCX1) mRNA, complete cds
674	9919	19048	4.8	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
674	9919	19049	4.8	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
680	11973		1.28	0.0E+00	X57147.1	NT	Human endogenous retrovirus pHE.1 (ERV8)
689	9932	19063	17.16	0.0E+00	4504424	NT	Homo sapiens high-mobility group (nonhistone chromosomal) protein 1 (HMG1) mRNA
694	9937	19067	4.7	0.0E+00	AB028012.1	NT	Homo sapiens mRNA for KIAA1089 protein, partial cds
704	9948	19082	3.3	0.0E+00	7857488	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
716	9958	19096	106.67	0.0E+00	AA614537.1	EST_HUMAN	np48401.s1 NCL CGAP_Br.1.1 Homo sapiens cDNA clone IMAGE:1129633 3' similar to gb:X57352 INTERFERON-INDUCIBLE PROTEIN 1-8U (HUMAN);
720	9962	19100	4.1	0.0E+00	M60875.1	NT	Human von Willebrand factor gene, exons 23 through 34
720	9962	19101	4.1	0.0E+00	M60875.1	NT	Human von Willebrand factor gene, exons 23 through 34
730	9972	19110	1.35	0.0E+00	5032192	NT	Homo sapiens TNF receptor-associated factor 1 (TRAF1) mRNA

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1307	10523	19882	2.46	0.0E+00	5174748	NT	Homo sapiens Wolfram syndrome (WFS) mRNA
1307	10523	19883	2.46	0.0E+00	5174748	NT	Homo sapiens Wolfram syndrome (WFS) mRNA
1307	10523	19884	2.46	0.0E+00	5174748	NT	Homo sapiens Wolfram syndrome (WFS) mRNA
1308	10524		3.13	0.0E+00	AF096158.1	NT	Homo sapiens protein phosphatase 2A BR gamma subunit gene, exon 5
1318	11860	19886	1.32	0.0E+00	7657529	NT	Homo sapiens rhabdoid tumor deletion region protein 1 (RTDR1), mRNA
1318	11860	19897	1.32	0.0E+00	7657529	NT	Homo sapiens rhabdoid tumor deletion region protein 1 (RTDR1), mRNA
1323	10538	19702	1.51	0.0E+00	5803146	NT	Homo sapiens ring finger protein 9 (RNF9), mRNA
1324	10539	19703	2.45	0.0E+00	4508004	NT	Homo sapiens zinc finger protein 173 (ZNF173) mRNA
1326	10541	19704	0.83	0.0E+00	Y07829.2	NT	Homo sapiens RFB30 gene for RING finger protein
1327	10542	19705	0.88	0.0E+00	5803146	NT	Homo sapiens ring finger protein 9 (RNF9), mRNA
1328	10543	19706	2.48	0.0E+00	4508004	NT	Homo sapiens zinc finger protein 173 (ZNF173) mRNA
1330	10545	19708	4.21	0.0E+00	AB011149.1	NT	Homo sapiens mRNA for KIAA0577 protein, complete cds
1331	10546	19709	5.75	0.0E+00	7681985	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
1332	10547	19710	5.16	0.0E+00	7681985	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
1333	10548	19711	4.94	0.0E+00	8567387	NT	Homo sapiens period (Drosophila) homolog 3 (PER3), mRNA
1333	10548	19712	4.94	0.0E+00	8567387	NT	Homo sapiens period (Drosophila) homolog 3 (PER3), mRNA
1345	10550	19725	2.1	0.0E+00	M14123.1	NT	Human endogenous retrovirus HERV-K10
1402	10616	19780	1.83	0.0E+00	BE257855.1	EST_HUMAN	601109792F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350471 5'
1402	10616	19781	1.83	0.0E+00	BE257855.1	EST_HUMAN	601109792F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350471 5'
1412	10625	19791	1.3	0.0E+00	AJ250014.1	NT	Homo sapiens mRNA for Familial Cylindromatosis cyl gene
1421	10634	19803	0.81	0.0E+00	AI208756.1	EST_HUMAN	qg38b06.x1 Soares_testis_NHT.Homo sapiens cDNA clone IMAGE:1837427 3' similar to WP:T27A1.5 CE14213 ;
1422	10635	19804	44.87	0.0E+00	6042208	NT	RAN, member RAS oncogene family.Homo sapiens RAN, member RAS oncogene family (RAN), mRNA
1431	10644	19816	2.73	0.0E+00	7705565	NT	Homo sapiens KIAA1114 protein (KIAA1114), mRNA
1431	10644	19817	2.73	0.0E+00	7705565	NT	Homo sapiens KIAA1114 protein (KIAA1114), mRNA
1433	10646	19818	7.99	0.0E+00	AJ238063.1	NT	Homo sapiens partial AF-4 gene, exons 2 to 7 and Alu repeat elements
1441	10655	19829	3.3	0.0E+00	AF038280.1	NT	Homo sapiens alpha1-6fucosyltransferase (alpha1-6FucT) gene, exon 7
1458	10672	19844	3.25	0.0E+00	AL132999.1	NT	Novel human gene on chromosome 20
1463	10676	19849	2.08	0.0E+00	D87077.1	NT	Human mRNA for KIAA0240 gene, partial cds
1468	10679	19852	9.32	0.0E+00	6912457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
1468	10681	19854	2.31	0.0E+00	7681985	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
1468	10681	19855	2.31	0.0E+00	7681985	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
1500	10713	19885	1.18	0.0E+00	7708434	NT	Homo sapiens h-IDC for homolog of Drosophila headcase (LOC51698), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1512	10726	18888	3.05	0.0E+00	AA481172.1	EST_HUMAN	aa34a03.r1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:315116 5'
1518	10732	18901	111.36	0.0E+00	AF023860.1	NT	Carcopithecus aethiops cyclophilin A mRNA, complete cds
1518	10732	18902	111.36	0.0E+00	AF023860.1	NT	Carcopithecus aethiops cyclophilin A mRNA, complete cds
1520	10734	18905	1.22	0.0E+00	AW976097.1	EST_HUMAN	EST388208 MAGE resequences, MAGN Homo sapiens cDNA
1520	10734	18906	1.22	0.0E+00	AW976097.1	EST_HUMAN	EST388208 MAGE resequences, MAGN Homo sapiens cDNA
1521	10735	18907	1.09	0.0E+00	D10884.1	NT	Bovine mRNA for neurocalcin
1523	10737		4.77	0.0E+00	U76027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
1524	10738	18910	5.07	0.0E+00	4505404	NT	Homo sapiens transmembrane glycoprotein (GPNMB) mRNA
1524	10738	18911	5.07	0.0E+00	4505404	NT	Homo sapiens transmembrane glycoprotein (GPNMB) mRNA
1525	10739	18912	2.92	0.0E+00	7662405	NT	Homo sapiens KIAA0857 protein (KIAA0857), mRNA
1526	10740		6.07	0.0E+00	7656972	NT	Homo sapiens TNF-inducible protein CG12-1 (CG12-1), mRNA
1531	10745	18918	3.68	0.0E+00	M89478.1	NT	Human transglutaminase mRNA, complete cds
1533	10747	18919	0.95	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
1533	10747	18920	0.95	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
1534	11697		72.34	0.0E+00	4506854	NT	Homo sapiens ribosomal protein L5 (RPL5) mRNA
1535	10748	18921	74.68	0.0E+00	M14189.1	NT	Human laminin receptor (2H5 epitope) mRNA, 5' end
1545	10759	18932	13.15	0.0E+00	4503098	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
1551	10765		2.44	0.0E+00	D00333.1	NT	human c-yes-2 gene
1559	10773	18946	8.95	0.0E+00	Z83738.1	NT	H. sapiens H12B/e gene
1560	10774	18947	2.11	0.0E+00	5821480	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
1560	10774	18948	2.11	0.0E+00	5821480	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
1561	10775	18949	9.8	0.0E+00	AV680831.1	EST_HUMAN	AV680831 GKC Homo sapiens cDNA clone GKBOF02 5'
1561	10775	18950	9.8	0.0E+00	AV680831.1	EST_HUMAN	AV680831 GKC Homo sapiens cDNA clone GKBOF02 5'
1564	11698	18953	3.17	0.0E+00	AB040905.1	NT	Homo sapiens mRNA for KIAA1472 protein, partial cds
1568	10781	18954	1.39	0.0E+00	AF157476.1	NT	Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds
1570	10783	18957	3.7	0.0E+00	7662183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
1570	10783	18958	3.7	0.0E+00	7662183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
1572	10785	18959	43.92	0.0E+00	5729876	NT	Homo sapiens heat shock 70kD protein 10 (HSC71) (HSPA10), mRNA
1572	10785	18960	43.92	0.0E+00	5729876	NT	Homo sapiens heat shock 70kD protein 10 (HSC71) (HSPA10), mRNA
1574	10787	18962	1.25	0.0E+00	M81803.1	NT	Human sodium channel mRNA
1588	10801	18977	8.91	0.0E+00	H26973.1	EST_HUMAN	yo76c06.s1 Soares adult brain N26-HB55 Homo sapiens cDNA clone IMAGE:183948 3'
1598	10810	18987	9.48	0.0E+00	AB046826.1	NT	Homo sapiens mRNA for KIAA1609 protein, partial cds
1598	10810	18988	8.46	0.0E+00	AB046826.1	NT	Homo sapiens mRNA for KIAA1609 protein, partial cds

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1615	10828	20003	1.28	0.0E+00	AW444637.1	EST_HUMAN	UI-H-B13-giw-c-04-0-U1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733284 3'
1640	10854	20034	1.25	0.0E+00	BE144384.1	EST_HUMAN	MR0-HT0166-191199-004-b11 HT0166 Homo sapiens cDNA
1640	10854	20035	1.25	0.0E+00	BE144364.1	EST_HUMAN	MR0-HT0166-191199-004-b11 HT0166 Homo sapiens cDNA
1644	10858	20039	13.17	0.0E+00	AI768104.1	EST_HUMAN	wg81b07.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2371477 3' similar to TR:Q62788 Q62788 CYS2/HIS2 ZINC FINGER PROTEIN.;
1645	10859	20040	3.17	0.0E+00	AF057177.1	NT	Homo sapiens T-cell receptor gamma V1 gene region
1648	10862	20043	2.18	0.0E+00	M29580.1	NT	Human zinc-finger protein 7 (ZFP7) mRNA, complete cds
1648	10862	20044	2.18	0.0E+00	M29580.1	NT	Human zinc-finger protein 7 (ZFP7) mRNA, complete cds
1650	10864	20048	39.38	0.0E+00	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
1651	10865	20047	1.68	0.0E+00	7857065	NT	Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG) mRNA
1655	10869	20050	1	0.0E+00	BE222374.1	EST_HUMAN	hu11d05.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166281 3' similar to TR:O95147 O95147 MKP-1 LIKE PROTEIN TYROSINE PHOSPHATASE ;
1655	10869	20051	1	0.0E+00	BE222374.1	EST_HUMAN	MKP-1 LIKE PROTEIN TYROSINE PHOSPHATASE ;
1657	10870	20053	1.59	0.0E+00	4557810	NT	Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 2 (GABRG2) mRNA
1660	10873	20056	4.81	0.0E+00	H30132.1	EST_HUMAN	yc68e08.r1 Soares breast 3NbHBst Homo sapiens cDNA clone IMAGE:182248 5' similar to gb:M64089 GAMMA-GLUTAMYL TRANSPEPTIDASE 5 PRECURSOR (HUMAN);
1660	10873	20057	4.81	0.0E+00	H30132.1	EST_HUMAN	yc68e08.r1 Soares breast 3NbHBst Homo sapiens cDNA clone IMAGE:182248 5' similar to gb:M64089 GAMMA-GLUTAMYL TRANSPEPTIDASE 5 PRECURSOR (HUMAN);
1662	10875	20059	5.52	0.0E+00	Z80780.1	NT	H. sapiens H2B/h gene
1665	10878	20060	5.52	0.0E+00	Z80780.1	NT	H. sapiens H2B/h gene
1674	10886	20072	5.65	0.0E+00	8923841	NT	Homo sapiens high-mobility group (nonhistone chromosomal) protein 17 (HMG17) mRNA
1677	10889	20075	1	0.0E+00	5453855	NT	Homo sapiens FOXJ2 forhead factor (LOC55810) mRNA
1682	10884	20082	2.52	0.0E+00	4826973	NT	Homo sapiens pericentriolar material 1 (PCM1) mRNA
1688	10900	20089	5.88	0.0E+00	AB026542.1	NT	Homo sapiens RNA binding motif protein, Y chromosome, family 1, member A1 (RBM1A1) mRNA
1690	10902		2.24	0.0E+00	S94400.1	NT	Homo sapiens WAVE2 mRNA for WASP-family protein, complete cds
1699	10911	20098	1.48	0.0E+00	4557538	NT	TCR zeta [human, Genomic/mRNA, 365 nt, segment 1 of 8]
1718	10930	20115	2.86	0.0E+00	AF273841.1	NT	Homo sapiens sulfate carrier family 26 (sulfate transporter), member 2 (SLC28A2) mRNA
1755	12001		57.99	0.0E+00	4508718	NT	Homo sapiens SMCY (SMCY) gene, complete cds
1759	10970	20155	1.64	0.0E+00	4557558	NT	Homo sapiens ribosomal protein S2 (RPS2) mRNA
1759	10970	20156	1.64	0.0E+00	4557558	NT	Homo sapiens E1A binding protein p300 (EP300) mRNA
1761	10972	20159	2.04	0.0E+00	U63963.1	NT	Homo sapiens E1A binding protein p300 (EP300) mRNA
1784	12002	20163	5.71	0.0E+00	4505332	NT	Human CSF-1 receptor (FMS) gene, complete cds, and (SMF) gene, partial cds
							Homo sapiens nuclear autoantigenic sperm protein (histone-binding) (NASP) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1765	10975	20184	1.37	0.0E+00	AA113030.1	EST_HUMAN	zr65c08.e1 Stratiogene Hela cell s3 637216 Homo sapiens cDNA clone IMAGE:563056 3'
1776	10988	20178	18.75	0.0E+00	U14987.1	NT	Human ribosomal protein L21 mRNA, complete cds
1778	10988	20181	16.18	0.0E+00	AB002331.1	NT	Human mRNA for KIAA0333 gene, partial cds
1779	10989	20182	14.48	0.0E+00	4502284	NT	Homo sapiens activating transcription factor 4 (tax-responsive enhancer element B87) (ATF4) mRNA
1779	10989	20183	14.48	0.0E+00	4502284	NT	Homo sapiens activating transcription factor 4 (tax-responsive enhancer element B87) (ATF4) mRNA
1779	10989	20184	14.48	0.0E+00	4502284	NT	Homo sapiens activating transcription factor 4 (tax-responsive enhancer element B87) (ATF4) mRNA
1802	11011	20203	7.84	0.0E+00	6005855	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
1802	11011	20204	7.84	0.0E+00	6005855	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
1811	11020	20212	1.4	0.0E+00	AB032978.1	NT	Homo sapiens mRNA for KIAA1152 protein, partial cds
1811	11020	20213	1.4	0.0E+00	AB032978.1	NT	Homo sapiens mRNA for KIAA1152 protein, partial cds
1815	11023	20215	3.22	0.0E+00	4828783	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA
1815	11023	20216	3.22	0.0E+00	4828783	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA
1816	11024	20217	7.42	0.0E+00	U07147.1	NT	Human retinal degeneration slow (RDS) gene, exon 1
1816	11024	20218	7.42	0.0E+00	U07147.1	NT	Human retinal degeneration slow (RDS) gene, exon 1
1819	11027	20221	1.23	0.0E+00	AW207280.1	EST_HUMAN	U1-H-B11-afn-f-07-Q-U1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:272333 3'
1819	11027	20222	1.23	0.0E+00	AW207280.1	EST_HUMAN	U1-H-B11-afn-f-07-Q-U1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:272333 3'
1841	11049	20239	2.89	0.0E+00	BE277465.1	EST_HUMAN	601178184F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3547239 5'
1841	11049	20240	2.89	0.0E+00	BE277465.1	EST_HUMAN	601178184F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3547239 5'
1859	11063	20257	1.73	0.0E+00	BE006282.1	EST_HUMAN	RC2-BN0128-200300-012-504 BN0128 Homo sapiens cDNA
1868	11065	20285	1.4	0.0E+00	7657390	NT	Homo sapiens nuclear protein (NP220), mRNA
1868	11065	20286	1.4	0.0E+00	7657390	NT	Homo sapiens nuclear protein (NP220), mRNA
1881	11088	20288	3.1	0.0E+00	4506384	NT	Homo sapiens RAD1 (S. pombe) homolog (RAD1) mRNA, and translated products
1881	11088	20289	3.1	0.0E+00	4506384	NT	Homo sapiens RAD1 (S. pombe) homolog (RAD1) mRNA, and translated products
1898	11103	20295	7.07	0.0E+00	AB037788.1	NT	Homo sapiens mRNA for KIAA1367 protein, partial cds
1900	11107		1.45	0.0E+00	AF157476.1	NT	Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds
1901	12005	20289	1.73	0.0E+00	M88478.1	NT	Human transglutaminase mRNA, complete cds
1901	12005	20300	1.73	0.0E+00	M88478.1	NT	Human transglutaminase mRNA, complete cds
1906	11112	20307	1.52	0.0E+00	4507464	NT	Homo sapiens transforming growth factor, beta 3 (TGFB3), mRNA
1908	11112	20308	1.52	0.0E+00	4507464	NT	Homo sapiens transforming growth factor, beta 3 (TGFB3), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1909	11114	20310	1.16	0.0E+00	7637038	NT	Homo sapiens death receptor 6 (DR6), mRNA
1911	11116		8.63	0.0E+00	AF240788.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
1916	11121		3.42	0.0E+00	M55632.1	NT	Human topoisomerase I pseudogene 1
1918	12006	20317	1.66	0.0E+00	5901803	NT	Homo sapiens butyrophilin, subfamily 3, member A2 (BTN3A2), mRNA
1920	11124	20319	1.35	0.0E+00	BE018068.1	EST_HUMAN	bb73f11.yt NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3048045 5'
1928	11130	20324	1.24	0.0E+00	4809282	NT	Homo sapiens histidine aminonitrilase (HAL) mRNA
1928	11130	20325	1.24	0.0E+00	4809282	NT	Homo sapiens histidine aminonitrilase (HAL) mRNA
1936	11140		1.01	0.0E+00	AL163252.2	NT	Homo sapiens chromosome 21 segment HS21G052
1938	11142	20338	1.12	0.0E+00	8400716	NT	Homo sapiens nebulin (NEB), mRNA
1938	11142	20339	1.12	0.0E+00	8400716	NT	Homo sapiens nebulin (NEB), mRNA
1939	11143	20340	7	0.0E+00	4826638	NT	Homo sapiens actinin, alpha 4 (ACTN4) mRNA
1939	11143	20341	7	0.0E+00	4826638	NT	Homo sapiens actinin, alpha 4 (ACTN4) mRNA
1949	11153	20355	1.05	0.0E+00	AB018333.1	NT	Homo sapiens mRNA for KIAA0760 protein, partial cds
1949	11153	20356	1.05	0.0E+00	AB018333.1	NT	Homo sapiens mRNA for KIAA0760 protein, partial cds
1955	11159	20360	1.34	0.0E+00	M33782.1	NT	Human TFEB protein mRNA, partial cds
1955	11159	20361	1.34	0.0E+00	M33782.1	NT	Human TFEB protein mRNA, partial cds
1957	11161	20362	1.72	0.0E+00	AW183024.1	EST_HUMAN	x89901.xt NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2878913 3'
1957	11161	20363	1.72	0.0E+00	AW183024.1	EST_HUMAN	x89901.xt NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2878913 3'
1959	11162	20364	9.82	0.0E+00	6912457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
1959	11162	20365	9.82	0.0E+00	6912457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
1960	11164	20367	12.58	0.0E+00	7682095	NT	Homo sapiens KIAA0408 gene product (KIAA0408), mRNA
1961	11165	20368	1.05	0.0E+00	AB011149.1	NT	Homo sapiens mRNA for KIAA0377 protein, complete cds
1962	11166	20369	1.04	0.0E+00	Z47558.1	NT	H. sapiens genes for semenogelin I and semenogelin II
1962	11166	20370	1.04	0.0E+00	Z47558.1	NT	H. sapiens genes for semenogelin I and semenogelin II
1968	11173	20379	4.4	0.0E+00	AB040948.1	NT	Homo sapiens mRNA for KIAA1513 protein, partial cds
1990	11183	20402	1.15	0.0E+00	AF273841.1	NT	Homo sapiens SMCY (SMCY) gene, complete cds
1990	11183	20403	1.15	0.0E+00	AF273841.1	NT	Homo sapiens SMCY (SMCY) gene, complete cds
2020	11221	20429	1.38	0.0E+00	7708742	NT	Homo sapiens TP53TG3a (TP53TG3a), mRNA
2024	11225	20433	28.23	0.0E+00	BE743215.1	EST_HUMAN	601573895F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3835188 5'
2024	11225	20434	28.23	0.0E+00	BE743215.1	EST_HUMAN	601573895F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3835188 5'
2026	11227	20435	0.95	0.0E+00	4503648	NT	Homo sapiens coagulation factor IX (plasma thromboplastic component, Christmas disease, hemophilia B) (FX) mRNA
2027	11228	20436	1.44	0.0E+00	BF207688.1	EST_HUMAN	601861974F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:4081483 5'

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2028	11228	20437	6.57	0.0E+00	AU140831.1	EST_HUMAN	AU140831 PLACE4 Homo sapiens cDNA clone PLACE400321 5'
2030	11231	20439	1.7	0.0E+00	AA077589.1	EST_HUMAN	7B22E10 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B22E10
2030	11231	20440	1.7	0.0E+00	AA077589.1	EST_HUMAN	7B22E10 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B22E10
2032	11233		4.04	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
2034	11235		2.43	0.0E+00	4585963	NT	Homo sapiens phosphodiesterase 8A, cGMP-specific, rod, alpha (PDE8A), mRNA
2035	11236	20443	2.31	0.0E+00	Z42396.1	EST_HUMAN	HSC01C021 normalized infant brain cDNA Homo sapiens cDNA clone c-01c02
2037	11238		2.23	0.0E+00	A1244247.1	EST_HUMAN	qv0008.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:1988871 3' similar to contains Alu repetitive element
2042	11243	20452	7.59	0.0E+00	BE87725.1	EST_HUMAN	601485148F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3887747 5'
2044	11245	20454	4.44	0.0E+00	BF316325.1	EST_HUMAN	601902604F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4135320 5'
2044	11245	20455	4.44	0.0E+00	BF316325.1	EST_HUMAN	601902604F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4135320 5'
2050	11251	20463	4.16	0.0E+00	BE697125.1	EST_HUMAN	RC3-CT0413-270700-022-410 CT0413 Homo sapiens cDNA
2050	11251	20464	4.16	0.0E+00	BE697125.1	EST_HUMAN	RC3-CT0413-270700-022-410 CT0413 Homo sapiens cDNA
2056	11267	20471	2.15	0.0E+00	L00620.1	NT	Human plasma membrane calcium ATPase isoform 2 (APT2B2) mRNA, complete cds
2056	11267	20472	2.15	0.0E+00	L00620.1	NT	Human plasma membrane calcium ATPase isoform 2 (APT2B2) mRNA, complete cds
2061	11282	20478	1.54	0.0E+00	4758489	NT	Homo sapiens GTP binding protein 1 (GTPBP1) mRNA
2065	11286	20479	1.29	0.0E+00	BE500995.1	EST_HUMAN	P50443 SULFATE TRANSPORTER ;
2084	11284		4.59	0.0E+00	BE767064.1	EST_HUMAN	QV1-GN0065-140800-318-c10 GN0065 Homo sapiens cDNA
2085	11285		1.21	0.0E+00	AF018963.1	NT	Homo sapiens X-linked juvenile retinoschisis protein (XLR51) gene, exon 8 and complete cds
2087	11287	20500	8.37	0.0E+00	BF027562.1	EST_HUMAN	601672089F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954785 5'
2088	11288	20501	1.73	0.0E+00	BE072624.1	EST_HUMAN	PMO-BT0547-210300-004-F04 BT0547 Homo sapiens cDNA
2090	11290	20502	4.32	0.0E+00	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
2092	11292	20504	4.24	0.0E+00	AW752708.1	EST_HUMAN	IL3-CT0219-271099-022-G10 CT0219 Homo sapiens cDNA
2093	11293	20505	4.83	0.0E+00	A1904640.1	EST_HUMAN	QV-BT065-020399-092 BT065 Homo sapiens cDNA
2093	11293	20506	4.83	0.0E+00	A1904640.1	EST_HUMAN	QV-BT065-020399-092 BT065 Homo sapiens cDNA
2146	11344		4.65	0.0E+00	L14787.1	NT	Human DNA-binding protein mRNA, 3' end
2152	11350	20566	1.31	0.0E+00	BE274696.1	EST_HUMAN	601122339F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3346898 5'
2154	11352	20569	1.28	0.0E+00	D87685.1	NT	Human mRNA for KIAA0244 gene, partial cds
2155	11353	20570	78.41	0.0E+00	AV738288.1	EST_HUMAN	AV738288 CB Homo sapiens cDNA clone CBNBDE08 5'
2155	11353	20571	78.41	0.0E+00	AV738288.1	EST_HUMAN	AV738288 CB Homo sapiens cDNA clone CBNBDE08 5'
2157	11355	20573	4.48	0.0E+00	AA831691.1	EST_HUMAN	cc32a01.at1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1567898 3'
2161	11359	20577	47.03	0.0E+00	BF344434.1	EST_HUMAN	602034828F1 NCI_CGAP_Bim84 Homo sapiens cDNA clone IMAGE:4150734 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2278	11473	20698	1.81	0.0E+00	6325468	NT	Homo sapiens flavin containing monooxygenase 3 (FMO3), mRNA
2285	11480	20702	3.99	0.0E+00	BE678095.1	EST_HUMAN	7122a02.x1 NCI_CGAP_GLL1 Homo sapiens cDNA clone IMAGE:3285370 3' similar to TR:O84939 O84939 KIAA0857 PROTEIN;
2288	11483	20704	8.5	0.0E+00	AF044571.1	NT	Homo sapiens phosphatase kinase alpha subunit (PHKA2) gene, exon 32
2289	11484	20705	2.07	0.0E+00	AI826542.1	EST_HUMAN	1567c08.x1 NCI_CGAP_U2 Homo sapiens cDNA clone IMAGE:2283182 3'
2291	11486	20706	2.04	0.0E+00	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
2294	11489	20708	19.82	0.0E+00	7682401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
2294	11489	20709	19.82	0.0E+00	7682401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
2297	11492	20712	7.66	0.0E+00	5903178	NT	Homo sapiens sperm specific antigen 2 (SSFA2), mRNA
2297	11492	20713	7.66	0.0E+00	5903178	NT	Homo sapiens sperm specific antigen 2 (SSFA2), mRNA
2303	11497	20716	3.58	0.0E+00	7682007	NT	Homo sapiens KIAA0218 gene product (KIAA0218), mRNA
2303	11497	20717	3.58	0.0E+00	7682007	NT	Homo sapiens KIAA0218 gene product (KIAA0218), mRNA
2307	11501	20722	2.32	0.0E+00	D83778.1	NT	Human mRNA for KIAA0194 gene, partial cds
2307	11501	20723	2.32	0.0E+00	D83778.1	NT	Human mRNA for KIAA0194 gene, partial cds
2317	11511	20731	2.36	0.0E+00	5174878	NT	Homo sapiens signal regulatory protein, beta, 1 (SIRP-BETA-1) mRNA
2321	11514	20735	3.85	0.0E+00	AU131142.1	EST_HUMAN	AU131142 NT2RP3 Homo sapiens cDNA clone NT2RP3002084 5'
2322	11515		65.13	0.0E+00	BE794028.1	EST_HUMAN	601588843F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3941003 5'
2323	11518	20738	17.63	0.0E+00	7682017	NT	Homo sapiens KIAA0244 protein (KIAA0244), mRNA
2324	11517	20737	1.62	0.0E+00	4758497	NT	Homo sapiens hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase) (H6PD), mRNA
2324	11517	20738	1.62	0.0E+00	4758497	NT	Homo sapiens hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase) (H6PD), mRNA
2325	11518						Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
2327	11620	20740	18.2	0.0E+00	AF280107.1	NT	polypeptide 5 (CYP3A5) gene, partial cds
2327	11620	20741	16.28	0.0E+00	AU118082.1	EST_HUMAN	AU118082 HEMBA1 Homo sapiens cDNA clone HEMBA1002839 5'
2327	11620	20742	16.28	0.0E+00	AU118082.1	EST_HUMAN	AU118082 HEMBA1 Homo sapiens cDNA clone HEMBA1002839 5'
2328	11621	20743	16.29	0.0E+00	AU118082.1	EST_HUMAN	AU118082 HEMBA1 Homo sapiens cDNA clone HEMBA1002839 5'
2345	11538		1.72	0.0E+00	8923088	NT	Homo sapiens hypothetical protein FLJ20081 (FLJ20081), mRNA
2377	11570	20780	4.01	0.0E+00	BE814424.1	EST_HUMAN	MRO-BN0070-090800-028-d12 BN0070 Homo sapiens cDNA
			1.85	0.0E+00	AU118582.1	EST_HUMAN	AU118582 HEMBA1 Homo sapiens cDNA clone HEMBA1008155 5'
2379	11572		3.76	0.0E+00	AJ042035.1	EST_HUMAN	α80b02.x1 Soares NIHMPu_S1 Homo sapiens cDNA clone IMAGE:1660883 3' similar to TR:O08602
2381	11574	20783	4.62	0.0E+00	8923820	NT	O08682 230KDA PHOSPHATIDYLINOSITOL 4-KINASE.;
							Homo sapiens hypothetical protein FLJ20893 (FLJ20893), mRNA
2383	11578	20784	1.68	0.0E+00	AW303998.1	EST_HUMAN	xv1507.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813221 3' similar to TR:O54924 O54924 EXO84.;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2385	11578		1.46	0.0E+00	BE895605.1	EST_HUMAN	601432608F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918168 5'
2396	11589		30.25	0.0E+00	AB005622.1	EST_HUMAN	AB005622 HeLa cDNA (T.Noma) Homo sapiens cDNA similar to adenylate kinase isozyme 2
2399	11592	20810	4.93	0.0E+00	8008002	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A) mRNA
2403	11595	20814	1.61	0.0E+00	D85606.1	NT	Homo sapiens gene for cholesteryltransferin type-A receptor, complete cds
2403	11595	20815	1.61	0.0E+00	D85606.1	NT	Homo sapiens gene for cholesteryltransferin type-A receptor, complete cds
2411	11603	20824	2.27	0.0E+00	AF106275.1	NT	Homo sapiens gene for cholesteryltransferin type-A receptor, complete cds
2415	11606	20828	2.38	0.0E+00	BF345274.1	EST_HUMAN	Homo sapiens immunoglobulin-like transcript 1c variant 4 (ILT1c) gene, exon 6
2422	11613	20836	4.8	0.0E+00	5728777	NT	602018058F1 NCL_CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4163870 5'
2430	11621	20842	1.25	0.0E+00	U13668.1	NT	Homo sapiens collagen, type XII, alpha 1 (COL12A1), mRNA
2430	11621	20843	1.26	0.0E+00	U13668.1	NT	Human G protein-coupled receptor (GPR1) gene, complete cds
2431	11622	20844	131.32	0.0E+00	BF569144.1	EST_HUMAN	Human G protein-coupled receptor (GPR1) gene, complete cds
2440	11631	20852	2.8	0.0E+00	AW466922.1	EST_HUMAN	602184558T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300383 3'
2442	11633	20853	6.93	0.0E+00	AW501010.1	EST_HUMAN	h04h04.x1 NCL_CGAP_K612 Homo sapiens cDNA clone IMAGE:2872759 3'
							UI-HF-BP0p-als-c-07-Q-J1.1 NIH_MGC_51 Homo sapiens cDNA clone IMAGE:3072780 5'
							q22306.x1 NCL_CGAP_Lym6 Homo sapiens cDNA clone IMAGE:1882435 3' similar to contains element
							MIH repetitive element:
2451	11642		1.22	0.0E+00	AI287878.1	EST_HUMAN	Homo sapiens protein kinase, AMP-activated, alpha 2 catalytic subunit (PRKAA2) mRNA
2457	11648	20869	1.84	0.0E+00	5453965	NT	Homo sapiens protein kinase, AMP-activated, alpha 2 catalytic subunit (PRKAA2) mRNA
2457	11648	20870	1.84	0.0E+00	5453965	NT	Homo sapiens protein kinase, AMP-activated, alpha 2 catalytic subunit (PRKAA2) mRNA
2470	11661		2.3	0.0E+00	AW813853.1	EST_HUMAN	RC3-ST0197-300300-018-c04 ST0187 Homo sapiens cDNA
2475	11668	20885	70.13	0.0E+00	BE785542.1	EST_HUMAN	601592530F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3846518 5'
2478	11114	20310	3.28	0.0E+00	7667038	NT	Homo sapiens death receptor 6 (DR6), mRNA
2477	11667	20886	2.58	0.0E+00	BF509482.1	EST_HUMAN	UIH-B14-ec2-b-08-Q-J1.s1 NCL_CGAP_Sub88 Homo sapiens cDNA clone IMAGE:3086535 3'
2480	11670	20888	2.03	0.0E+00	Z32684.2	NT	Homo sapiens mRNA for membrane transport protein (XK gene)
2482	11672		3.62	0.0E+00	5453871	NT	Homo sapiens platelet-derived growth factor receptor-like (PDGFR) mRNA
2485	11675	20882	2.44	0.0E+00	BE910378.1	EST_HUMAN	601503356F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3905148 5'
2486	11676	20893	6.91	0.0E+00	7657498	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
2487	11677	20894	2.18	0.0E+00	8023340	NT	Homo sapiens hypothetical protein FLJ20368 (FLJ20368), mRNA
2488	11678	20895	8.81	0.0E+00	U83239.1	NT	Human Sec82 (Sec82) mRNA, complete cds
2494	11684	20901	14.6	0.0E+00	BE96480.1	EST_HUMAN	601508211F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3909886 5'
2498	11687	20908	6.8	0.0E+00	BE975511.1	EST_HUMAN	601489241F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3891371 5'
2498	11687	20907	5.8	0.0E+00	BE975511.1	EST_HUMAN	601489241F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3891371 5'
2498	11688	20908	2.84	0.0E+00	AF114027.1	EST_HUMAN	AF114027 Homo sapiens lung fetus Homo sapiens cDNA clone ESF8
2518	11705	20918	1.69	0.0E+00	BE938921.1	EST_HUMAN	601064738F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451161 5'
2522	11710	20926	56.3	0.0E+00	AU143277.1	EST_HUMAN	AU143277 Y79AA1 Homo sapiens cDNA clone Y79AA1001673 5'
2522	11710	20927	56.3	0.0E+00	AU143277.1	EST_HUMAN	AU143277 Y79AA1 Homo sapiens cDNA clone Y79AA1001673 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2523	11711	20928	35.33	0.0E+00	BE202896.1	EST_HUMAN	601105312F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2887955 5'
2523	11711	20929	35.33	0.0E+00	BE202896.1	EST_HUMAN	601105312F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2887955 5'
2524	11712	20930	1.33	0.0E+00	BF223041.1	EST_HUMAN	7q27h12x1 NCI CGAP_G08 Homo sapiens cDNA clone IMAGE: 3' similar to TR:O00248 O00248
2527	11715	20932	8.27	0.0E+00	AF245505.1	NT	HYPOTHETICAL 9.3 KD PROTEIN;
2558	11954	20964	1.76	0.0E+00	AB037836.1	NT	Homo sapiens adican mRNA, complete cds
2558	11954	20965	1.76	0.0E+00	AB037836.1	NT	Homo sapiens mRNA for KIAA1415 protein, partial cds
2566	11745	20970	9.26	0.0E+00	BF513835.1	EST_HUMAN	Homo sapiens mRNA for KIAA1415 protein, partial cds
2566	11745	20970	1.76	0.0E+00	BF672818.1	EST_HUMAN	UI-H-BW1-amp-f-12-Q-J1.81 NCI CGAP_Sub7 Homo sapiens cDNA clone IMAGE:4293612 5'
2568	11762	20975	2.87	0.0E+00	BE616695.1	EST_HUMAN	602152653F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:3621786 5'
2570	11755	20976	0.91	0.0E+00	BF204131.1	EST_HUMAN	601279873F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3621786 5'
2570	11755	20976	0.91	0.0E+00	BF204131.1	EST_HUMAN	601279873F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:4111411 5'
2574	11759	20979	3.98	0.0E+00	AB037742.1	NT	601889073F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4111411 5'
2575	11780	20980	2.79	0.0E+00	5032150	NT	601889073F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4111411 5'
2576	11784	20985	6.29	0.0E+00	AB037859.1	NT	Homo sapiens mRNA for KIAA1438 protein, partial cds
2579	11765	20983	2.26	0.0E+00	BE785445.1	EST_HUMAN	Homo sapiens mRNA for KIAA1438 protein, partial cds
2579	11765	20987	2.26	0.0E+00	BE785445.1	EST_HUMAN	601590108F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944304 5'
2582	11768	20988	1.03	0.0E+00	BE283328.1	EST_HUMAN	601590108F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944304 5'
2589	11775	20996	11.88	0.0E+00	BE782472.1	EST_HUMAN	601143722F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3051389 5'
2591	11777	20998	0.91	0.0E+00	AB020710.1	NT	601143722F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3939222 5'
2599	11784	21004	3.6	0.0E+00	4504688	NT	Homo sapiens mRNA for KIAA0803 protein, partial cds
2608	11792	21011	4.33	0.0E+00	AF173227.1	NT	Homo sapiens IMP (inosine monophosphate) dehydrogenase 1 (IMPDH1) mRNA
2612	11766	21012	1.91	0.0E+00	AB011108.1	NT	Homo sapiens IMP (inosine monophosphate) dehydrogenase 1 (IMPDH1) mRNA
2613	11797	21013	2.06	0.0E+00	AU133385.1	EST_HUMAN	Homo sapiens guanylate cyclase-activating protein 2 (GUCA1B) gene, exon 1
2614	11798	21014	0.92	0.0E+00	M69225.1	NT	Homo sapiens mRNA for KIAA0536 protein, partial cds
2617	11801	21017	3.04	0.0E+00	AU130403.1	EST_HUMAN	Homo sapiens mRNA for KIAA0536 protein, partial cds
2617	11801	21018	3.04	0.0E+00	AU130403.1	EST_HUMAN	Homo sapiens mRNA for KIAA0536 protein, partial cds
2620	11804	21021	1.65	0.0E+00	AW887015.1	EST_HUMAN	AU133385 NT2RP4 Homo sapiens cDNA clone NT2RP4001984 5'
2623	11807	21024	1.42	0.0E+00	BF000018.1	EST_HUMAN	Human bullous pemphigoid antigen (BPAG1) mRNA, complete cds
2624	11808	21025	14.04	0.0E+00	BE383165.1	EST_HUMAN	AU130403 NT2RP3 Homo sapiens cDNA clone NT2RP3000779 5'
2625	11809	21046	2.6	0.0E+00	BE531263.1	NT	AU130403 NT2RP3 Homo sapiens cDNA clone NT2RP3000779 5'
2649	11832	21054	0.9	0.0E+00	8922843	NT	AU130403 NT2RP3 Homo sapiens cDNA clone NT2RP3000779 5'
2659	11840	21054	1.28	0.0E+00	AB037732.1	NT	AU130403 NT2RP3 Homo sapiens cDNA clone NT2RP3000779 5'

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2681	11863		33.03	0.0E+00	AA316723.1	EST_HUMAN	EST188414 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to ribosomal protein L29
2682	11864	21078	30.31	0.0E+00	BE794894.1	EST_HUMAN	601589625F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943591 5'
2687	11868	21082	4.57	0.0E+00	U36253.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 5
2689	11870	21084	1.69	0.0E+00	AF110763.1	NT	Homo sapiens skeletal muscle LIM-protein 1 (FHL-1) gene, complete cds
2684	11874	21088	80.93	0.0E+00	BE798376.1	EST_HUMAN	601591891F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3945983 5'
2695	11875	21089	1.08	0.0E+00	BF680632.1	EST_HUMAN	602155923F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4287132 5'
2688	12025	21093	28.45	0.0E+00	BE563433.1	EST_HUMAN	601335485F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3889564 5'
2699	11878		3.2	0.0E+00	AV721847.1	EST_HUMAN	AV721847 HTB Homo sapiens cDNA clone HTBBYE09 5'
2701	11880	21098	2.18	0.0E+00	5174488	NT	Homo sapiens spermatogenesis associated PD1 (KIAA0757) mRNA
2701	11880	21097	2.18	0.0E+00	5174488	NT	Homo sapiens spermatogenesis associated PD1 (KIAA0757) mRNA
2702	11881	21098	1.13	0.0E+00	8923441	NT	Homo sapiens hypothetical protein FLJ20477 (FLJ20477), mRNA
2702	11881	21099	1.13	0.0E+00	8923441	NT	Homo sapiens hypothetical protein FLJ20477 (FLJ20477), mRNA
2703	11882	21100	2.55	0.0E+00	AF290195.1	NT	Homo sapiens hypertension-related calcium-regulated gene mRNA, complete cds
2704	11883		83.21	0.0E+00	AV651066.1	EST_HUMAN	AV651066 GLC Homo sapiens cDNA clone GLCGLD07 3'
2705	11884	21101	6.42	0.0E+00	BF377897.1	EST_HUMAN	CM1-TN0141-250900-439-508 TN0141 Homo sapiens cDNA
2705	11884	21102	5.42	0.0E+00	BF377897.1	EST_HUMAN	CM1-TN0141-250900-439-508 TN0141 Homo sapiens cDNA
2712	11891	21109	14.18	0.0E+00	BE747183.1	EST_HUMAN	601580903F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3928472 5'
2724	11903		1.33	0.0E+00	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
2726	11904	21120	4.31	0.0E+00	BF514110.1	EST_HUMAN	UHL-BW1-asmw-07-Q.U1.s1 NCJ CGAP Sub7 Homo sapiens cDNA clone IMAGE:3071340 3'
2738	11915	21128	4.15	0.0E+00	BF677894.1	EST_HUMAN	602085579F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4248915 5'
2741	11920	21135	1.04	0.0E+00	7427522	NT	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), mRNA
2744	11923	21137	18.85	0.0E+00	AV725534.1	EST_HUMAN	AV725534 HTC Homo sapiens cDNA clone HTCCCA03 5'
2744	11923	21138	18.85	0.0E+00	AV725534.1	EST_HUMAN	AV725534 HTC Homo sapiens cDNA clone HTCCCA03 5'
2746	11925		13.22	0.0E+00	AI879183.1	EST_HUMAN	au55604.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2518663 5' similar to SW-R13A_HUMAN P40428 60S RIBOSOMAL PROTEIN L13A ;
2749	11928	21143	2.75	0.0E+00	BF530661.1	EST_HUMAN	602071957F1 NCJ CGAP Bm87 Homo sapiens cDNA clone IMAGE:4214879 5'
2760	11929	21144	43.65	0.0E+00	BE872768.1	EST_HUMAN	601450912F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3854842 5'
2762	11931	21145	3.13	0.0E+00	AU131494.1	EST_HUMAN	AU131494 NT2RP3 Homo sapiens cDNA clone NT2RP3002872 5'
2752	11931	21146	3.13	0.0E+00	AU131494.1	EST_HUMAN	AU131494 NT2RP3 Homo sapiens cDNA clone NT2RP3002872 5'
2753	11932	21147	94.45	0.0E+00	BE300344.1	EST_HUMAN	600944784F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2860806 5'
2753	11932	21148	94.45	0.0E+00	BE300344.1	EST_HUMAN	600944784F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2860806 5'
2758	9472	18803	2.6	0.0E+00	S76830.1	NT	glycoprotein D=Duffy group antigen [human, blood, Genomic DNA, 3088 nt]
2761	11938		3.13	0.0E+00	AB033281.1	NT	Homo sapiens BTRCP2 mRNA for F-box and WD-repeats protein isoform C, complete cds

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2767	9882	19125	2.16	0.0E+00	AF284750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
2767	9882	19126	2.16	0.0E+00	AF284750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
2771	10272	19423	5.49	0.0E+00	4503202	NT	Homo sapiens cytochrome P450, subfamily I (dioxin-inducible), polypeptide 1 (glaucoma 3, primary infantile) (CYP1B1) mRNA
2771	10272	19424	5.49	0.0E+00	4503202	NT	Homo sapiens cytochrome P450, subfamily I (dioxin-inducible), polypeptide 1 (glaucoma 3, primary infantile) (CYP1B1) mRNA
2789	12028	21156	4.21	0.0E+00	X85080.1	NT	H. sapiens serine hydroxymethyltransferase pseudogene
2790	12030		1.26	0.0E+00	AF068824.1	NT	Homo sapiens 6-aminocaproate synthase 2 (ALAS2) gene, complete cds
2791	12031		1.42	0.0E+00	AB040960.1	NT	Homo sapiens mRNA for KIAA1527 protein, partial cds
2797	12037		1.15	0.0E+00	AJ238852.1	NT	Homo sapiens partial rpl3 gene for ribosomal protein L3, U82 snRNA, U83a snRNA and U83b snRNA genes
2798	12038	21160	2.34	0.0E+00	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
2802	12042	21163	2.17	0.0E+00	M80802.1	NT	Human AHNAC nucleoprotein mRNA, 5' end
2804	12044	21165	1.42	0.0E+00	BE164504.1	EST_HUMAN	PMO-HT0343-281298-003-e02 HT0343 Homo sapiens cDNA
2804	12044	21166	1.42	0.0E+00	BE164504.1	EST_HUMAN	PMO-HT0343-281298-003-e02 HT0343 Homo sapiens cDNA
2808	12046		1.59	0.0E+00	X73428.1	NT	H. sapiens lds gene for HLH type transcription factor
2808	12048		2.79	0.0E+00	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C088
2808	12049	21168	1.22	0.0E+00	7019584	NT	Homo sapiens zinc finger protein 221 (ZNF221), mRNA
2808	12049	21170	1.22	0.0E+00	7019584	NT	Homo sapiens zinc finger protein 221 (ZNF221), mRNA
2808	12049	21171	1.22	0.0E+00	7019584	NT	Homo sapiens zinc finger protein 221 (ZNF221), mRNA
2811	12051	21172	1.03	0.0E+00	M88478.1	NT	Human transglutaminase mRNA, complete cds
2815	12054	21177	25.36	0.0E+00	D50657.1	NT	Homo sapiens gamma-cytoplasmic actin (ACTGP3) pseudogene
2815	12054	21178	25.36	0.0E+00	D50657.1	NT	Homo sapiens gamma-cytoplasmic actin (ACTGP3) pseudogene
2818	12057	21181	3.87	0.0E+00	AL088857.1	NT	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes
2819	12058		10.77	0.0E+00	Y10858.1	NT	H. sapiens mRNA for nuclear DNA helicase II
2820	12059		1.01	0.0E+00	AF152303.1	NT	Homo sapiens protocadherin alpha C1 (PCDH-alpha-C1) mRNA, complete cds
2821	12060	21182	125.82	0.0E+00	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
2821	12060	21183	125.82	0.0E+00	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
2833	12072	21194	2.68	0.0E+00	4507280	NT	Homo sapiens serine/threonine kinase 9 (STK9) mRNA
2838	12076	21188	1.36	0.0E+00	AL047589.1	EST_HUMAN	DKFZp568G0821_r1 688 (synonym: hute1) Homo sapiens cDNA clone DKFZp568G0821
2837	12076	21189	1.1	0.0E+00	7661863	NT	Homo sapiens KIAA0054 gene product, Helicase (KIAA0054), mRNA
2837	12076	21200	1.1	0.0E+00	7661863	NT	Homo sapiens KIAA0054 gene product, Helicase (KIAA0054), mRNA
2838	12077		1.88	0.0E+00	4503098	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
2840	12079	21202	6.06	0.0E+00	BE081896.1	EST_HUMAN	QV2-BT0636-130400-138-H03 BT0636 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2840	12079	21203	6.06	0.0E+00	BE01898.1	EST_HUMAN	QV2-BT0638-130400-138-h03 BT0638 Homo sapiens cDNA
2845	12084	21211	1.41	0.0E+00	6808918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
2845	12084	21212	1.41	0.0E+00	6808918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
2848	12087	21216	2.94	0.0E+00	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C008
2848	12087	21217	2.94	0.0E+00	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C008
2849	12088	21218	1.07	0.0E+00	AA216579.1	EST_HUMAN	z86b11.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:583517 3' similar to contains Alu repetitive element
2856	12094		4.27	0.0E+00	Y19210.1	NT	Homo sapiens H1b5 gene for hair keratin, exons 1 to 9
2859	12097	21227	1.07	0.0E+00	4758279	NT	Homo sapiens EphA4 (EPHA4) mRNA
2860	12098	21228	47.88	0.0E+00	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
2861	12099	21229	2.25	0.0E+00	AI561002.1	EST_HUMAN	tn18407.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2167881 3' similar to TR:O18247
2861	12099	21229	2.25	0.0E+00	AI561002.1	EST_HUMAN	O18247 F44E7.2 PROTEIN. ;
2861	12099	21230	2.26	0.0E+00	AI561002.1	EST_HUMAN	tn18407.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2167881 3' similar to TR:O18247
2863	12101	21232	1.52	0.0E+00	P52740	SWISSPROT	O18247 F44E7.2 PROTEIN. ;
2864	12102	21233	1.33	0.0E+00	AF152338.1	NT	ZINC FINGER PROTEIN 132
2878	12116	21245	2.8	0.0E+00	AB033063.1	NT	Homo sapiens proteodherin gamma C4 (PCDH-gamma-C4) mRNA, complete cds
2878	12116	21246	2.8	0.0E+00	AB033063.1	NT	Homo sapiens mRNA for KIAA1267 protein, partial cds
2878	12117	21247	5.69	0.0E+00	AB040941.1	NT	Homo sapiens mRNA for KIAA1267 protein, partial cds
2879	12117	21248	5.68	0.0E+00	AB040941.1	NT	Homo sapiens mRNA for KIAA1508 protein, partial cds
2882	12120	21251	6.58	0.0E+00	7681903	NT	Homo sapiens KIAA0100 gene product (KIAA0100), mRNA
2882	12120	21252	6.56	0.0E+00	7681903	NT	Homo sapiens KIAA0100 gene product (KIAA0100), mRNA
2883	12121	21253	3.32	0.0E+00	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (MLLT4) mRNA
2883	12121	21254	3.32	0.0E+00	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (MLLT4) mRNA
2888	12125	21258	1.33	0.0E+00	BF110702.1	EST_HUMAN	7n40d03.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3567028 3' similar to TR:Q9VLN1
2888	12125	21258	1.33	0.0E+00	BF110702.1	EST_HUMAN	Q9VLN1 CG17283 PROTEIN. ;
2888	12125	21259	1.33	0.0E+00	BF110702.1	EST_HUMAN	7n40d03.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3567028 3' similar to TR:Q9VLN1
2888	12125	21259	1.33	0.0E+00	BF110702.1	EST_HUMAN	Q9VLN1 CG17283 PROTEIN. ;
2898	12134	21270	2.63	0.0E+00	4505084	NT	Homo sapiens melanoma antigen, family B, 4 (MAGEB4), mRNA
2898	12134	21271	2.63	0.0E+00	4505084	NT	Homo sapiens melanoma antigen, family B, 4 (MAGEB4), mRNA
2898	12136	21273	1.31	0.0E+00	4885214	NT	Homo sapiens v-erb-a avian erythroblastic leukemia viral oncogene homolog-like 4 (ERBB4) mRNA
2898	12136	21274	1.31	0.0E+00	4885214	NT	Homo sapiens v-erb-a avian erythroblastic leukemia viral oncogene homolog-like 4 (ERBB4) mRNA

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2902	12140	21277	1.23	0.0E+00	AB011083.1	NT	Homo sapiens mRNA for KIAA0511 protein, partial cds
2908	12144	21280	1.94	0.0E+00	4758827	NT	Homo sapiens neurodin III (NRXN3) mRNA
2907	12145		0.98	0.0E+00	X88494.1	NT	H. sapiens mRNA for M phase phosphoprotein 10
2910	12148	21283	1.37	0.0E+00	AB033034.1	NT	Homo sapiens mRNA for KIAA1208 protein, partial cds
2912	12150	21284	1.32	0.0E+00	X15309.1	NT	H. sapiens NF-H gene, exon 4
2912	12150	21285	1.32	0.0E+00	X15309.1	NT	H. sapiens NF-H gene, exon 4
2914	12152	21287	10.32	0.0E+00	AF108275.1	NT	Homo sapiens immunoglobulin-like transcript 1c variant 4 (ILT1c) gene, exon 6
2928	12166		1.27	0.0E+00	AI149860.1	EST_HUMAN	q43109.x1 Soares_testis NHT Homo sapiens cDNA clone IMAGE:1752809 3'
2938	12178	21310	0.91	0.0E+00	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
2938	12178	21311	0.91	0.0E+00	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
2939	12177	21312	3.28	0.0E+00	AB004894.1	NT	Homo sapiens mRNA for PKU-alpha, partial cds
2951	12189	21322	1.83	0.0E+00	7662273	NT	Homo sapiens KIAA0737 gene product (KIAA0737), mRNA
2952	12180	21323	2.25	0.0E+00	5729755	NT	Homo sapiens calcium channel, voltage-dependent, gamma subunit 3 (CACNG3), mRNA
2952	12180	21324	2.25	0.0E+00	5729755	NT	Homo sapiens calcium channel, voltage-dependent, gamma subunit 3 (CACNG3), mRNA
2963	12201	21335	2.39	0.0E+00	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
2963	12201	21338	2.39	0.0E+00	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
2991	12228		0.68	0.0E+00	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
2993	12230	21382	1.2	0.0E+00	M74088.1	NT	Human displacement protein (CCAAT) mRNA
3002	12238	21368	0.65	0.0E+00	4508882	NT	Homo sapiens samengolgin 1 (SEMG1) mRNA
3004	12240	21370	1.08	0.0E+00	AW976286.1	EST_HUMAN	EST388375 MAGE resequences, MAGN Homo sapiens cDNA
3009	12245		4.68	0.0E+00	AF189553.1	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds
3012	12248	21378	10.7	0.0E+00	5579469	NT	Homo sapiens heat shock 70kD protein 1 (HSPA1A), mRNA
3012	12248	21379	10.7	0.0E+00	5579469	NT	Homo sapiens heat shock 70kD protein 1 (HSPA1A), mRNA
3014	12250		7.18	0.0E+00	AL359403.1	NT	Isoform 2 of a novel human mRNA from chromosome 22
3018	12254	21383	3.07	0.0E+00	AF017433.1	NT	Homo sapiens putative transcription factor CR53 (CR53) mRNA, partial cds
3021	12257						Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM5 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel α
3042	12279	21407	2.58	0.0E+00	AF198779.1	NT	Human germline gene 16.1 for Ig lambda L-chain C region (IgLC16.1)
3047	12283		3.54	0.0E+00	X03520.1	NT	Homo sapiens F-box protein FBL5 (FBL5) mRNA, complete cds
3051	12287	21413	1.89	0.0E+00	AF198355.1	NT	Homo sapiens melanoma-associated antigen (MAGE-G1) gene, complete cds
3070	12308	21428	4.81	0.0E+00	AF064589.1	NT	Homo sapiens melanoma-associated antigen (MAGE-G1) gene, complete cds
3071	12307	21429	10.45	0.0E+00	AF265208.1	NT	Homo sapiens SWI-SNF complex protein p270 mRNA, partial cds
3076	12312	21433	4.31	0.0E+00	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
3076	12312	21433	4.31	0.0E+00	7662139	NT	Homo sapiens KIAA0469 gene product (KIAA0469), mRNA

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3077	12313	21434	1.49	0.0E+00	AF042075.1	NT	Homo sapiens olfactory receptor-like protein (OLFR 42B) gene, OLFR 42B-9110 allele, partial cds
3106	12341	21468	2.95	0.0E+00	4826783	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA
3113	12348	21476	54.11	0.0E+00	L20841.1	NT	Human ferritin heavy chain mRNA, complete cds
3117	12352	21480	1.3	0.0E+00	AB011121.1	NT	Homo sapiens mRNA for KIAA0549 protein, partial cds
3117	12352	21481	1.3	0.0E+00	AB011121.1	NT	Homo sapiens mRNA for KIAA0549 protein, partial cds
3124	12359	21488	38.75	0.0E+00	T94870.1	EST_HUMAN	y632703 s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:119453 3' similar to SP:S20539
3140	12375	21508	1.17	0.0E+00	BF243338.1	EST_HUMAN	S29539 BASIC PROTEIN, 23k -
3142	12377	21507	1.02	0.0E+00	AI968086.1	EST_HUMAN	601878507F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4107433 5'
3147	12382	21514	4.89	0.0E+00	X98922.1	NT	wu12h10.x1 NCL_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2516803 3'
3147	12382	21515	4.89	0.0E+00	X98922.1	NT	H1.sapiens mRNA for gamma-glutamyltransferase
3168	12391	21525	1.61	0.0E+00	4758827	NT	H1.sapiens mRNA for gamma-glutamyltransferase
3168	12391	21526	1.81	0.0E+00	4758827	NT	Homo sapiens neurodin III (NIRXN3) mRNA
3164	12398	21534	10.08	0.0E+00	4504658	NT	Homo sapiens neurodin III (NIRXN3) mRNA
3183	12418	21562	10.77	0.0E+00	M28699.1	NT	Homo sapiens interleukin 1 receptor, type I (IL1R1) mRNA
3186	12421	21554	7.27	0.0E+00	4502088	NT	Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds
3192	12427	21562	0.97	0.0E+00	4758055	NT	Homo sapiens solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 6 (SLC25A5), nuclear gene encoding mitochondrial protein, mRNA
3192	12427	21563	0.97	0.0E+00	4758055	NT	Homo sapiens CREB binding protein (Rubinstein-Taybi syndrome) (CREBBP) mRNA
3184	12429	21564	7.38	0.0E+00	AA774783.1	EST_HUMAN	Homo sapiens CREB binding protein (Rubinstein-Taybi syndrome) (CREBBP) mRNA
3202	12437	21572	5.8	0.0E+00	AF286598.1	NT	aa87b11.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:971133 3'
3202	12437	21573	5.8	0.0E+00	AF286598.1	NT	Homo sapiens angiotensin binding protein 1 mRNA, complete cds
3215	12449	21581	1.45	0.0E+00	4557590	NT	Homo sapiens angiotensin binding protein 1 mRNA, complete cds
3220	12454	21587	0.86	0.0E+00	4507720	NT	Homo sapiens fibrillin 1 (Marfan syndrome) (FBN1) mRNA
3228	12462	21594	1.77	0.0E+00	AF019413.1	NT	Homo sapiens titin (TTN) mRNA
3231	12465	21597	4.91	0.0E+00	AF055084.1	NT	Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SK12W), RD, complement factor B (Bf), and complement component C2 (C2) genes, >
3234	12468	21599	1.25	0.0E+00	7682125	NT	Homo sapiens very large G-protein coupled receptor-1 (VLGR1) mRNA, complete cds
3234	12468	21600	1.25	0.0E+00	7682125	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
3242	14465	21607	3.5	0.0E+00	4502014	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
3242	14465	21608	3.5	0.0E+00	4502014	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
3259	12492	21623	3.47	0.0E+00	AF265208.1	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA

Table 4

Single Exon Probes Expressed In HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3260	12463	21624	1.11	0.0E+00	8822624	NT	Homo sapiens hypothetical protein FLJ20895 (FLJ20895), mRNA
3274	12507	21638	1.26	0.0E+00	7657038	NT	Homo sapiens death receptor 6 (DR6), mRNA
3285	12516	21847	0.74	0.0E+00	4885312	NT	Homo sapiens G protein-coupled receptor 24 (GPR24), mRNA
3288	12527	21658	8.17	0.0E+00	AI589284.1	EST_HUMAN	U6808.x2 NCL CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2222535 3' similar to SW:RL11_RAT
3308	12536	21688	3.01	0.0E+00	AF128883.1	NT	P25121 60S RIBOSOMAL PROTEIN L11, contains Alu repetitive element
3308	12536	21689	3.01	0.0E+00	AF128883.1	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 1-6
3307	12537	21670	0.98	0.0E+00	7657213	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 1-6
3307	12537	21671	0.98	0.0E+00	7657213	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 1-6
3308	12539	21673	1.61	0.0E+00	4502582	NT	Homo sapiens homonally upregulated neu tumor-associated kinase (HUNK), mRNA
3308	12539	21674	1.61	0.0E+00	4502582	NT	Homo sapiens homonally upregulated neu tumor-associated kinase (HUNK), mRNA
3312	12542	21678	12.9	0.0E+00	AF111163.1	NT	Homo sapiens caspase 8, apoptosis-related cysteine protease (CASP8) mRNA
3314	12544	21678	0.93	0.0E+00	AB040940.1	NT	Homo sapiens caspase 8, apoptosis-related cysteine protease (CASP8) mRNA
3321	12560	21684	0.79	0.0E+00	BE778039.1	EST_HUMAN	Homo sapiens pyrin (MEFV) gene, complete cds
3333	12602	21700	0.85	0.0E+00	AI832569.1	EST_HUMAN	Homo sapiens mRNA for KIAA1507 protein, partial cds
3374	12602	21738	2.97	0.0E+00	AU123664.1	EST_HUMAN	60148495F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3868246 5'
3381	12608	21741	0.84	0.0E+00	7363436	NT	W61004.x1 NCL CGAP_G08 Homo sapiens cDNA clone IMAGE:2305279 3' similar to TR:Q91929 Q91929
3381	12608	21742	0.84	0.0E+00	7363436	NT	ZINC FINGER PROTEIN ;
3384	12611	21744	1.38	0.0E+00	7706239	NT	AU123664 NT2RM2 Homo sapiens cDNA clone NT2RM200735 5'
3385	12612	21745	1.16	0.0E+00	AF211189.1	NT	Homo sapiens olfactory receptor, family 10, subfamily C, member 1 (OR10C1), mRNA
3389	12618		1.19	0.0E+00	AW897015.1	EST_HUMAN	Homo sapiens olfactory receptor, family 10, subfamily C, member 1 (OR10C1), mRNA
3403	12629	21759	3.18	0.0E+00	7662401	NT	Homo sapiens neuroblastoma-empirical protein (LOC51584), mRNA
3403	12629	21760	3.18	0.0E+00	7662401	NT	Homo sapiens T-type calcium channel alpha1 subunit Alpha1A isoform (CACNA1A) mRNA, complete cds
3404	12630	21761	0.96	0.0E+00	4502398	NT	MR1-SN0033-100400-001-c08 SN0033 Homo sapiens cDNA
3408	12632	21762	2.09	0.0E+00	5803087	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
3415	11870	21084	3.07	0.0E+00	AF110783.1	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
3419	12644	21773	2.84	0.0E+00	7657038	NT	Homo sapiens beaded filament structural protein 1, filensin (BFSP1) mRNA
3422	12647	21777	8.12	0.0E+00	K02380.1	NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 2 (LILRA2), mRNA
3424	12649	21779	0.95	0.0E+00	7427522	NT	Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds
3427	12652	21782	2.08	0.0E+00	4557746	NT	Homo sapiens death receptor 6 (DR6), mRNA
							Bacteriophage P1 replication region including repA, parA, and parB genes and IncA, IncB, and IncC
							Incompatibility determinants
							Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), mRNA
							Homo sapiens met proto-oncogene (hepatocyte growth factor receptor) (MET) mRNA

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3432	12657	21767	4.07	0.0E+00	AI935159.1	EST_HUMAN	wp14d10.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2484819 3' similar to TR:O73634 O73634 NEURAL CELL ADHESION MOLECULE.;
3432	12657	21768	4.07	0.0E+00	AI935159.1	EST_HUMAN	wp14d10.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2484819 3' similar to TR:O73634 O73634 NEURAL CELL ADHESION MOLECULE.;
3438	12681	21793	2.57	0.0E+00	AJ278120.1	NT	Homo sapiens mRNA for putative ankyrin-repeat containing protein (ORF1)
3442	12687	21801	2.8	0.0E+00	6552332	NT	Homo sapiens v-fos FBJ murine osteosarcoma viral oncogene homolog (FOS), mRNA
3442	12687	21802	2.8	0.0E+00	6552332	NT	Homo sapiens v-fos FBJ murine osteosarcoma viral oncogene homolog (FOS), mRNA
3448	12673	21808	1.89	0.0E+00	M14123.1	NT	Human endogenous retrovirus HERV-K10
3452	12677	21812	7.14	0.0E+00	U43283.1	NT	Human MDS1A (AML1/MDS1 fusion) mRNA, partial cds
3460	12685	21820	2.98	0.0E+00	AF045452.1	NT	Homo sapiens cell-line KG1 transcriptional regulatory protein p54 mRNA, complete cds
3460	12685	21821	2.98	0.0E+00	AF045452.1	NT	Homo sapiens cell-line KG1 transcriptional regulatory protein p54 mRNA, complete cds
3468	12683	21830	1.05	0.0E+00	AF231922.1	NT	Homo sapiens chromosome 21 unknown mRNA
3476	12700	21838	1.23	0.0E+00	4508028	NT	Homo sapiens zinc finger protein 45 (a Kruppel-associated box (KRAB) domain polypeptide) (ZNF46) mRNA
3478	12703	21838	1.95	0.0E+00	BE304781.1	EST_HUMAN	601143853F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3051373 5'
3479	12703	21839	1.95	0.0E+00	BE304781.1	EST_HUMAN	601143853F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3051373 5'
3482	12708	21842	1.24	0.0E+00	4828795	NT	Homo sapiens potassium voltage-gated channel, Isk-related family, member 2 (KCNE2) mRNA
3484	12708	21845	1.98	0.0E+00	O14867	SWISSPROT	TRANSCRIPTION REGULATOR PROTEIN BACH1 (BTB AND CNC HOMOLOG-1) (HA2303)
3488	12712	21848	0.74	0.0E+00	AI384007.1	EST_HUMAN	ts35g12.x1 Soares_NIHMPu_S1 Homo sapiens cDNA clone IMAGE:2088742 3' similar to TR:O00498
3508	12730	21867	0.61	0.0E+00	AB032979.1	NT	O00498 MYASTHENIA GRAVIS AUTOANTIGEN GRAVIN;
3508	12730	21868	0.61	0.0E+00	AB032979.1	NT	Homo sapiens mRNA for KIAA1153 protein, partial cds
3514	12738	21878	0.95	0.0E+00	AB029019.1	NT	Homo sapiens mRNA for KIAA1098 protein, partial cds
3518	12740	21877	0.89	0.0E+00	AV701869.1	EST_HUMAN	AV701869 ADB Homo sapiens cDNA clone ADBDAH08 5'
3517	12741	21878	5.33	0.0E+00	4508984	NT	Homo sapiens semenogelin II (SEMG2) mRNA
3518	12742	21882	2.19	0.0E+00	AF078868.1	NT	Homo sapiens homologous yeast-44.2 protein mRNA, complete cds
3528	12750	21882	1.74	0.0E+00	AL133204.1	NT	Nevel human gene mapping to chromosome X
3529	12752	21885	0.84	0.0E+00	AB040909.1	NT	Homo sapiens mRNA for KIAA1476 protein, partial cds
3540	12763	21894	0.9	0.0E+00	8823087	NT	Homo sapiens hypothetical protein FLJ20080 (FLJ20080), mRNA
3548	12772	21900	0.98	0.0E+00	6897248	NT	Homo sapiens sal (Drosophila)-like 1 (SALL1), mRNA
3549	12772	21901	0.98	0.0E+00	6897248	NT	Homo sapiens sal (Drosophila)-like 1 (SALL1), mRNA
3550	12773		1.1	0.0E+00	AI081907.1	EST_HUMAN	ox77c11.x1 Soares_NIHMPu_S1 Homo sapiens cDNA clone IMAGE:1682356 3' similar to WP:11984.4 CE13742;
3552	12775	21904	1.13	0.0E+00	6325463	NT	Homo sapiens butyrophilin, subfamily 3, member A3 (BTN3A3), mRNA

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3558	12781		5.31	0.0E+00	AW852217.1	EST_HUMAN	QV0-CT0225-230300-169-e01 CT0225 Homo sapiens cDNA
3562	12785	21815	1.05	0.0E+00	4504294	NT	Homo sapiens H3 histone family, member K (H3FK), mRNA
3566	12789		0.6	0.0E+00	AF118846.1	NT	Homo sapiens gamma-glutamylcysteine synthetase (GLCLC) gene, partial cds
3567	12790	21816	8.28	0.0E+00	BF676393.1	EST_HUMAN	602084583F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4248598 5'
3571	12784		1.08	0.0E+00	AA888715.1	EST_HUMAN	cc94h06.s1 NCI_CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1584043 3' similar to contains MER29.b2
3581	12803	21828	0.72	0.0E+00	AW937977.1	EST_HUMAN	QV0-DT0047-170200-123-g01 DT0047 Homo sapiens cDNA
3584	12816		1.18	0.0E+00	4826967	NT	Homo sapiens retinoblastoma-binding protein 2 (RBBP2) mRNA
3586	12817	21837	0.7	0.0E+00	AW864693.1	EST_HUMAN	hi84g01.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2878024 3'
3588	12817	21838	0.7	0.0E+00	AW864693.1	EST_HUMAN	hi84g01.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2878024 3'
3601	12822	21944	0.82	0.0E+00	7682318	NT	Homo sapiens KIAA0806 gene product (KIAA0806), mRNA
3608	12828	21848	1.13	0.0E+00	4557752	NT	Homo sapiens midline 1 (Opitz/BBB syndrome) (MID1) mRNA
3608	12828	21850	1.13	0.0E+00	4557752	NT	Homo sapiens midline 1 (Opitz/BBB syndrome) (MID1) mRNA
3628	12847	21865	1.9	0.0E+00	DB7327.1	NT	Homo sapiens mRNA for G protein-coupled inward rectifier potassium channel, complete cds
3630	12861		30.7	0.0E+00	7689491	NT	Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GAPD), mRNA
3648	12869	21886	2.32	0.0E+00	AB026542.1	NT	Homo sapiens WAVE2 mRNA for WASP-family protein, complete cds
3650	12871	21888	2.49	0.0E+00	AB007886.2	NT	Homo sapiens mRNA for KIAA0408 protein, partial cds
3651	12872	21889	3.61	0.0E+00	AF124250.1	NT	Homo sapiens SH2-containing protein Nsp2 mRNA, complete cds
3651	12872	21890	3.61	0.0E+00	AF124250.1	NT	Homo sapiens SH2-containing protein Nsp2 mRNA, complete cds
3659	12880	21999	1.62	0.0E+00	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
3659	12880	22000	1.62	0.0E+00	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
3660	12881	22001	1.03	0.0E+00	AB002331.1	NT	Human mRNA for KIAA0333 gene, partial cds
3660	12881	22002	1.03	0.0E+00	AB002331.1	NT	Human mRNA for KIAA0333 gene, partial cds
3663	12884	22005	1.57	0.0E+00	AW851714.1	EST_HUMAN	MR2-CT0222-281090-005-e05 CT0222 Homo sapiens cDNA
3665	12886	22007	1.9	0.0E+00	5729828	NT	Homo sapiens matrix metalloproteinase 24 (membrane-inserted) (MMP24), mRNA
3667	12888	22009	1.54	0.0E+00	AB018339.1	NT	Homo sapiens mRNA for KIAA0786 protein, partial cds
3669	12890	22011	1.87	0.0E+00	O14867	SWISSPROT	TRANSCRIPTION REGULATOR PROTEIN BACH1 (BTB AND CNC HOMOLOG 1) (HA2303)
3680	12901	22021	1.01	0.0E+00	5729733	NT	Homo sapiens activator of S phase kinase (ASK) mRNA
3680	12901	22022	1.01	0.0E+00	5729733	NT	Homo sapiens activator of S phase kinase (ASK) mRNA
3684	12905	22024	5.05	0.0E+00	AW288134.1	EST_HUMAN	UHH-BW0-qls-e-12-O-UJ.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2733022 3'
3684	12905	22025	5.05	0.0E+00	AW288134.1	EST_HUMAN	UHH-BW0-qls-e-12-O-UJ.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2733022 3'
3710	12930	22048	1.27	0.0E+00	AB004630.1	NT	Human gene for Type XIX collagen a1 chain, exon 6
3711	12931	22049	1.11	0.0E+00	AA463858.1	EST_HUMAN	aa08g01.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:812486 5' similar to SW:KRB4_SHEEP P02445 KERATIN, HIGH-SULFUR MATRIX PROTEIN, IIB4. [1];

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3715	12835	22053	0.9	0.0E+00	AB020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
3718	12838	22055	4.28	0.0E+00	7657488	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
3728	12947	22065	1.04	0.0E+00	AB037835.1	NT	Homo sapiens mRNA for KIAA1414 protein, partial cds
3742	12962	22077	11.29	0.0E+00	7682183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
3745	12983	22080	33.84	0.0E+00	4506718	NT	Homo sapiens ribosomal protein S2 (RPS2) mRNA
3810	13028		0.68	0.0E+00	AF195858.1	NT	Homo sapiens DNA mismatch repair protein (MLH3) gene, complete cds
3811	13029	22138	2.52	0.0E+00	AF178733.1	NT	Pan troglodytes effector receptor (PTR208) gene, partial cds
3814	13032	22142	2.35	0.0E+00	7657488	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
3814	13032	22143	2.35	0.0E+00	7657488	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
3818	13038	22148	2.12	0.0E+00	4756011	NT	Homo sapiens RAB9, member RAS oncogene family (RAB9) mRNA
3818	13037	22149	0.99	0.0E+00	10181138	NT	Mus musculus junctional protein 1 (Jp1-pending), mRNA
3820	13038	22160	1.18	0.0E+00	AF127851.1	NT	Gorilla gorilla effector receptor (GG071) gene, partial cds
3820	13038	22151	1.18	0.0E+00	AF127851.1	NT	Gorilla gorilla effector receptor (GG071) gene, partial cds
3821	13039	22162	1.3	0.0E+00	AI377689.1	EST_HUMAN	168210.X1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2091307 3'
3822	13040		1.16	0.0E+00	AF152486.1	NT	Homo sapiens protocadherin beta 3 (PCDH-beta3) mRNA, complete cds
3823	13041	22153	3.87	0.0E+00	4758199	NT	Homo sapiens desmoplakin (DPI, DPII) (DSP) mRNA
3825	13043	22154	15.35	0.0E+00	S78885.1	NT	Homo sapiens ATP-sensitive inwardly rectifying K-channel subunit (KCNJ8/BIR1) gene, complete cds
3828	13044	22155	2.43	0.0E+00	7710148	NT	Homo sapiens methyl CpG binding protein 2 (MECP2), mRNA
3827	13045	22156	1.87	0.0E+00	7682183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
3833	13050	22160	1.08	0.0E+00	6912735	NT	Homo sapiens transient receptor potential channel 5 (TRPC5), mRNA
3837	13054	22167	6.52	0.0E+00	4503178	NT	Homo sapiens chromosome X open reading frame 5 (CXORF5) mRNA
3837	13054	22168	6.52	0.0E+00	4503178	NT	Homo sapiens chromosome X open reading frame 5 (CXORF5) mRNA
3839	13056	22171	3.62	0.0E+00	U09412.1	NT	Human zinc finger protein ZNF134 mRNA, complete cds
3840	13057	22172	0.82	0.0E+00	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
3843	13060	22174	1.28	0.0E+00	4828783	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA
3845	13062	22176	2.53	0.0E+00	4758171	NT	Homo sapiens SC35-interacting protein 1 (SRRP128), mRNA
3847	13064	22178	0.8	0.0E+00	AF090117.1	NT	Homo sapiens amphiphylin gene, partial cds
3856	13072	22187	2.52	0.0E+00	AI884727.1	EST_HUMAN	wk01f01.x1 NCL_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2411085 3' similar to TRIO43340
3857	13073	22188	1.05	0.0E+00	AL163248.2	NT	O43340 R28830_2; contains element PTR7 repetitive element;
3860	13078	22182	15.3	0.0E+00	4508742	NT	Homo sapiens chromosome 21 segment HS21C048
3862	13078	22184	1.81	0.0E+00	AL040338.1	EST_HUMAN	Homo sapiens ribosomal protein S8 (RPS8), mRNA
							DKFZp434N0413_r1_434 (synonym: hbs3) Homo sapiens cDNA clone DKFZp434N0413 5'

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Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3867	13083	22200	0.98	0.0E+00	6005887	NT	Homo sapiens AP1 gamma subunit binding protein 1 (AP1GBP1), mRNA
3867	13083	22201	0.98	0.0E+00	6005887	NT	Homo sapiens AP1 gamma subunit binding protein 1 (AP1GBP1), mRNA
3868	13084	22202	2.93	0.0E+00	4504138	NT	Homo sapiens glutamate receptor, metabotropic 3 (GRM3) mRNA
3869	13085		1.91	0.0E+00	4505078	NT	Homo sapiens melanoma antigen, family B, 1 (MAGEB1) mRNA
3873	13089	22205	1.28	0.0E+00	AF149412.1	NT	Homo sapiens HBP17 heparin-binding and FGF-binding protein gene, complete cds
3882	13098	22215	1.08	0.0E+00	4508758	NT	Homo sapiens tyrosine receptor 3 (RYR3) mRNA
3886	13102	22219	2.26	0.0E+00	4585642	NT	Homo sapiens zinc finger protein (KIAA0412) mRNA
3893	13109	22227	4	0.0E+00	BF355285.1	EST_HUMAN	RC3-H10860-170800-011-a12 HT0860 Homo sapiens cDNA
3899	13115	22232	2.47	0.0E+00	AF129533.1	NT	Homo sapiens F-box protein Fbl3b (FBL3B) mRNA, partial cds
3902	13118	22235	1	0.0E+00	U86281.1	NT	Homo sapiens olfactory receptor (OR7-141) gene, partial cds
3902	13118	22236	1	0.0E+00	U86281.1	NT	Homo sapiens olfactory receptor (OR7-141) gene, partial cds
3908	13122	22240	4.33	0.0E+00	BE378602.1	EST_HUMAN	Homo sapiens cDNA clone IMAGE:3608600 5'
3914	13130	22247	0.91	0.0E+00	AW680740.1	EST_HUMAN	PM3-LT0031-100100-003-109 LT0031 Homo sapiens cDNA
3915	13131	22248	1.01	0.0E+00	BE264988.1	EST_HUMAN	PM3-LT0031-100100-003-109 LT0031 Homo sapiens cDNA clone IMAGE:3637774 5'
3915	13131	22249	1.01	0.0E+00	BE264988.1	EST_HUMAN	PM3-LT0031-100100-003-109 LT0031 Homo sapiens cDNA clone IMAGE:3637774 5'
3953	13168	22281	5.67	0.0E+00	AF116195.1	NT	Homo sapiens cancer-testis antigen CT10 (CT10) gene, complete cds
3953	13168	22282	5.67	0.0E+00	AF116195.1	NT	Homo sapiens cancer-testis antigen CT10 (CT10) gene, complete cds
3963	13178		4.8	0.0E+00	M23910.1	NT	Homo sapiens cancer-testis antigen DPw4-beta-2 pseudogene, exon 2
3965	13180		5.59	0.0E+00	AL163303.2	NT	Human MHC class II lymphocyte antigen DPw4-beta-2 pseudogene, exon 2
3974	13188	22288	3.74	0.0E+00	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C0084
3982	13198	22304	1.95	0.0E+00	AL163288.2	NT	Homo sapiens chromosome 21 segment HS21C0088
3984	13208		82.29	0.0E+00	4503470	NT	Homo sapiens chromosome 21 segment HS21C0093
4002	13215		1.09	0.0E+00	AI657078.1	EST_HUMAN	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
4005	13217	22321	1.87	0.0E+00	U09368.1	NT	tt55g08.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2244734 3' similar to TR:060309 080309
4023	13234	22339	15.84	0.0E+00	AB015610.1	NT	KIAA0563 PROTEIN. ;
4032	13242		3.9	0.0E+00	AJ238617.1	NT	Human zinc finger protein ZNF133
4042	13252	22353	1.68	0.0E+00	AL163203.2	NT	Chlorococcus aesthus mRNA for ribosomal protein S4X, complete cds
4043	13253	22354	3.29	0.0E+00	AJ277276.1	NT	Homo sapiens mRNA for UGA suppressor tRNA-associated antigenic protein (RNA48 gene)
4043	13253	22355	3.29	0.0E+00	AJ277276.1	NT	Homo sapiens chromosome 21 segment HS21C0083
4050	13260	22362	11.29	0.0E+00	5032026	NT	Homo sapiens mRNA for rpsa-2 (rpsa gene)
4050	13260	22363	11.29	0.0E+00	5032026	NT	Homo sapiens mRNA for rpsa-2 (rpsa gene)
4050	13260	22363	11.29	0.0E+00	5032026	NT	Homo sapiens retinoblastoma-binding protein 4 (RBBP4) mRNA
4050	13260	22363	11.29	0.0E+00	5032026	NT	Homo sapiens retinoblastoma-binding protein 4 (RBBP4) mRNA
4050	13260	22363	11.29	0.0E+00	5032026	NT	Homo sapiens phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylamidazole synthetase (GART) mRNA
4050	13271	22373	1.03	0.0E+00	4503914	NT	

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4066	13276	22377	5.4	0.0E+00	4885308	NT	Homo sapiens G protein-coupled receptor 21 (GPR21), mRNA
4067	13277	22378	1.63	0.0E+00	AB006625.1	NT	Homo sapiens mRNA for KIAA0287 gene, partial cds
4070	13280	22379	0.59	0.0E+00	4758807	NT	Homo sapiens ras GTPase activating protein-like (NGAP) mRNA
4071	13281	22380	9.39	0.0E+00	11419297	NT	Homo sapiens IMP (inosine monophosphate) dehydrogenase 1 (IMPDH1), mRNA
4072	13282	22381	5.92	0.0E+00	AL096857.1	NT	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes
4080	13280	22389	4.73	0.0E+00	AF165527.1	NT	Homo sapiens DGCR8 (DGCR8) mRNA, complete cds
4089	10363	19513	1.01	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
4089	10363	19514	1.01	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
4089	13304	22403	0.99	0.0E+00	5901805	NT	Homo sapiens bulkyphillin, subfamily 3, member A2 (BTNA2), mRNA
4097	13305	22404	1.08	0.0E+00	4503854	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (60kD) (GABPA), mRNA
4097	13305	22405	1.08	0.0E+00	4503854	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (60kD) (GABPA), mRNA
4100	12741	21878	0.59	0.0E+00	4506984	NT	Homo sapiens semenogelin II (SEMG2) mRNA
4102	13309	22408	0.98	0.0E+00	8922391	NT	Homo sapiens hypothetical protein FLJ10378 (FLJ10378), mRNA
4102	13309	22409	0.98	0.0E+00	8922391	NT	Homo sapiens hypothetical protein FLJ10378 (FLJ10378), mRNA
4108	13315	22413	0.81	0.0E+00	AB020702.1	NT	Homo sapiens mRNA for KIAA0895 protein, partial cds
4115	13322	22422	6.13	0.0E+00	A1982597.1	EST_HUMAN	wu04d04.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2515975 3'
4115	13322	22423	6.13	0.0E+00	A1982597.1	EST_HUMAN	wu04d04.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2515975 3'
4118	13324	22425	1.2	0.0E+00	BE184856.1	EST_HUMAN	MR1-HT0707-100500-001-e02 HT0707 Homo sapiens cDNA
4118	13324	22426	1.2	0.0E+00	BE184856.1	EST_HUMAN	MR1-HT0707-100500-001-e02 HT0707 Homo sapiens cDNA
4122	13328		5.85	0.0E+00	BE274217.1	EST_HUMAN	601120778F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2867690 5'
4128	13334	22432	0.98	0.0E+00	AB032851.1	NT	Homo sapiens mRNA for KIAA1125 protein, partial cds
4128	13334	22433	0.98	0.0E+00	AB032851.1	NT	Homo sapiens mRNA for KIAA1125 protein, partial cds
4130	13336	22435	2.13	0.0E+00	5729725	NT	Homo sapiens nuclear receptor coactivator 3 (NCOA3), mRNA
4138	13344		6.07	0.0E+00	AW675598.1	EST_HUMAN	ba51f04.x1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2800095 3' similar to SW:TH12_BOVIN
4143	13349	22449	1.61	0.0E+00	AW408788.1	EST_HUMAN	Q95108 MITOCHONDRIAL THIOPREDOXIN PRECURSOR ;
4145	13351	22452	1.52	0.0E+00	8922468	NT	UI-HF-BMD-adx-e-02-Q-UL1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3063147 5'
4145	13351	22453	1.52	0.0E+00	8922468	NT	Homo sapiens hypothetical protein FLJ10498 (FLJ10498), mRNA
4154	13360		2.25	0.0E+00	5174632	NT	Homo sapiens polycystic kidney disease (polycystin) and REJ (sperm receptor for egg jelly, see urchin homolog)-like (PKDREJ) mRNA
4165	13369	22468	1.08	0.0E+00	AB037739.1	NT	Homo sapiens mRNA for KIAA1318 protein, partial cds
4174	13378	22477	10.79	0.0E+00	AA401438.1	EST_HUMAN	zu68h07.a1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:743187 3' similar to contains Alu repetitive element; contains element MER35 repetitive element ;

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4174	13378	22478	10.79	0.0E+00	AA401438.1	EST_HUMAN	zu68h07.a1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:743197 3' similar to contains Alu repetitive element; contains element MER35 repetitive element;
4177	13381	22482	1.36	0.0E+00	AF157478.1	NT	Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds
4191	13395	22495	1.8	0.0E+00	7882125	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
4201	9301	18403	6.72	0.0E+00	AA228128.1	EST_HUMAN	zf59c04.l1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:687560 5' similar to TR:G222811 G222811 ALPHA 1 CHAIN OF TYPE XII COLLAGEN;
4201	9301	18404	6.72	0.0E+00	AA228128.1	EST_HUMAN	zf59c04.l1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:687560 5' similar to TR:G222811 G222811 ALPHA 1 CHAIN OF TYPE XII COLLAGEN;
4208	13409	22502	4.97	0.0E+00	4758188	NT	Homo sapiens desmoplakin (DPI, DPII) (DSP) mRNA
4208	13409	22503	4.97	0.0E+00	4758199	NT	Homo sapiens desmoplakin (DPI, DPII) (DSP) mRNA
4215	13418		0.92	0.0E+00	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
4248	13449	22540	0.98	0.0E+00	AJ010770.1	NT	Homo sapiens hyperion gene, exons 1-50
4259	13462	22554	2.79	0.0E+00	J02610.1	NT	Homo sapiens apolipoprotein B-100 mRNA, complete cds
4273	13478	22573	0.84	0.0E+00	AW838889.1	EST_HUMAN	PM2-DT0023-080300-004-a08 DT0023 Homo sapiens cDNA
4281	13484	22582	0.83	0.0E+00	4828827	NT	Homo sapiens myelodysplasia syndrome 1 (MDS1) mRNA
4281	13484	22583	0.83	0.0E+00	4828827	NT	Homo sapiens myelodysplasia syndrome 1 (MDS1) mRNA
4283	13486	22585	3.57	0.0E+00	AF174590.1	NT	Homo sapiens F-box protein Fbx4 (FBL4) mRNA, partial cds
4288	13491	22588	1.38	0.0E+00	6808918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
4288	13491	22589	1.39	0.0E+00	6808918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
4280	13492		2.48	0.0E+00	AI188844.1	EST_HUMAN	qd23f08.x1 Soares_placenta_80weeks_2NHP8669W Homo sapiens cDNA clone IMAGE:1724578 3' similar to contains MER20.b2 MER20 repetitive element;
4284	13495		4.58	0.0E+00	U14520.1	NT	Human CBFA3 (Cbfa3) gene, partial cds
4288	13496	22595	0.64	0.0E+00	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (MLL T4) mRNA
4318	13517	22612	1.43	0.0E+00	6583384	NT	Homo sapiens protein kinase C, nu (PRKGN), mRNA
4318	13517	22613	1.43	0.0E+00	6583384	NT	Homo sapiens protein kinase C, nu (PRKGN), mRNA
4323	13524	22619	1.16	0.0E+00	U10991.1	NT	Human G2 protein mRNA, partial cds
4323	13524	22620	1.16	0.0E+00	U10991.1	NT	Human G2 protein mRNA, partial cds
4334	13535	22628	8.99	0.0E+00	6912281	NT	Homo sapiens COMPLEMENT COMPONENT C1q RECEPTOR (C1QR), mRNA
4354	13558		1.34	0.0E+00	AF153047.2	NT	Homo sapiens gap junction protein connexin-38 (CX38) gene, complete cds
4384	13588	22661	4.84	0.0E+00	L14591.1	NT	Homo sapiens plasma membrane calcium ATPase isoform 1 (ATP2B1) gene, alternative splice products, partial cds
4388	13570	22668	6.52	0.0E+00	Z80780.1	NT	H. sapiens H2B/h gene
4388	13570	22667	6.52	0.0E+00	Z80780.1	NT	H. sapiens H2B/h gene

Table 4

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4368	13571	22668	1.2	0.0E+00	AW166933.1	EST_HUMAN	xg88e10.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2835514 3' similar to TR:P97365 P97365
4375	13577	22674	1.54	0.0E+00	X60483.1	NT	ZINC FINGER PROTEIN 64 ;
4375	13577	22675	1.54	0.0E+00	X60483.1	NT	H.sapiens H4/d gene for H4 histone
4380	13581	22681	9.12	0.0E+00	7682091	NT	H.sapiens H4/d gene for H4 histone
4380	13581	22682	9.12	0.0E+00	7682091	NT	Homo sapiens KIAA0390 gene product (KIAA0390), mRNA
4388	13589	22691	1.03	0.0E+00	X82338.1	NT	Homo sapiens KIAA0390 gene product (KIAA0390), mRNA
4391	13582	22695	18.08	0.0E+00	4885126	NT	Homo sapiens Menkes disease gene, exon 4
4392	13583	22698	1.77	0.0E+00	AJ271736.1	NT	Homo sapiens caudal type homeo box transcription factor 4 (CDX4), mRNA
4393	13594		0.96	0.0E+00	AL163207.2	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
4398	13597	22698	4.78	0.0E+00	AB037781.1	NT	Homo sapiens chromosome 21 segment HS21C007
4424	13624	22719	1.16	0.0E+00	7019450	NT	Homo sapiens mRNA for KIAA1360 protein, partial cds
4435	13635		8.37	0.0E+00	AF195953.1	NT	Homo sapiens myosin regulatory light chain interacting protein (MIR), mRNA
4442	13642	22733	26.88	0.0E+00	AJ249765.1	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds
4442	13642	22734	26.88	0.0E+00	AJ249765.1	NT	Homo sapiens ACTN2 gene for alpha-Actinin 2, exon 10
4446	13645	22740	0.87	0.0E+00	W28179.1	EST_HUMAN	Homo sapiens ACTN2 gene for alpha-Actinin 2, exon 10
4446	13645	22741	0.87	0.0E+00	W28179.1	EST_HUMAN	24q7 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
4484	13682		2.27	0.0E+00	AF200626.1	NT	24q7 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
4487	13685		1.02	0.0E+00	M14123.1	NT	Homo sapiens HPS1 gene, intron 5
4488	13686	22778	0.72	0.0E+00	AA228126.1	EST_HUMAN	Human endogenous retrovirus HERV-K10
4488	13686	22777	0.72	0.0E+00	AA228126.1	EST_HUMAN	z58c04.r1 Soares_NIHMPu_S1 Homo sapiens cDNA clone IMAGE:867590 5' similar to TR:G222811
4504	13701	22785	13.33	0.0E+00	AW084864.1	EST_HUMAN	G222811 ALPHA 1 CHAIN OF TYPE XI COLLAGEN ;
4506	14471		2.11	0.0E+00	8051819	NT	z58c04.r1 Soares_NIHMPu_S1 Homo sapiens cDNA clone IMAGE:867590 5' similar to TR:G222811
4510	13706		8.68	0.0E+00	AL163207.2	NT	z58c04.r1 Soares_NIHMPu_S1 Homo sapiens cDNA clone IMAGE:867590 5' similar to TR:G222811
4512	13708	22801	3.69	0.0E+00	AW381570.1	EST_HUMAN	PM1-HT0305-101168-002-403 HT0305 Homo sapiens cDNA
4517	13713	22806	1.93	0.0E+00	AJ278120.1	NT	Homo sapiens mRNA for putative ankyrin-repeat containing protein (ORF1)
4517	13713	22807	1.93	0.0E+00	AJ278120.1	NT	Homo sapiens mRNA for putative ankyrin-repeat containing protein (ORF1)
4519	13715	22809	1.19	0.0E+00	4758487	NT	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA
4520	13716	22810	1.72	0.0E+00	AF108830.1	NT	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA
4524	13720	22815	1.43	0.0E+00	Z65526.1	NT	Homo sapiens serine-threonine protein kinase (MINBH) mRNA, complete cds
4528	13724	22820	1.14	0.0E+00	AF111163.1	NT	H.sapiens pancreatic polypeptide receptor PP1 gene
							Homo sapiens pyrin (MEFV) gene, complete cds

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Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4528	13724	22821	1.14	0.0E+00	AF111163.1	NT	Homo sapiens pyrin (MEFV) gene, complete cds
4538	14472	22829	4.41	0.0E+00	6005973	NT	Homo sapiens zinc finger protein 195 (ZNF195), mRNA
4541	13738	22834	7.2	0.0E+00	AF208161.1	NT	Homo sapiens zinc finger protein 195 (ZNF195), mRNA
4548	13741	22841	1.23	0.0E+00	AF152337.1	NT	Homo sapiens synectin precursor, mRNA, complete cds
4549	13744	22845	1.3	0.0E+00	AF152337.1	NT	Homo sapiens synectin precursor, mRNA, complete cds
4561	13755	22863	33.93	0.0E+00	5454175	NT	Homo sapiens zinc finger protein 211 (ZNF211), mRNA
					4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
4588	13762	22858	16.98	0.0E+00	4505016	NT	Homo sapiens low density lipoprotein receptor-related protein 8 (LRP8) mRNA, and translated products
4572	13768	22861	1.1	0.0E+00	4503098	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
4577	13771	22867	1.06	0.0E+00	4502556	NT	Homo sapiens calcium/calmodulin-dependent protein kinase IV (CAMK4) mRNA
4580	13774		1.11	0.0E+00	BE871808.1	EST_HUMAN	601447832F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3852127 5'
4583	13777		2.88	0.0E+00	L35485.1	NT	Homo sapiens diuronate sulphate sulphonase (IDS) gene, complete cds
4585	13778	22870	12.98	0.0E+00	7662091	NT	Homo sapiens KIAA0390 gene product (KIAA0390), mRNA
4585	13779	22871	12.98	0.0E+00	7662091	NT	Homo sapiens KIAA0390 gene product (KIAA0390), mRNA
4602	13788	22888	2.61	0.0E+00	AF143314.1	NT	Homo sapiens PTEN (P.TEN) gene, exons 3 through 5
						NT	Homo sapiens mRNA for G7c protein (G7c gene located in the class III region of the major histocompatibility complex)
4605	13788	22889	11.6	0.0E+00	AJ245418.1	NT	Homo sapiens mRNA for G7c protein (G7c gene located in the class III region of the major histocompatibility complex)
4605	13788	22890	11.6	0.0E+00	AJ245418.1	NT	Homo sapiens mRNA for KIAA0785 protein, partial cds
4607	13801	22891	0.73	0.0E+00	AB018338.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
4615	13809		0.64	0.0E+00	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
4628	13820		1.54	0.0E+00	AA174072.1	EST_HUMAN	zp18g08.s1 Stratagene fetal retina 837202 Homo sapiens cDNA clone IMAGE:609854 3'
4628	13822		1.75	0.0E+00	7657410	NT	Homo sapiens odz (odd Oz/ten-m, Drosophila) homolog 1 (ODZ1), mRNA
4630	13824		5.76	0.0E+00	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4631	13826	22913	1.18	0.0E+00	H92741.1	EST_HUMAN	y82b01.s1 Soares pineal gland_N3HPG Homo sapiens cDNA clone IMAGE:231721 3'
4631	13826	22914	1.18	0.0E+00	H92741.1	EST_HUMAN	y82b01.s1 Soares pineal gland_N3HPG Homo sapiens cDNA clone IMAGE:231721 3'
4632	13826	22915	1.92	0.0E+00	AF184110.1	NT	Homo sapiens cyclophilin-related protein (NIKTR) gene, complete cds
4633	13827	22916	5.71	0.0E+00	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
4634	13828		1.78	0.0E+00	AB037521.1	NT	Homo sapiens gene for natriuretic protein, partial cds
4638	13832	22920	1.07	0.0E+00	AB007868.2	NT	Homo sapiens mRNA for KIAA0408 protein, partial cds
4643	13837	22926	36.33	0.0E+00	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
4643	13837	22927	36.33	0.0E+00	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
4644	13838	22928	2.55	0.0E+00	AF167441.1	NT	Mus musculus E-cadherin binding protein E7 mRNA, complete cds
4654	13848	22940	1.04	0.0E+00	L78810.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4854	13848	22841	1.04	0.0E+00	L78810.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
4854	13848	22842	1.04	0.0E+00	L78810.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
4855	13849	22843	1.68	0.0E+00	AB028870.1	NT	Homo sapiens mRNA for KIAA1047 protein, partial cds
4855	13849	22844	1.68	0.0E+00	AB028870.1	NT	Homo sapiens mRNA for KIAA1047 protein, partial cds
4862	13850	22854	7.88	0.0E+00	Y18880.1	NT	Human endogenous retrovirus type K (HERV-K), gag, pol and env genes
4868	13862	22863	2.3	0.0E+00	BE081527.1	EST_HUMAN	QV2-BT0635-160400-142-H05 BT0635 Homo sapiens cDNA
4869	13863	22864	1.23	0.0E+00	AA418246.1	EST_HUMAN	z96b07.s1 Soares_Nhlh1Pu_S1 Homo sapiens cDNA clone IMAGE:767605 3'
4875	13869		2.11	0.0E+00	AF086841.1	NT	Homo sapiens truncated tenascin XB (TNXB) gene, partial cds and TNXA gene recombination breakpoint region
4883	13875	22875	1.02	0.0E+00	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
4883	13875	22876	1.02	0.0E+00	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
4884	13876	22877	2.48	0.0E+00	AB037820.1	NT	Homo sapiens mRNA for KIAA1389 protein, partial cds
4884	13876	22878	2.48	0.0E+00	AB037820.1	NT	Homo sapiens mRNA for KIAA1389 protein, partial cds
4885	13877	22879	2.47	0.0E+00	M74089.1	NT	Human displacement protein (CCAAT) mRNA
4887	13878	22881	1.63	0.0E+00	AW284800.1	EST_HUMAN	UI-H-B12-sh1-c-05-Q-U1.s1 NCI CGAP Sub4 Homo sapiens cDNA clone IMAGE:2726792 3'
4887	13878	22882	1.63	0.0E+00	AW284800.1	EST_HUMAN	UI-H-B12-sh1-c-05-Q-U1.s1 NCI CGAP Sub4 Homo sapiens cDNA clone IMAGE:2726792 3'
4889	13881	22883	2.61	0.0E+00	6453812	NT	Homo sapiens butyrophilin, subfamily 2, member A2 (BTN2A2), mRNA
4889	13881	22884	2.61	0.0E+00	6453812	NT	Homo sapiens butyrophilin, subfamily 2, member A2 (BTN2A2), mRNA
4890	9419	18553	0.78	0.0E+00	T56945.1	EST_HUMAN	ya83g04.i2 Stratiogene fetal spleen (#837205) Homo sapiens cDNA clone IMAGE:88310 5'
4890	9419	18554	0.78	0.0E+00	T56945.1	EST_HUMAN	ya83g04.i2 Stratiogene fetal spleen (#837205) Homo sapiens cDNA clone IMAGE:88310 5'
4893	13884		1.01	0.0E+00	BE278730.1	EST_HUMAN	601158935F1 NIH_MGC 21 Homo sapiens cDNA clone IMAGE:3505521 5'
4724	13915	23016	12.07	0.0E+00	M80902.1	NT	Human ATRAK nucleoprotein mRNA, 5' and
4727	13918	23019	2.83	0.0E+00	M69197.1	NT	Human haptoglobin and haptoglobin-related protein (HP and HPR) genes, complete cds
4727	13918	23020	2.93	0.0E+00	M69197.1	NT	Human haptoglobin and haptoglobin-related protein (HP and HPR) genes, complete cds
4727	13918	23021	1.32	0.0E+00	AF184110.1	NT	Homo sapiens cyclophilin-related protein (NIKTR) gene, complete cds
4733	13924	23028	0.61	0.0E+00	7682479	NT	Homo sapiens KIAA1084 protein (KIAA1084), mRNA
4735	13926	23029	1.85	0.0E+00	7682181	NT	Homo sapiens KIAA0563 gene product (KIAA0563), mRNA
4740	13931	23035	1.12	0.0E+00	U07563.1	NT	Human proto-oncogene tyrosine-protein kinase (ABL) gene, exon 1a and exons 2-10, complete cds
4745	13936	23040	0.98	0.0E+00	AL098857.1	NT	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes
4763	13944		0.95	0.0E+00	X58467.1	NT	Human CYP2D7AP pseudogene for cytochrome P450 2D6
4770	13959	23060	1.19	0.0E+00	AF026801.1	NT	Homo sapiens alpha-3 type IX collagen (COL9A3) gene, promoter region, and exons 1-28
4772	13961	23062	1.2	0.0E+00	6677700	NT	Homo sapiens G-protein coupled receptor (RE2), mRNA
4772	13961	23063	1.2	0.0E+00	6677700	NT	Homo sapiens G-protein coupled receptor (RE2), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4775	13964	23068	0.88	0.0E+00	7018320	NT	Homo sapiens protein d008 (AD013), mRNA
4775	13964	23067	0.88	0.0E+00	7018320	NT	Homo sapiens protein d008 (AD013), mRNA
4798	13985	23060	1.99	0.0E+00	AW44637.1	EST_HUMAN	UI-H-B13-ajw-c-04-U1.s1 NCJ_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733284 3'
4801	13990	23098	1.24	0.0E+00	AF903134.1	NT	Homo sapiens aldehyde dehydrogenase 12 (ALDH12) mRNA, complete cds
4804	13993		1.63	0.0E+00	AF083242.1	NT	Homo sapiens HSPC024-iso mRNA, complete cds
4853	14042	23135	0.67	0.0E+00	J00191.1	NT	Human MHC class I transplantation antigen (hla) gene
4853	14042	23136	0.67	0.0E+00	J00191.1	NT	Human MHC class I transplantation antigen (hla) gene
4880	14048		5.78	0.0E+00	AF240788.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
4882	14050	23144	1.87	0.0E+00	X97205.1	NT	M.fascicularis mRNA for metalloprotease-like, disintegrin-like protein, IVa
4884	14052	23146	2.5	0.0E+00	AF084479.1	NT	Homo sapiens Williams-Buren syndrome deletion transcript 9 (WBSCR9) mRNA, complete cds
4885	14053	23147	1.79	0.0E+00	AF097416.1	NT	Mus musculus zinc finger transcription factor Kalso mRNA, complete cds
4886	14054	23148	5.28	0.0E+00	4503768	NT	Homo sapiens fragile X mental retardation 2 (FMR2) mRNA
4888	14056	23150	17.49	0.0E+00	4885048	NT	Homo sapiens actin, alpha, cardiac muscle (ACTC), mRNA
4889	14057	23151	1.01	0.0E+00	P52740	SWISSPROT	ZINC FINGER PROTEIN 132
4871	14059	23153	1.92	0.0E+00	8922180	NT	Homo sapiens hypothetical protein DKFZp782E1312 (DKFZp782E1312), mRNA
4874	14062	23157	5.78	0.0E+00	8923080	NT	Homo sapiens hypothetical protein FLJ20073 (FLJ20073), mRNA
4878	14066	23161	1.05	0.0E+00	7681978	NT	Homo sapiens KIAA0187 gene product (KIAA0187), mRNA
4879	14067	23162	1.61	0.0E+00	M94081.1	NT	Human Tcr-C-delta gene, exons 1-4; Tcr-V-delta gene, exons 1-2; T-cell receptor alpha (Tcr-alpha) gene, J1-J81 segments; and Tcr-C-alpha gene, exons 1-4
4878	14067						
4881	14069	23163	1.61	0.0E+00	M94081.1	NT	Human Tcr-C-delta gene, exons 1-4; Tcr-V-delta gene, exons 1-2; T-cell receptor alpha (Tcr-alpha) gene, J1-J81 segments; and Tcr-C-alpha gene, exons 1-4
4881	14069	23165	1.73	0.0E+00	X94628.1	NT	H.sapiens MeCP-2 gene
4881	14069	23166	1.73	0.0E+00	X94628.1	NT	H.sapiens MeCP-2 gene
4884	14072	23169	3.1	0.0E+00	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
4895	14083	23176	1.21	0.0E+00	5032150	NT	Homo sapiens TATA box binding protein (TBP)-associated factor, RNA polymerase II, 28kD (TAF21)
4905	14083	23186	1.59	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
4907	14085	23188	3.28	0.0E+00	X92841.1	NT	H.sapiens MICA gene
4908	14087	23190	2.44	0.0E+00	4585642	NT	Homo sapiens zinc finger protein (KIAA0412) mRNA
4910	14088	23191	0.94	0.0E+00	AB037894.1	NT	Homo sapiens mRNA for KIAA1443 protein, partial cds
4911	14089	23192	1.88	0.0E+00	AB014533.1	NT	Homo sapiens mRNA for KIAA0633 protein, partial cds
4912	14100	23163	2.45	0.0E+00	6877848	NT	Mus musculus zinc finger protein interacting with K protein 1 (Zfk1); mRNA
4913	14101	23184	1.89	0.0E+00	5174590	NT	Homo sapiens meningioma expressed antigen 6 (colled-coil proline-rich) (MGEA6), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4915	14103	23198	8.44	0.0E+00	4758189	NT	Homo sapiens desmoplakin (DPI, DPII) (DSP) mRNA
4917	14105	23188	1.31	0.0E+00	5174560	NT	Homo sapiens meningioma expressed antigen 8 (coiled-coil proline-rich) (MGEA6), mRNA
4917	14105	23188	1.31	0.0E+00	5174560	NT	Homo sapiens meningioma expressed antigen 8 (coiled-coil proline-rich) (MGEA6), mRNA
4921	14109	23205	33.09	0.0E+00	AF055068.1	NT	Homo sapiens MHC class 1 region
4923	14111		3.19	0.0E+00	4505508	NT	Homo sapiens oploid receptor, delta 1 (OPRD1) mRNA
4924	14112	23208	3.02	0.0E+00	AF081711.1	NT	Homo sapiens splice variant AKAP350 mRNA, partial cds
4936	14123	23218	3.83	0.0E+00	4503884	NT	Homo sapiens farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase, dimethylallyltransferase, geranyltransferase) (FPPS) mRNA
4938	14125	23220	8.87	0.0E+00	4557472	NT	Homo sapiens chloride channel 5 (nephrolithiasis 2, X-linked, Dent disease) (CLCN5) mRNA
4938	14125	23221	8.87	0.0E+00	4557472	NT	Homo sapiens chloride channel 5 (nephrolithiasis 2, X-linked, Dent disease) (CLCN5) mRNA
4946	14133		0.62	0.0E+00	AI291128.1	EST_HUMAN	qin1505.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1881921 3' similar to TR:Q61632
4972	14159	23250	1.28	0.0E+00	AL163284.2	NT	EN-2/LACZ FUSION PROTEIN
4981	14168	23258	1.19	0.0E+00	AW452728.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C084
4988	14170	23267	0.98	0.0E+00	4502398	NT	UI-H-B13-ctv-F-02-Q-UJ.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3058691 3'
4992	14170		10.64	0.0E+00	U14697.1	NT	Homo sapiens beaded filament structural protein 1, filensin (BFSP1) mRNA
5003	14180	23280	1.08	0.0E+00	M10978.1	NT	Human ribosomal protein L21 mRNA, complete cds
5005	14182		3.04	0.0E+00	BE408863.1	EST_HUMAN	Human endogenous retroviral DNA (4-1), complete proviral segment
5009	14188	23285	5.9	0.0E+00	4758189	NT	601303728F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638118 5'
5016	14202	23289	1.87	0.0E+00	7682401	NT	Homo sapiens desmoplakin (DPI, DPII) (DSP) mRNA
5019	14206	23291	2.07	0.0E+00	AB026866.1	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
5032	14217	23301	2.25	0.0E+00	8923441	NT	Homo sapiens mRNA for KIAA1043 protein, partial cds
5032	14217	23302	2.25	0.0E+00	8923441	NT	Homo sapiens hypothetical protein FLJ20477 (FLJ20477), mRNA
5046	14228	23311	0.76	0.0E+00	AA601246.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ20477 (FLJ20477), mRNA
5046	14228	23312	0.76	0.0E+00	AA601246.1	EST_HUMAN	no14g09.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100704 3' similar to TR:E239140
5046	14229	23313	0.76	0.0E+00	AA601246.1	EST_HUMAN	E239140 SPALT PROTEIN
5049	14231	23315	1.68	0.0E+00	AF161463.1	EST_HUMAN	no14g09.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100704 3' similar to TR:E239140
5049	14231	23316	1.68	0.0E+00	AF161463.1	NT	E239140 SPALT PROTEIN
						NT	Homo sapiens HSPC114 mRNA, complete cds
						NT	Homo sapiens HSPC114 mRNA, complete cds
5051	14233	23318	3.31	0.0E+00	U82671.2	NT	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), caltactin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and L1>

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5051	14233	23319	3.31	0.0E+00	U82871.2	NT	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), caltractin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and L1>
5057	9498	18630	0.81	0.0E+00	AF195658.1	NT	Homo sapiens DNA mismatch repair protein (MLH3) gene, complete cds
5059	14239		1.1	0.0E+00	AL050253.1	NT	H. sapiens mRNA similar to D29763 mouse mRNA for seizure-related gene product 6. Shares domains with BMP's, Tolloid, Sushi repeat proteins
5081	14241		1.06	0.0E+00	4758225	NT	Homo sapiens E2F transcription factor 2 (E2F2) mRNA
5073	14253	23336	1.24	0.0E+00	AF016705.1	NT	Homo sapiens E6-AP ubiquitin-protein ligase (UBE3A) gene, exon 3
5078	14256	23339	0.85	0.0E+00	U53588.1	NT	Homo sapiens MHC class 1 region
5087	14287		1.48	0.0E+00	AL183209.2	NT	Homo sapiens chromosome 21 segment HS21C009
5089	14289		33.47	0.0E+00	D50857.1	NT	Homo sapiens gamma-globin gene (HBB) pseudogene
5097	14277	23361	1.02	0.0E+00	AF207880.1	NT	Mus musculus testis 2 (Tsh2) gene, partial cds
5115	14265	23363	2.87	0.0E+00	X52888.1	NT	Bacillus amyloliquefaciens sacB gene for levansucrase (EC 2.4.1.10)
5116	14286	23364	0.86	0.0E+00	X72781.1	NT	Human endogenous retrovirus mRNA for gag protein
5128	14307	23398	0.89	0.0E+00	AF272663.1	NT	Homo sapiens gephyrin mRNA, complete cds
5133	14311	23402	0.99	0.0E+00	AF240835.1	NT	Homo sapiens vascular endothelial cadherin 2 mRNA, complete cds
5133	14311	23403	0.99	0.0E+00	AF240835.1	NT	Homo sapiens vascular endothelial cadherin 2 mRNA, complete cds
5134	14312	23404	1.22	0.0E+00	5454153	NT	Homo sapiens cyclophilin (USA-CYP) mRNA
5138	14316	23407	0.95	0.0E+00	AA683288.1	EST_HUMAN	ae82b04.s1 Stratogene schizo brain S11 Homo sapiens cDNA clone IMAGE:1020367 3'
5148	14326	23418	2.49	0.0E+00	11421001	NT	Homo sapiens HEF like Protein (HEFL), mRNA
5158	14335	23425	1.75	0.0E+00	Y12477.1	NT	Homo sapiens putative GPR37 gene, exon 2
5158	14335	23426	1.75	0.0E+00	Y12477.1	NT	Homo sapiens putative GPR37 gene, exon 2
5159	14338	23427	1.23	0.0E+00	Y08032.1	NT	Human endogenous retrovirus-K, LTR U5 and gag gene
5172	14351	23439	0.95	0.0E+00	5802091	NT	Homo sapiens solute carrier family 6 (inositol transporters), member 3 (SLC6A3), mRNA
5174	14352	23440	1.5	0.0E+00	AF124250.1	NT	Homo sapiens SH2-containing protein Nup2 mRNA, complete cds
5187	14363	23450	0.63	0.0E+00	7706245	NT	Homo sapiens 4F2 light chain (LOC51587), mRNA
5187	14363	23451	0.63	0.0E+00	7706245	NT	Homo sapiens 4F2 light chain (LOC51587), mRNA
5188	14364	23452	1.06	0.0E+00	7692421	NT	Homo sapiens KIAA0971 protein (KIAA0971), mRNA
5189	14365	23453	0.98	0.0E+00	4828795	NT	Homo sapiens potassium voltage-gated channel, Isk-related family, member 2 (KCNE2) mRNA
5188	14374	23461	2.03	0.0E+00	U26555.1	NT	Human versican V2 core protein precursor splice-variant mRNA, complete cds
5202	14377	23464	0.94	0.0E+00	U71601.1	NT	Human zinc finger protein zfp47 (zfp47) mRNA, partial cds
5210	14385	23470	1.18	0.0E+00	4757889	NT	Homo sapiens chromosome 8 open reading frame 1 (C8ORF1) mRNA
5211	14386	23471	1.16	0.0E+00	AF195658.1	NT	Homo sapiens DNA mismatch repair protein (MLH3) gene, complete cds
5216	14473	23476	1.05	0.0E+00	AF167338.1	NT	Homo sapiens interleukin 1 receptor accessory protein (IL1RAP) gene, exon 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5219	14393	23478	0.76	0.0E+00	AF231922.1	NT	Homo sapiens chromosome 21 unknown mRNA
5220	14394	23479	1.22	0.0E+00	4826777	NT	Homo sapiens jumonji (mouse) homolog (JMU) mRNA
5230	14404	23487	1.66	0.0E+00	7657203	NT	Homo sapiens acidic 82 kDa protein mRNA (HSU15552), mRNA
5238	14412		1.31	0.0E+00	AB040948.1	NT	Homo sapiens mRNA for KIAA1513 protein, partial cds
5276	14448	23521	1.28	0.0E+00	7662109	NT	Homo sapiens KIAA0426 gene product (KIAA0426), mRNA
5280	14451		1.98	0.0E+00	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
5282	14453	23523	1.82	0.0E+00	4503764	NT	Homo sapiens flavin containing monooxygenase 1 (FMO1) mRNA
5287	14458	23526	23.87	0.0E+00	7662177	NT	Homo sapiens KIAA0555 gene product (KIAA0555), mRNA
5287	14458	23527	23.87	0.0E+00	7662177	NT	Homo sapiens KIAA0555 gene product (KIAA0555), mRNA
5298	14485		3.15	0.0E+00	AF063093.1	NT	Homo sapiens aconitase (ACO2) gene, nuclear gene encoding mitochondrial protein, exon 15
5302	14534	23537	2.19	0.0E+00	AF137288.1	NT	Homo sapiens keratin 12 (KRT12) gene, complete cds
5302	14534	23538	2.19	0.0E+00	AF137288.1	NT	Homo sapiens keratin 12 (KRT12) gene, complete cds
5313	14545	23614	1.76	0.0E+00	9256579	NT	Homo sapiens protocadherin alpha 13 (PCDHA13), mRNA
5321	14553	23623	3.91	0.0E+00	BE931080.1	EST_HUMAN	RC3-GN0076-310800-013-b03 GN0078 Homo sapiens cDNA
5325	14557	23627	3.45	0.0E+00	AF182034.1	NT	Homo sapiens polycystic kidney disease-like 2 protein (PKDL2) mRNA, complete cds
5325	14557	23628	3.45	0.0E+00	AF182034.1	NT	Homo sapiens polycystic kidney disease-like 2 protein (PKDL2) mRNA, complete cds
5331	14562	23635	1.86	0.0E+00	X56163.1	NT	H. sapiens immunoglobulin heavy chain gene, variable region
5331	14562	23638	1.86	0.0E+00	X56163.1	NT	H. sapiens immunoglobulin heavy chain gene, variable region
5388	14617	23730	6.44	0.0E+00	BE975498.1	EST_HUMAN	7110-06.x1 NCL_CGAP_CELL1 Homo sapiens cDNA clone IMAGE:3284250 3'
5389	14618	23731	1.72	0.0E+00	BE220753.1	EST_HUMAN	h189a02.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3165194 3' similar to SW:Y054_HUMAN
5390	14619	23732	1.68	0.0E+00	BE784412.1	EST_HUMAN	P42694 HYPOTHETICAL PROTEIN KIAA0054 ;
5390	14619	23733	1.68	0.0E+00	BE784412.1	EST_HUMAN	601589422F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943804 5'
5392	14621	23735	5.3	0.0E+00	M26908.1	NT	601589422F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943804 5'
5394	14623	23736	3.48	0.0E+00	A1791363.1	EST_HUMAN	Homo sapiens eosinophil peroxidase (EPP) gene, exon 7
5396	18053	23740	4.35	0.0E+00	11421038	NT	chr8:8a09.y6 NCL_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1472152 5' similar to gb:M18512 IG
5402	14630		2.86	0.0E+00	BF665962.1	EST_HUMAN	HEAVY CHAIN PRECURSOR V-J REGION (HUMAN);
5410	14638	23766	2.1	0.0E+00	BF526328.1	EST_HUMAN	Homo sapiens SP4 transcription factor (SP4), mRNA
5410	14638	23767	2.1	0.0E+00	BF526328.1	EST_HUMAN	602118928F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4278254 5'
5421	18224	24643	2.57	0.0E+00	4557384	NT	602071372F1 NCL_CGAP_Bm84 Homo sapiens cDNA clone IMAGE:4214272 5'
5425	14652	23786	4.72	0.0E+00	AF257737.1	NT	602071372F1 NCL_CGAP_Bm84 Homo sapiens cDNA clone IMAGE:4214272 5'
5426	14652	23789	4.72	0.0E+00	AF257737.1	NT	Homo sapiens Bloom syndrome (BLM) mRNA
5436	14663	23816	1.92	0.0E+00	11420819	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
							Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
							Homo sapiens olfactory receptor, family 2, subfamily F, member 1 (OR2F1), mRNA

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5447	14873	23832	3.27	0.0E+00	BF528831.1	EST_HUMAN	602042322F1 NCJ_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4178888 5'
5447	14873	23833	3.27	0.0E+00	BF528831.1	EST_HUMAN	602042322F1 NCJ_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4178888 5'
5450	14878	23835	2.69	0.0E+00	BF313139.1	EST_HUMAN	601887858F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126815 5'
5457	14883	24033	4.38	0.0E+00	11434392	NT	Homo sapiens calcium channel, voltage-dependent, alpha 1G subunit (CACNA1G), mRNA
5476	14703		3.14	0.0E+00	AW867316.1	EST_HUMAN	MRO-SND0037-030400-001-h07 SN0037 Homo sapiens cDNA
5485	14711	24067	1.95	0.0E+00	BE282889.1	EST_HUMAN	601105291F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2887803 5'
5485	14711	24068	1.95	0.0E+00	BE282889.1	EST_HUMAN	601105291F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2887803 5'
5485	14721	24078	1.84	0.0E+00	11420819	NT	Homo sapiens olfactory receptor, family 2, subfamily F, member 1 (OR2F1), mRNA
5485	14721	24078	1.84	0.0E+00	11420819	NT	Homo sapiens olfactory receptor, family 2, subfamily F, member 1 (OR2F1), mRNA
5485	14725	24084	4.29	0.0E+00	AF084254.1	NT	Homo sapiens very long-chain acyl-CoA synthetase homolog 1 mRNA, complete cds
5489	14725	24085	4.29	0.0E+00	AF084254.1	NT	Homo sapiens very long-chain acyl-CoA synthetase homolog 1 mRNA, complete cds
5502	14728	24089	3.04	0.0E+00	AJ224839.1	NT	Homo sapiens Surf-5 and Surf-6 genes
5502	14728	24090	3.04	0.0E+00	AJ224839.1	NT	Homo sapiens Surf-5 and Surf-6 genes
5513	14738	24103	7.42	0.0E+00	M85719.1	EST_HUMAN	EST02238 Fetal brain, Striatum (cat#836208) Homo sapiens cDNA clone HFBCM48
5518	14743	24110	5.68	0.0E+00	AW405472.1	EST_HUMAN	U1-HF-BL0-adj-4-02-0-U1.F1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3081858 5'
5530	14754	24121	2.09	0.0E+00	AW361877.1	EST_HUMAN	PM3-CT0263-091289-007-h05 CT0263 Homo sapiens cDNA
5530	14754	24122	2.09	0.0E+00	AW361877.1	EST_HUMAN	PM3-CT0263-091289-007-h05 CT0263 Homo sapiens cDNA
5530	14754	24123	2.09	0.0E+00	AW361877.1	EST_HUMAN	PM3-CT0263-091289-007-h05 CT0263 Homo sapiens cDNA
5531	14755	24124	2.03	0.0E+00	U38281.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 13
5565	14790	24161	1.72	0.0E+00	AJ006345.1	NT	Homo sapiens KVLQT1 gene
5565	14790	24162	1.72	0.0E+00	AJ006345.1	NT	Homo sapiens KVLQT1 gene
5575	14798	24172	5.12	0.0E+00	11416801	NT	Homo sapiens protocadherin beta 2 (PCDH2), mRNA
5580	14804	24177	7.34	0.0E+00	BE560082.1	EST_HUMAN	601345141F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677843 5'
5581	14805	24178	3.28	0.0E+00	U86861.1	NT	Human L-type calcium channel beta-1 subunit (CACNLB1) gene, exon 13B and isoform beta-1B, complete cds
5581	14805	24179	3.28	0.0E+00	U86861.1	NT	Human L-type calcium channel beta-1 subunit (CACNLB1) gene, exon 13B and isoform beta-1B, complete cds
5588	14812	24188	1.89	0.0E+00	BF338835.1	EST_HUMAN	602036272F1 NCJ_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4184321 5'
5590	14814	24188	3.15	0.0E+00	BE273983.1	EST_HUMAN	601104462F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3347463 5'
5596	14820	24197	2.21	0.0E+00	BF569905.1	EST_HUMAN	602185852F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310078 5'
5615	14838	24216	2.14	0.0E+00	AF217289.1	NT	Homo sapiens cadherin 20 (CDH20) mRNA, complete cds
5616	14839	24217	2.44	0.0E+00	BE828144.1	EST_HUMAN	RC5-ET0027-210800-022-G10 ET0027 Homo sapiens cDNA
5619	14842	24220	2.87	0.0E+00	BE958636.1	EST_HUMAN	601645287F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3830453 5'
5640	14884		2.25	0.0E+00	AF012618.1	NT	Homo sapiens familial mental retardation protein 2 (FMR2) gene, exon 14

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5842	14866	24249	3.34	0.0E+00	BE280197.1	EST_HUMAN	601159515F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:350323 5'
5845	14868	24253	2.68	0.0E+00	BE889610.1	EST_HUMAN	601512630F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3914238 5'
5863	18061	24275	10.36	0.0E+00	9789898	NT	Homo sapiens potassium voltage-gated channel, Shal-related subfamily, member 2 (KCND2), mRNA
5878	14899	24292	9.4	0.0E+00	U34825.1	NT	Human T cell surface glycoprotein CD-6 mRNA, complete cds
5879	14899	24293	9.4	0.0E+00	U34825.1	NT	Human T cell surface glycoprotein CD-6 mRNA, complete cds
5725	14943	24339	1.68	0.0E+00	BE378007.1	EST_HUMAN	601236276F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608490 5'
5738	14955	24364	3.41	0.0E+00	U45982.1	NT	Human G protein-coupled receptor GPR-9-6 gene, complete cds
5748	14967	24368	4.14	0.0E+00	AA204740.1	EST_HUMAN	zfp81403.1 Stratagene INT neuron (#037233) Homo sapiens cDNA clone IMAGE:848005 5' similar to TR:G854195 Q854195 LEUKOCYTE SURFACE PROTEIN. ;
5749	14968	24367	3.88	0.0E+00	11545913	NT	Homo sapiens xylosyltransferase II (XT2), mRNA
5749	14968	24368	3.88	0.0E+00	11545913	NT	Homo sapiens xylosyltransferase II (XT2), mRNA
5763	14982	24381	4.68	0.0E+00	BE257173.1	EST_HUMAN	601109532F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3350822 5'
5779	14997	24389	1.73	0.0E+00	11435630	NT	Homo sapiens peptide transporter 3 (LOC51286), mRNA
5808	15023		8.8	0.0E+00	AV650020.1	EST_HUMAN	AV650020 GLC Homo sapiens cDNA clone GLOCAD09 3'
5810	15027	24428	3.35	0.0E+00	AW575598.1	EST_HUMAN	U1HF-BLD-acc-g-12-Q-U1.s1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3058751 3'
5812	15029	24430	3.9	0.0E+00	H01255.1	EST_HUMAN	y27b03.1 Soares placenta Nid2HP Homo sapiens cDNA clone IMAGE:149933 5'
5817	15034	24435	1.7	0.0E+00	X15377.1	NT	Human gene for the light and heavy chains of myeloperoxidase
5821	15038	24438	4.44	0.0E+00	BE735989.1	EST_HUMAN	601305368F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3639616 5'
5821	15038	24440	4.44	0.0E+00	BE735989.1	EST_HUMAN	601305368F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3639616 5'
5823	15040	24442	23.08	0.0E+00	AU119245.1	EST_HUMAN	AU119245 HEMBA1 Homo sapiens cDNA clone HEMBA1005360 5'
5823	15040	24443	23.08	0.0E+00	AU119245.1	EST_HUMAN	AU119245 HEMBA1 Homo sapiens cDNA clone HEMBA1005360 5'
5831	15048	24452	4.25	0.0E+00	BE283153.1	EST_HUMAN	601105344F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2887963 5'
5831	15048	24463	4.25	0.0E+00	BE283153.1	EST_HUMAN	601105344F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2887963 5'
5867	15104	24515	2.57	0.0E+00	AF190860.1	NT	Homo sapiens low voltage-activated T-type calcium channel alpha 1G splice variant CavT.1a (CACNA1G) mRNA, complete cds
5883	15110	24521	3.97	0.0E+00	AW163640.1	EST_HUMAN	au86h08.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2784159 5' similar to TR:O15390 O15390 GT24. [3] TR:O43840 TR:O43208 ;
5893	15110	24522	3.97	0.0E+00	AW163640.1	EST_HUMAN	au86h08.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2784159 5' similar to TR:O15390 O15390 GT24. [3] TR:O43840 TR:O43208 ;
5906	15123	24532	5.08	0.0E+00	BE798973.1	EST_HUMAN	601587561F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3941847 5'
5908	15125	24533	7.6	0.0E+00	BE889813.1	EST_HUMAN	601512058F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913311 5'
5908	15125	24534	7.6	0.0E+00	BE889813.1	EST_HUMAN	601512058F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913311 5'
5914	15131	24540	4.93	0.0E+00	L24463.1	NT	Human antigen CD27 gene, exons 1-2

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Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5918	15135	24544	2.28	0.0E+00	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
5918	15136	24545	2.28	0.0E+00	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
5924	15141	24552	3.32	0.0E+00	6005983	NT	Homo sapiens zona pellucida glycoprotein 3A (sperm receptor) (ZP3A), mRNA
5927	15143	24554	4.12	0.0E+00	AI638412.1	EST_HUMAN	U31111.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2242413 3' similar to SW:WNT3_MOUSE
5928	15144	24555	1.71	0.0E+00	L32832.1	NT	P17553 WNT-3 PROTO-ONCOGENE PROTEIN PRECURSOR.
5933	15149	24558	4	0.0E+00	AA434584.1	EST_HUMAN	Homo sapiens zinc finger homeodomain protein (ATBF1-A) mRNA, complete cds
5978	15182	24609	7.22	0.0E+00	BE168131.1	EST_HUMAN	PM3-HT0520-230200-002-c08 HT0520 Homo sapiens cDNA
5990	15272	24701	3.28	0.0E+00	AA190755.1	EST_HUMAN	zp88a03.r1 Stratiogene HeLa cell s3 637218 Homo sapiens cDNA clone IMAGE:927282 5'
5997	15278	24710	5.7	0.0E+00	AI940621.1	EST_HUMAN	IL3-ST0024-230769-001-B01 ST0024 Homo sapiens cDNA
5997	15279	24711	5.7	0.0E+00	AI940621.1	EST_HUMAN	IL3-ST0024-230769-001-B01 ST0024 Homo sapiens cDNA
6002	15284	24717	1.76	0.0E+00	11435826	NT	Homo sapiens CD8 antigen (CD8), mRNA
6022	14512	23570	13.42	0.0E+00	BE807889.1	EST_HUMAN	601443687F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847687 5'
6022	14512	23571	13.42	0.0E+00	BE807889.1	EST_HUMAN	601443687F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847687 5'
6023	15231	24650	2.29	0.0E+00	BE550182.1	EST_HUMAN	7b49R03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3231581 3' similar to SW:GG95_HUMAN
6023	15231	24651	2.29	0.0E+00	BE550182.1	EST_HUMAN	Q08379 GOLGIN-95.
6036	15244	24686	1.69	0.0E+00	BF088376.1	EST_HUMAN	Q08379 GOLGIN-95.
6039	15247	24689	1.94	0.0E+00	AA195108.1	EST_HUMAN	CM1-HT0877-080900-397-g11 HT0877 Homo sapiens cDNA
6049	15211		11.49	0.0E+00	11034810	NT	zr34g03.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:865332 5'
6051	15219	24639	2.71	0.0E+00	BF569905.1	EST_HUMAN	Homo sapiens catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein) (CTNND2), mRNA
6058	15227		2.04	0.0E+00	J03089.1	NT	(CTNND2), mRNA
6061	15251	24673	3.02	0.0E+00	AF217289.1	NT	802185852F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310078 5'
6061	15251	24674	3.02	0.0E+00	AF217289.1	NT	Human MYCL2 gene, complete cds
6066	14513	23572	2.97	0.0E+00	BE262941.1	EST_HUMAN	Homo sapiens cadherin 20 (CDH20) mRNA, complete cds
6080	14528	23548	6.31	0.0E+00	Z37876.1	NT	Homo sapiens cadherin 20 (CDH20) mRNA, complete cds
6081	14527	23549	2.22	0.0E+00	Z37876.1	NT	Homo sapiens melanoma antigen, family B, 2 (MAGEB2), mRNA
6081	14527	23550	2.22	0.0E+00	Z37876.1	NT	801148934F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3501828 5'
6082	14528	23551	2.98	0.0E+00	AF257737.1	EST_HUMAN	H. sapiens mRNA for latent transforming growth factor-beta binding protein (LTBP-2)
6082	14528	23552	2.98	0.0E+00	AF257737.1	NT	H. sapiens mRNA for latent transforming growth factor-beta binding protein (LTBP-2)
6088	15288	24720	2.39	0.0E+00	BF569905.1	EST_HUMAN	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
6090	15291	24724	3.87	0.0E+00	L01978.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6098	15298	24730	5.25	0.0E+00	BF308998.1	EST_HUMAN	601889823F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4123948 5'
6101	15301	24733	2.33	0.0E+00	U41302.1	NT	Human chromosome 16 creatine transporter (SLC6A8) and (CDM) paralogous genes, complete cds
6137	15321	24758	2.28	0.0E+00	AU133213.1	EST_HUMAN	AU133213 NT2RP4 Homo sapiens cDNA clone NT2RP4001558 5'
6150	15334	23537	2.53	0.0E+00	AU143708.1	EST_HUMAN	AU143708 Y79AA1 Homo sapiens cDNA clone Y79AA1002385 5'
6165	14534	23538	2.38	0.0E+00	AF137286.1	NT	Homo sapiens keratin 12 (KRT12) gene, complete cds
6165	14534	23538	2.38	0.0E+00	AF137286.1	NT	Homo sapiens keratin 12 (KRT12) gene, complete cds
6174	15358	24794	4.35	0.0E+00	11436889	NT	Homo sapiens vitamin D (1,25-dihydroxyvitamin D3) receptor (VDR), mRNA
6174	15358	24795	4.35	0.0E+00	11436889	NT	Homo sapiens vitamin D (1,25-dihydroxyvitamin D3) receptor (VDR), mRNA
6188	15370	24810	34.37	0.0E+00	AI128344.1	EST_HUMAN	qc67a07.x1 Soares_placenta_8to9weeks_2NbhP8b9W Homo sapiens cDNA clone IMAGE:1714844 3' similar to SW:ARSD_HUMAN P61889 ARYL SULFATASE D PRECURSOR ; contains element HGR repetitive element ;
6188	15370	24811	34.37	0.0E+00	AI128344.1	EST_HUMAN	qc67a07.x1 Soares_placenta_8to9weeks_2NbhP8b9W Homo sapiens cDNA clone IMAGE:1714844 3' similar to SW:ARSD_HUMAN P61889 ARYL SULFATASE D PRECURSOR ; contains element HGR repetitive element ;
6190	15372	24813	4.12	0.0E+00	11426392	NT	Homo sapiens myosin, heavy polypeptide 8, skeletal muscle, perinatal (MYH8), mRNA
6190	15372	24814	4.12	0.0E+00	11426392	NT	Homo sapiens myosin, heavy polypeptide 8, skeletal muscle, perinatal (MYH8), mRNA
6192	15374		14	0.0E+00	BF337376.1	EST_HUMAN	602035089F1 NCI_CGAP_Brm64 Homo sapiens cDNA clone IMAGE:4182839 5'
6194	15378	24818	2.38	0.0E+00	AA128453.1	EST_HUMAN	zn60f09.r1 Stratiogene muscle 937209 Homo sapiens cDNA clone IMAGE:562601 5' similar to TR:G808562 G808562 NEBULIN ;
6213	15394		2.23	0.0E+00	AU118807.1	EST_HUMAN	AU118807 HEMBA1 Homo sapiens cDNA clone HEMBA1003969 5'
6214	15395	24838	1.95	0.0E+00	AF005213.1	NT	Homo sapiens ankyrin 1 (ANK1) mRNA, complete cds
6214	15395	24839	1.95	0.0E+00	AF005213.1	NT	Homo sapiens ankyrin 1 (ANK1) mRNA, complete cds
6223	15404	24845	7.18	0.0E+00	X70172.1	NT	H.sapiens DNA for ZNGP2 pseudogene, exon 4
6225	15408	24847	9.65	0.0E+00	U45448.1	NT	Human P2x1 receptor mRNA, complete cds
6225	15408	24848	9.65	0.0E+00	U45448.1	NT	Human P2x1 receptor mRNA, complete cds
6231	15412	24853	2.5	0.0E+00	AW950516.1	EST_HUMAN	EST362588 IMAGE resequences, MAGA Homo sapiens cDNA
6260	15441	24880	2.71	0.0E+00	AW238326.1	EST_HUMAN	xb39a05.y1 NCI_CGAP_Lu31 Homo sapiens cDNA clone IMAGE:2578640 5' similar to TR:Q08050 Q08050 HNF3/TFH TRANSCRIPTION FACTOR GENESIS ;
6270	15450	24889	4.1	0.0E+00	11427135	NT	Homo sapiens glucagon-like peptide 2 receptor (GLP2R), mRNA
6281	15461	24903	2.21	0.0E+00	AW405827.1	EST_HUMAN	UI-HF-BL0-abs-4-07-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3057489 5'
6317	15497	24941	4.45	0.0E+00	AI752581.1	EST_HUMAN	cn17d05.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn17d05 random

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6317	15487	24842	4.45	0.0E+00	AI752561.1	EST_HUMAN	cn17d05.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NIH7BC_cn17d05 random
6374	15554	25011	2.08	0.0E+00	6912735	NT	Homo sapiens transient receptor potential channel 5 (TRPC5), mRNA
6377	15557	25013	5.62	0.0E+00	BF217905.1	EST_HUMAN	Homo sapiens cDNA clone IMAGE:4103729 5'
6381	15561	25017	3.89	0.0E+00	AU128622.1	EST_HUMAN	601885465F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:4103729 5'
6382	15572	25028	6.76	0.0E+00	4501848	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
6396	15575	25030	5.9	0.0E+00	BE739870.1	EST_HUMAN	601583158F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3947385 5'
6395	15575	25031	5.9	0.0E+00	BE739870.1	EST_HUMAN	601583158F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3947385 5'
6407	15588	25047	2.02	0.0E+00	BE787610.1	EST_HUMAN	601481713F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3884258 5'
6407	15588	25048	2.02	0.0E+00	BE787610.1	EST_HUMAN	601481713F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3884258 5'
6449	15646	25114	3.8	0.0E+00	BE787610.1	EST_HUMAN	601481713F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3884258 5'
6457	15654	25123	3.92	0.0E+00	M34872.1	NT	601305958F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3638803 5'
6457	15654	25124	3.92	0.0E+00	M34872.1	NT	Human amyloid-beta protein (APP) gene, exon 11
6468	15665	25136	2.95	0.0E+00	AA397551.1	EST_HUMAN	Human amyloid-beta protein (APP) gene, exon 11
6471	15668	25137	6.84	0.0E+00	AU142402.1	EST_HUMAN	z181b04.r1 Strategene schizo brain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR:G300482
6479	15678	25171	7.08	0.0E+00	BF673096.1	EST_HUMAN	G300482 POL-REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT) :
6510	15706	25171	3.93	0.0E+00	AW500549.1	EST_HUMAN	AU142402 Y78AA1 Homo sapiens cDNA clone Y78AA1000277 5'
6514	15710	25174	12.31	0.0E+00	AW157233.1	EST_HUMAN	602153008F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4284128 5'
6556	15752	25214	2.38	0.0E+00	11427235	NT	UI-HF-BNO-ek1-f01-Q-U1.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077488 5'
6556	15752	25215	2.38	0.0E+00	11427235	NT	UI-HF-BNO-ek1-f01-Q-U1.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077488 5'
6574	15770		5.05	0.0E+00	AA398511.1	EST_HUMAN	TR:O60463 O60463 TYPE-2 PHOSPHATIDIC ACID PHOSPHOHYDROLASE. (1):
6604	15800		3.33	0.0E+00	BE980767.1	EST_HUMAN	601431238F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916588 5'
6610	15806	25262	3.19	0.0E+00	4758895	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA
6610	15806	25263	3.19	0.0E+00	4758895	NT	Homo sapiens mitogen-activated protein kinase kinase 13 (MAP3K13), mRNA
6626	15822	25282	4.61	0.0E+00	X98922.1	NT	Homo sapiens mitogen-activated protein kinase kinase 13 (MAP3K13), mRNA
6626	15822	25283	4.61	0.0E+00	X98922.1	NT	H. sapiens mRNA for gamma-glutamyltransferase
6626	15822	25284	4.61	0.0E+00	X98922.1	NT	H. sapiens mRNA for gamma-glutamyltransferase
6650	15845		2.28	0.0E+00	AW513513.1	EST_HUMAN	H. sapiens mRNA for gamma-glutamyltransferase
6652	15847	25306	9.98	0.0E+00	D52650.1	EST_HUMAN	601431238F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916588 5'

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Table 4
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6861	15856	25315	6.79	0.0E+00	BE378495.1	EST_HUMAN	801239488F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3808708 5'
6863	15858	25317	2.22	0.0E+00	AA410545.1	EST_HUMAN	z32a04.r1 Soares ovary tumor NbtHOT Homo sapiens cDNA clone IMAGE:724082 5'
6861	15886	25345	10.28	0.0E+00	AA982527.1	EST_HUMAN	cr60g02.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1602104 3' similar to gb:M36072 60S RIBOSOMAL PROTEIN L7A (HUMAN);
6894	15889	25349	5.08	0.0E+00	10947037	NT	Homo sapiens ankyrin 1, erythrocytic (ANK1), transcript variant 1, mRNA
6894	15889	25350	5.08	0.0E+00	10947037	NT	Homo sapiens ankyrin 1, erythrocytic (ANK1), transcript variant 1, mRNA
6708	15903	25385	2.95	0.0E+00	AV718377.1	EST_HUMAN	AV718377 FHTB Homo sapiens cDNA clone FHTBAAF11 5'
6711	15906	25385	2.26	0.0E+00	AU124051.1	EST_HUMAN	AU124051 NT2RM2 Homo sapiens cDNA clone NT2RM2001575 5'
6739	15934	25393	8.1	0.0E+00	AW592233.1	EST_HUMAN	h48a09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2935098 3'
6739	15934	25394	8.1	0.0E+00	AW592233.1	EST_HUMAN	h48a09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2935098 3'
6782	15957	25412	8	0.0E+00	11422857	NT	Homo sapiens tumor protein p73 (TP73), mRNA
6787	15962	25418	7.02	0.0E+00	AB020630.1	NT	Homo sapiens mRNA for KIAA0823 protein, partial cds
6787	15962	25419	7.02	0.0E+00	AB020630.1	NT	Homo sapiens mRNA for KIAA0823 protein, partial cds
6787	15962	25419	4.5	0.0E+00	7706838	NT	Homo sapiens polycystin-L (PKDL), mRNA
6788	15964	25422	3.18	0.0E+00	BE315402.1	EST_HUMAN	901141119F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3140740 5'
6783	15978	25436	3.18	0.0E+00	BE315402.1	EST_HUMAN	901141119F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3140740 5'
6783	15978	25437	2.37	0.0E+00	X14786.1	NT	Human mRNA for GABA-A receptor, alpha 1 subunit
6790	15985	25445	2.92	0.0E+00	AI954607.1	EST_HUMAN	wq34a12.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2473160 3' similar to SW:MGB3_HUMAN Q15480 MELANOMA-ASSOCIATED ANTIGEN B3 ;
6789	15994	25462	5.73	0.0E+00	9256595	NT	Homo sapiens protocadherin alpha 8 (PCDH8), mRNA
6802	15987	25455	2.77	0.0E+00	AW958311.1	EST_HUMAN	EST370381 IMAGE resequences, IMAGE Homo sapiens cDNA
6807	16002	25462	3.11	0.0E+00	BE794923.1	EST_HUMAN	601589294F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943463 5'
6822	16016	25481	2.65	0.0E+00	BE712515.1	EST_HUMAN	QV2-HT0698-250700-282-508 HT0698 Homo sapiens cDNA
6885	16055	25522	3.59	0.0E+00	11560151	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA
6889	15595	25057	3.59	0.0E+00	11560151	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA
6889	15595	25058	3.59	0.0E+00	11560151	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA
6891	15597	25061	12.21	0.0E+00	AI290909.1	EST_HUMAN	qnt09a06.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1881288 3' similar to SW:RL28_HUMAN P29316 60S RIBOSOMAL PROTEIN L23A ;
6891	15597	25062	12.21	0.0E+00	AI290909.1	EST_HUMAN	qnt09a06.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1881288 3' similar to SW:RL28_HUMAN P29316 60S RIBOSOMAL PROTEIN L23A ;
6802	16059	25527	4.68	0.0E+00	AF153466.1	NT	Homo sapiens polycystic kidney disease 2-like protein (PKD2L) gene, exon 8
6907	16095	25527	15.37	0.0E+00	BE255829.1	EST_HUMAN	801109942F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350722 5'
6908	16096	25562	24.85	0.0E+00	AW163779.1	EST_HUMAN	au86c04.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783142 5' similar to gb:M36072 60S RIBOSOMAL PROTEIN L7A (HUMAN);
6925	16118	25584	6.68	0.0E+00	C06158.1	EST_HUMAN	C06158 Human pancreatic islet Homo sapiens cDNA clone hbc5805

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6925	16118	25585	6.68	0.0E+00	C08158.1	EST_HUMAN	C08158 Human pancreatic islet Homo sapiens cDNA clone hbc5605
6927	16120	25588	5.28	0.0E+00	BE746216.1	EST_HUMAN	601578683F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3927548 5'
6942	16086	25554	2.48	0.0E+00	BE900549.1	EST_HUMAN	601673425F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3856238 5'
6955	16133	25602	3.1	0.0E+00	AF019084.1	NT	Homo sapiens keratin 2e (KRT2E) gene, complete cds
6955	16133	25603	3.1	0.0E+00	AF019084.1	NT	Homo sapiens keratin 2e (KRT2E) gene, complete cds
7001	16179	25650	2.7	0.0E+00	S78488.1	NT	AlGF=androgen-induced growth factor AlGF [human, placenta, Genomic/mRNA, 498 nt, segment 5 of 5]
7001	16179	25651	2.7	0.0E+00	S78488.1	NT	AlGF=androgen-induced growth factor AlGF [human, placenta, Genomic/mRNA, 498 nt, segment 5 of 5]
7002	16180	25652	3.47	0.0E+00	BE56320.1	EST_HUMAN	601334603F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3888680 5'
7017	16194	25668	2.39	0.0E+00	AU132349.1	EST_HUMAN	AU132349 NT2RP3 Homo sapiens cDNA clone NT2RP3004260 5'
7017	16194	25669	2.39	0.0E+00	AU132349.1	EST_HUMAN	AU132349 NT2RP3 Homo sapiens cDNA clone NT2RP3004260 5'
7020	16197	25673	18.33	0.0E+00	BE740490.1	EST_HUMAN	601595558F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3949383 5'
7020	16197	25674	18.33	0.0E+00	BE740490.1	EST_HUMAN	601595558F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3949383 5'
7023	16200	25678	2.71	0.0E+00	7632067	NT	Homo sapiens KIAA0345 gene product (KIAA0345), mRNA
7034	16211	25687	3.28	0.0E+00	AU132349.1	EST_HUMAN	AU132349 NT2RP3 Homo sapiens cDNA clone NT2RP3004260 5'
7058	16233	25708	3.33	0.0E+00	BE280793.1	EST_HUMAN	601165227F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138786 5'
7059	16236	25709	9.74	0.0E+00	BE388700.1	EST_HUMAN	601286351F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3813045 5'
7059	16236	25710	9.74	0.0E+00	BE388700.1	EST_HUMAN	601286351F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3813045 5'
7062	16239	25712	6.83	0.0E+00	AW236289.1	EST_HUMAN	nt72601.x1 NCL CGAP_CML1 Homo sapiens cDNA clone IMAGE:2898977 3' similar to gbX02152_cds1 L-
7078	16255	25728	3.3	0.0E+00	AU143673.1	EST_HUMAN	LACTATE DEHYDROGENASE M CHAIN (HUMAN)
7078	16255	25729	3.3	0.0E+00	AU143673.1	EST_HUMAN	AU143673 Y79AA1 Homo sapiens cDNA clone Y79AA1002307 5'
7079	16256	25730	3.69	0.0E+00	AF072408.1	NT	Homo sapiens killer cell inhibitory receptor KIRCI gene, exons 2, 3, and 4
7081	16258	25732	2.51	0.0E+00	11421001	NT	Homo sapiens HEF like Protein (HEFL), mRNA
7081	16258	25733	2.51	0.0E+00	11421001	NT	Homo sapiens HEF like Protein (HEFL), mRNA
7091	16268	25745	2.83	0.0E+00	AU138637.1	EST_HUMAN	AU138637 PLACE1 Homo sapiens cDNA clone PLACE1004737 5'
7091	16268	25746	2.83	0.0E+00	AU138637.1	EST_HUMAN	AU138637 PLACE1 Homo sapiens cDNA clone PLACE1004737 5'
7103	16280	25749	2.85	0.0E+00	AA196387.1	EST_HUMAN	zp97n11.1 Stratiogene muscle 637208 Homo sapiens cDNA clone IMAGE:628197 5'
7125	16302	25783	2.32	0.0E+00	AF178308.1	NT	Homo sapiens KIF4 (KIF4) mRNA, complete cds
7139	16316	25787	12.52	0.0E+00	BE730772.1	EST_HUMAN	601570712F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3845403 5'
7139	16316	25788	12.52	0.0E+00	BE730772.1	EST_HUMAN	601570712F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3845403 5'
7187	16344	25822	4.03	0.0E+00	BF340331.1	EST_HUMAN	602037045F1 NCL CGAP_Bm84 Homo sapiens cDNA clone IMAGE:4184939 5'
7187	16344	25823	4.03	0.0E+00	BF340331.1	EST_HUMAN	602037045F1 NCL CGAP_Bm84 Homo sapiens cDNA clone IMAGE:4184939 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7198	16376	25857	2.47	0.0E+00	BF438218.1	EST_HUMAN	nb45e12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3285271 3'
7208	16383	25884	5.33	0.0E+00	AW517860.1	EST_HUMAN	xu74b01.x1 NCI_CGAP_Kid8 Homo sapiens cDNA clone IMAGE:2807401 3' similar to gb:MG8066 MOESIN (HUMAN);
7208	16385	25888	13.01	0.0E+00	BE549213.1	EST_HUMAN	601078764F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3464703 5'
7214	16391	25873	2.88	0.0E+00	BE781742.1	EST_HUMAN	601487418F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3870700 5'
7216	16393	25876	2.52	0.0E+00	BE082720.1	EST_HUMAN	RC2-BT0842-150200-012-d03 BT0842 Homo sapiens cDNA
7216	16393	25877	2.52	0.0E+00	BE082720.1	EST_HUMAN	RC2-BT0842-150200-012-d03 BT0842 Homo sapiens cDNA
7219	16398	25880	5.18	0.0E+00	BE743215.1	EST_HUMAN	601573885F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3835198 6'
7219	16398	25881	5.18	0.0E+00	BE743215.1	EST_HUMAN	601573885F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3835198 5'
7220	16451	25840	2.88	0.0E+00	AV711075.1	EST_HUMAN	AV711075 Cu Homo sapiens cDNA clone CUAAGG05 5'
7230	16451	25941	2.88	0.0E+00	AV711075.1	EST_HUMAN	AV711075 Cu Homo sapiens cDNA clone CUAAGG05 5'
7232	16453		6.94	0.0E+00	AW813783.1	EST_HUMAN	RC3-ST0197-120200-015-d03 ST0197 Homo sapiens cDNA
7239	16459	25948	7.82	0.0E+00	AW863583.1	EST_HUMAN	EST375836 IMAGE resequences, MAGH Homo sapiens cDNA
7262	16472	25983	2.36	0.0E+00	11431124 NT	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
7262	16472	25984	2.36	0.0E+00	11431124 NT	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
7254	16474	25988	2.18	0.0E+00	AW057821.1	EST_HUMAN	wy61109.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2553065 3' similar to TR:Q60568 Q60568 VDX;
7262	16481	25973	2.11	0.0E+00	BE243270.1	EST_HUMAN	TCAAP3D0917 Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project=TCAA Homo sapiens cDNA clone TCAAP0817
7263	16482	25974	5.84	0.0E+00	AI652239.1	EST_HUMAN	wb28a12.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2306974 3' similar to contains element MSR1 MSR1 repetitive element;
7263	16482	25975	5.84	0.0E+00	AI652239.1	EST_HUMAN	wb28a12.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2306974 3' similar to contains element MSR1 MSR1 repetitive element;
7273	16482	25983	4.32	0.0E+00	11545911 NT	NT	Homo sapiens NOD2 protein (NOD2), mRNA
7273	16482	25984	4.32	0.0E+00	11545911 NT	NT	Homo sapiens NOD2 protein (NOD2), mRNA
7287	16508	25987	2.37	0.0E+00	AW404795.1	EST_HUMAN	UI-HF-BLO-ecm-d-04-0-UJ.1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3058383 5'
7280	16509	26000	5.86	0.0E+00	11424829 NT	NT	Homo sapiens hypothetical protein FLJ20079 (FLJ20079), mRNA
7281	16510	26001	10.37	0.0E+00	4504536 NT	NT	Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1E (HTR1E), mRNA
7281	16510	26002	10.37	0.0E+00	4504536 NT	NT	Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1E (HTR1E), mRNA
7282	16511	26003	2.78	0.0E+00	AI691927.1	EST_HUMAN	wu32b08.x1 Soares_Dieckgraebe_colon_NHCD Homo sapiens cDNA clone IMAGE:2521715 3'
7285	16514	26007	2.95	0.0E+00	BE882109.1	EST_HUMAN	601505204F2 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3806885 5'
7289	16518	26008	14.1	0.0E+00	BE891630.1	EST_HUMAN	601434522F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3919838 5'
7301	16520	26010	1.93	0.0E+00	8923939 NT	NT	Homo sapiens myosin, heavy polypeptide 2, skeletal muscle, adult (MYH2), mRNA
7301	16520	26011	1.93	0.0E+00	8923939 NT	NT	Homo sapiens myosin, heavy polypeptide 2, skeletal muscle, adult (MYH2), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7315	16533	26022	12.28	0.0E+00	BE903304.1	EST_HUMAN	601674332F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3957343 5'
7316	14789	24160	2.45	0.0E+00	AA195805.1	EST_HUMAN	z95b11.1 Striatum muscle 837209 Homo sapiens cDNA clone IMAGE:627933 5' similar to gb:X03740
7337	16553	26042	6.57	0.0E+00	BE783488.1	EST_HUMAN	MYOSIN HEAVY CHAIN, SKELETAL MUSCLE (HUMAN);
7345	16561	26049	25.26	0.0E+00	AV727362.1	EST_HUMAN	601588828F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943015 5'
7345	16561	26050	25.26	0.0E+00	AV727362.1	EST_HUMAN	AV727362 HTC Homo sapiens cDNA clone HTCAQH06 5'
7356	16572	26084	18.75	0.0E+00	AW516055.1	EST_HUMAN	AV727362 HTC Homo sapiens cDNA clone HTCAQH06 5'
7362	16578	26089	1.96	0.0E+00	AU135741.1	EST_HUMAN	xy04g10.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2852226 3' similar to gb:M60864 40S
7367	16583	26072	3.09	0.0E+00	AW563333.1	EST_HUMAN	RIBOSOMAL PROTEIN S16 (HUMAN);
7367	16583	26073	3.09	0.0E+00	AW563333.1	EST_HUMAN	AU135741 PLACE1 Homo sapiens cDNA clone PLACE1002784 5'
7367	16583	26074	3.09	0.0E+00	AW563333.1	EST_HUMAN	hg13d02.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2945475 3' similar to contains
7368	16585	26075	1.79	0.0E+00	Z34887.1	NT	element MSR1 repetitive element;
7370	16585	26076	3.22	0.0E+00	F13069.1	EST_HUMAN	hg13d02.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2845475 3' similar to contains
7371	16583	26081	1.98	0.0E+00	D10083.1	NT	element MSR1 repetitive element;
7371	16583	26081	1.98	0.0E+00	D10083.1	NT	element MSR1 repetitive element;
7393	16607	26097	2.67	0.0E+00	AW338094.1	EST_HUMAN	hg13d02.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2945475 3' similar to contains
7394	16608	26098	5.93	0.0E+00	AW451230.1	EST_HUMAN	Hi.sapiens mRNA for H1 histamine receptor
7394	16608	26098	5.93	0.0E+00	AW451230.1	EST_HUMAN	HSC31C031 normalized infant brain cDNA Homo sapiens cDNA clone c-31c03
7398	9496		16.35	0.0E+00	4506632	NT	Homo sapiens RGH1 gene, retrovirus-like element
7398	16611	26101	2.2	0.0E+00	AB014567.1	NT	hw6801.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2832885 3' similar to gb:X17115 IG MU
7411	16623	26117	2.76	0.0E+00	BE288449.1	EST_HUMAN	CHAIN C REGION (HUMAN);
7427	16637	26130	1.88	0.0E+00	AB011117.1	NT	UIH-B13-eth-a-01-O-UJ.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2736849 3'
7443	16651	26143	2.9	0.0E+00	BE792155.1	EST_HUMAN	UIH-B13-eth-a-01-O-UJ.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2736849 3'
7444	16652		62.67	0.0E+00	BF684061.1	EST_HUMAN	Homo sapiens ribosomal protein L31 (RPL31) mRNA
7447	16655	26146	5.83	0.0E+00	AU118366.1	EST_HUMAN	Homo sapiens mRNA for KIAA0987 protein, partial cds
7448	16656		11.90	0.0E+00	AW236269.1	EST_HUMAN	801119248F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028219 5'
7453	16661	26150	8.59	0.0E+00	A1149808.1	EST_HUMAN	Homo sapiens mRNA for KIAA0545 protein, partial cds
7453	16661	26151	8.59	0.0E+00	A1149808.1	EST_HUMAN	801582046F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3939539 5'
7454	16662	26152	4.17	0.0E+00	AW391937.1	EST_HUMAN	802141405F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4302432 5'
							AU118366 HEMBA1 Homo sapiens cDNA clone HEMBA1003486 5'
							sn72b01.x1 NCI_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2669977 3' similar to gb:X02152_cds1 L-
							LACTATE DEHYDROGENASE M CHAIN (HUMAN);
							qf43c03.x1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:1762772 3'
							qf43c03.x1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:1762772 3'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7407	16875	26158	21.87	0.0E+00	11424726	NT	Homo sapiens insulin receptor (INSR), mRNA
7474	16882	26165	1.76	0.0E+00	BF340308.1	EST_HUMAN	602037014F1 NCI_CGAP_Bim64 Homo sapiens cDNA clone IMAGE:4164979 5'
7475	16883	26166	40.56	0.0E+00	BE261209.1	EST_HUMAN	601148357F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3163310 5'
7485	16882	26175	3.77	0.0E+00	U50326.1	NT	Human protein kinase C substrate 80K-H (PRKCSH) gene, exon 15-17
7489	16898	26180	2.19	0.0E+00	BE773036.1	EST_HUMAN	RC1-F10134-170700-012-07 FT0134 Homo sapiens cDNA
7489	16898	26181	2.19	0.0E+00	BE773036.1	EST_HUMAN	RC1-F10134-170700-012-07 FT0134 Homo sapiens cDNA
7510	16716	26203	19.32	0.0E+00	AA740782.1	EST_HUMAN	6032607.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1325412 3' similar to contains element
7517	16722	26212	3.85	0.0E+00	AF252303.1	NT	MSR1 repetitive element:
7530	16735	26225	6.93	0.0E+00	C05089.1	EST_HUMAN	Homo sapiens signaling lymphocytic activation molecule (SLAM) gene, exon 2
7537	16742	26233	2.19	0.0E+00	AA746375.1	EST_HUMAN	C05089 Human heart cDNA (Ynakamura) Homo sapiens cDNA clone 3NH4817
7537	16742	26234	2.19	0.0E+00	AA746375.1	EST_HUMAN	6058901.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1309008 5'
7547	16752	26246	2.05	0.0E+00	M78448.1	EST_HUMAN	6058901.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1309008 5'
7547	16752	26247	2.05	0.0E+00	M78448.1	EST_HUMAN	6058901.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1309008 5'
7550	16755	26248	7.75	0.0E+00	AL157808.1	EST_HUMAN	EST00588 Fetal brain, Striatum (cat833206) Homo sapiens cDNA clone HFBCC28
7560	16765	26256	13.17	0.0E+00	AU116988.1	EST_HUMAN	EST00588 Fetal brain, Striatum (cat833206) Homo sapiens cDNA clone HFBCC28
7572	16777	26270	2.02	0.0E+00	AV693656.1	EST_HUMAN	EST00588 Fetal brain, Striatum (cat833206) Homo sapiens cDNA clone HFBCC28
7580	16785	26278	2.07	0.0E+00	BF368563.1	EST_HUMAN	EST00588 Fetal brain, Striatum (cat833206) Homo sapiens cDNA clone HFBCC28
7603	16806	26302	3.42	0.0E+00	BE182380.1	EST_HUMAN	EST00588 Fetal brain, Striatum (cat833206) Homo sapiens cDNA clone HFBCC28
7603	16806	26303	3.42	0.0E+00	BE182380.1	EST_HUMAN	EST00588 Fetal brain, Striatum (cat833206) Homo sapiens cDNA clone HFBCC28
7605	16808		1.71	0.0E+00	AV701162.1	EST_HUMAN	DKFZp781J2118 r1 761 (synonym: harny2) Homo sapiens cDNA clone HEMBA1000424 5'
7618	16821	26316	3.77	0.0E+00	BE896423.1	EST_HUMAN	AU116988 HEMBA1 Homo sapiens cDNA clone GKCCNC03 5'
							AV693656 GK Homo sapiens cDNA clone GKCCNC03 5'
							IL3-NT0104-200500-143-A07 NT0104 Homo sapiens cDNA
							PM0-HT0845-060500-002-E05 HT0845 Homo sapiens cDNA
							PM0-HT0845-060500-002-E05 HT0845 Homo sapiens cDNA
							PM0-HT0845-060500-002-E05 HT0845 Homo sapiens cDNA
							AV701152 ADA Homo sapiens cDNA clone ADAAAD08 5'
							601439092F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3924142 5'
							bb78c04.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3048488 5' similar to gb:Y00345_cds1
							POLYADENYLATE-BINDING PROTEIN (HUMAN); gb:X65553 M.musculus mRNA for poly(A) binding
							protein (MOUSE);
7626	16828	26325	3.72	0.0E+00	BE018283.1	EST_HUMAN	601440446F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3925403 5'
7659	16859	26360	5.05	0.0E+00	BE897853.1	EST_HUMAN	601440446F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3925403 5'
7660	16860	26361	1.88	0.0E+00	AI459545.1	EST_HUMAN	601440446F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3925403 5'
7660	16860	26362	1.88	0.0E+00	AI459545.1	EST_HUMAN	601440446F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3925403 5'
7696	16897	26406	4.25	0.0E+00	4758827	NT	601440446F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3925403 5'
7698	16898	26407	19.73	0.0E+00	BF206561.1	EST_HUMAN	601440446F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3925403 5'
7704	16903	26412	20.68	0.0E+00	AW207734.1	EST_HUMAN	601440446F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3925403 5'
7708	16907	26415	6.88	0.0E+00	AB018260.1	NT	601440446F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3925403 5'
7708	16907	26416	6.88	0.0E+00	AB018260.1	NT	601440446F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3925403 5'

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7709	16908	26417	3.24	0.0E+00	BE206848.1	EST_HUMAN	ba04407.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823373 5' similar to TR:O76022 O76022 E1B-55KDA-ASSOCIATED PROTEIN. ;
7709	16908	26418	3.24	0.0E+00	BE206848.1	EST_HUMAN	ba04407.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823373 5' similar to TR:O76022 O76022 E1B-55KDA-ASSOCIATED PROTEIN. ;
7731	15482	24904	2.19	0.0E+00	L32632.1	NT	55KDA-ASSOCIATED PROTEIN. ;
7734	16931	26438	2.97	0.0E+00	BE148076.1	EST_HUMAN	Homo sapiens zinc finger homeodomain protein (ATBF1-A) mRNA, complete cds
7734	16931	26439	2.97	0.0E+00	BE148076.1	EST_HUMAN	55KDA-ASSOCIATED PROTEIN. ;
7767	16963	26475	4.84	0.0E+00	BF507876.1	EST_HUMAN	Homo sapiens zinc finger homeodomain protein (ATBF1-A) mRNA, complete cds
7767	16963	26478	4.84	0.0E+00	BF507876.1	EST_HUMAN	55KDA-ASSOCIATED PROTEIN. ;
7775	16970	26483	2.28	0.0E+00	AU135170.1	EST_HUMAN	RC3-H10230-040500-110-h04 HT0230 Homo sapiens cDNA
7780	16975	26488	10.51	0.0E+00	BE876401.1	EST_HUMAN	RC3-H10230-040500-110-h04 HT0230 Homo sapiens cDNA
7780	16975	26489	10.51	0.0E+00	BE876401.1	EST_HUMAN	RC3-H10230-040500-110-h04 HT0230 Homo sapiens cDNA
7788	16981	26494	1.86	0.0E+00	D87682.1	EST_HUMAN	UIH-B14-ack-b-10-U1.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085028 3'
7792	16986	26510	4.77	0.0E+00	AB037737.1	NT	UIH-B14-ack-b-10-U1.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085028 3'
7805	16998	26511	3.35	0.0E+00	AB037737.1	NT	UIH-B14-ack-b-10-U1.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone PLACE1001381 5'
7809	17002	26514	4.11	0.0E+00	AB037737.1	NT	AU135170 PLACE1 Homo sapiens cDNA clone IMAGE:3889207 5'
7809	17002	26515	4.11	0.0E+00	AB037737.1	NT	AU135170 PLACE1 Homo sapiens cDNA clone IMAGE:3889207 5'
7823	17015	26530	10.15	0.0E+00	BF578267.1	EST_HUMAN	601488828F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3889207 5'
7831	17023	26538	1.78	0.0E+00	AW328173.1	EST_HUMAN	601488828F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3889207 5'
7833	17025	26541	7.53	0.0E+00	M55083.1	EST_HUMAN	601488828F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3889207 5'
7836	17028	26548	41.44	0.0E+00	BF306896.1	EST_HUMAN	601488828F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3889207 5'
7841	17033	26549	3.52	0.0E+00	BF306896.1	EST_HUMAN	601488828F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3889207 5'
7841	17033	26549	3.52	0.0E+00	BF306896.1	EST_HUMAN	601488828F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3889207 5'
7848	17039	26556	26.43	0.0E+00	BE897051.1	EST_HUMAN	601488828F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3889207 5'
7870	17060	26594	4.97	0.0E+00	8923698	NT	601488828F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3889207 5'
7880	17068	26594	3.16	0.0E+00	BF207682.1	EST_HUMAN	601488828F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3889207 5'
7882	17070	26640	3.22	0.0E+00	BE206848.1	EST_HUMAN	601488828F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3889207 5'
7894	17110	26641	4.84	0.0E+00	BE206848.1	EST_HUMAN	601488828F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3889207 5'
7894	17110	26641	4.84	0.0E+00	BE206848.1	EST_HUMAN	601488828F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3889207 5'
7896	17112	26643	5.08	0.0E+00	AW753028.1	EST_HUMAN	601488828F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3889207 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7901	17117		3.33	0.0E+00	AA558707.1	EST_HUMAN	n42c08.s1 NCI_CGAP_P44 Homo sapiens cDNA clone IMAGE:1043342 similar to gb:M95178 ALPHA-ACTININ 1, CYTOSKELETAL ISOFORM (HUMAN);
7902	14543	23812	3.78	0.0E+00	AI834854.1	EST_HUMAN	wp08g08.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2484094 3'
7903	17118	26849	10.87	0.0E+00	AW327895.1	EST_HUMAN	dr02b08.x1 NIH_MGC_3 Homo sapiens cDNA clone IMAGE:2846919 5'
7921	18080	26887	1.71	0.0E+00	AW282776.1	EST_HUMAN	UIH-BWO-aj-q-07-q-UI.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2728509 3'
7934	17074	26801	2.83	0.0E+00	BE865609.2	EST_HUMAN	601659038R1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3885916 3'
7934	17074	26802	2.83	0.0E+00	BE865609.2	EST_HUMAN	601659038R1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3885916 3'
7935	17075	26803	4.8	0.0E+00	BE185656.1	EST_HUMAN	IL6-HT0731-020500-077-05 HT0731 Homo sapiens cDNA
7949	17088	26817	6.34	0.0E+00	AL048540.1	EST_HUMAN	DKFZp434G178_r1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434G178 5'
7949	17088	26818	6.34	0.0E+00	AL048540.1	EST_HUMAN	DKFZp434G178_r1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434G178 5'
7958	17087	26827	24.68	0.0E+00	AI923116.1	EST_HUMAN	wn83g03.x1 NCI_CGAP_UI1 Homo sapiens cDNA clone IMAGE:2452488 3' similar to gb:S37491 LAMININ RECEPTOR (HUMAN);
7962	17141	26873	7.88	0.0E+00	AA760913.1	EST_HUMAN	nz11c07.s1 NCI_CGAP_GC81 Homo sapiens cDNA clone IMAGE:1287468 3' similar to TR:Q13888 Q13888 ALKB HOMOLOG PROTEIN.;
7982	17141	26874	7.88	0.0E+00	AA760913.1	EST_HUMAN	nz11c07.s1 NCI_CGAP_GC81 Homo sapiens cDNA clone IMAGE:1287468 3' similar to TR:Q13888 Q13888 ALKB HOMOLOG PROTEIN.;
7987	17148	26880	2.47	0.0E+00	BE910548.1	EST_HUMAN	601501080F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3802928 5'
7975	18410	25898	6.48	0.0E+00	BE676347.1	EST_HUMAN	7027112.x1 NCI_CGAP_QLL1 Homo sapiens cDNA clone IMAGE:3811144 5'
7978	18413	25899	1.85	0.0E+00	BE615686.1	EST_HUMAN	601278335F1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3811144 5'
7978	18413	25900	1.85	0.0E+00	BE615686.1	EST_HUMAN	601278335F1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3811144 5'
8014	17153	26887	2.83	0.0E+00	L38891.1	NT	Homo sapiens polycystic kidney disease-associated protein (PKD1) gene, complete cds
8014	17153	26888	2.83	0.0E+00	L38891.1	NT	Homo sapiens polycystic kidney disease-associated protein (PKD1) gene, complete cds
8027	17164	26701	4.05	0.0E+00	AU138211.1	EST_HUMAN	AU138211 PLACE1 Homo sapiens cDNA clone PLACE1008077 5'
8040	17176	26716	3.92	0.0E+00	BE622317.1	EST_HUMAN	601441098F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918270 5'
8073	17208	26741	28.14	0.0E+00	BE748889.1	EST_HUMAN	601572186T1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3839012 3'
8073	17208	26742	28.14	0.0E+00	BE748889.1	EST_HUMAN	601572186T1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3839012 3'
8084	17219	26764	3.94	0.0E+00	AU141882.1	EST_HUMAN	AU141882 THYRO1 Homo sapiens cDNA clone THYRO1001398 5'
8084	17219	26755	3.94	0.0E+00	AU141882.1	EST_HUMAN	AU141882 THYRO1 Homo sapiens cDNA clone THYRO1001398 5'
8087	17222	26758	2.47	0.0E+00	AW006022.1	EST_HUMAN	wz81h01.x1 NCI_CGAP_Brm25 Homo sapiens cDNA clone IMAGE:2588226 3' similar to WP:F63H10.2 CE11040 ZINC FINGER, C2H2 TYPE.;
8091	18081	26762	4.52	0.0E+00	BF002333.1	EST_HUMAN	7h22b10.x1 NCI_CGAP_Cot16 Homo sapiens cDNA clone IMAGE:3316688 3' similar to TR:Q13458 Q13458 TRIO.;
8108	17242	26782	3.67	0.0E+00	AW387776.1	EST_HUMAN	MR4-ST0118-261069-012-b03 ST0118 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8108	17242	26783	3.87	0.0E+00	AW387776.1	EST_HUMAN	MR4-ST0118-281099-012-b03 ST0118 Homo sapiens cDNA
8126	17262	26805	4.34	0.0E+00	11435244	NT	Homo sapiens KIAA0247 gene product (KIAA0247), mRNA
8128	17262	26808	4.34	0.0E+00	11435244	NT	Homo sapiens KIAA0247 gene product (KIAA0247), mRNA
8133	17268	26810	7.52	0.0E+00	U36253.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 5
8135	17268	26812	17.97	0.0E+00	BE379254.1	EST_HUMAN	601237691F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608623 5'
8135	17268	26813	17.97	0.0E+00	BE379254.1	EST_HUMAN	601237691F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608623 5'
8149	17281	26826	2.37	0.0E+00	BE794758.1	EST_HUMAN	601590588F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944708 5'
8150	17282	26827	86.17	0.0E+00	BE879633.1	EST_HUMAN	601491821F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3894220 5'
8160	17282	26833	9.23	0.0E+00	BE408993.1	EST_HUMAN	601289403F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3628544 5'
8161	17283	26834	1.7	0.0E+00	BE148650.1	EST_HUMAN	MR0-HT0241-150500-011-802 HT0241 Homo sapiens cDNA
8162	17284	26835	1.74	0.0E+00	11427345	NT	Homo sapiens protein kinase, AMP-activated, alpha 2 catalytic subunit (PRKAA2), mRNA
8162	17284	26836	1.74	0.0E+00	11427345	NT	Homo sapiens protein kinase, AMP-activated, alpha 2 catalytic subunit (PRKAA2), mRNA
8162	17284	26837	1.74	0.0E+00	11427345	NT	Homo sapiens protein kinase, AMP-activated, alpha 2 catalytic subunit (PRKAA2), mRNA
8163	17285	26838	2.96	0.0E+00	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
8163	17285	26839	2.96	0.0E+00	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
8170	17302	26847	2.12	0.0E+00	AU132840.1	EST_HUMAN	AU132840 NT2RP4 Homo sapiens cDNA clone NT2RP4000928 5'
8173	17305	26849	4.04	0.0E+00	BE803372.1	EST_HUMAN	601676357F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3858835 5'
8182	17314	26856	2.31	0.0E+00	BF312552.1	EST_HUMAN	601897524F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4127089 5'
8182	17314	26857	2.31	0.0E+00	BF312552.1	EST_HUMAN	601897524F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4127089 5'
8184	17316	26859	3.09	0.0E+00	X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
8184	17316	26860	3.09	0.0E+00	X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
8191	17323		1.98	0.0E+00	W88994.1	EST_HUMAN	zh73d05.s1 Soerea fetal liver spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:417705 3'
8193	17325		2.05	0.0E+00	BE806402.1	EST_HUMAN	601489553F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3900386 5'
8204	17336	26876	2.78	0.0E+00	8635487	NT	Human endogenous retrovirus, complete genome
8218	18082		15.82	0.0E+00	BF309120.1	EST_HUMAN	601890634F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131416 5'
8224	17354	26891	75.29	0.0E+00	BE287175.1	EST_HUMAN	601177407F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532868 5'
8254	15576	25032	2.25	0.0E+00	6912481	NT	Homo sapiens atrophin-1 interacting protein 1; activin receptor interacting protein 1 (KIAA0705), mRNA
8254	15576	25033	2.25	0.0E+00	6912481	NT	Homo sapiens atrophin-1 interacting protein 1; activin receptor interacting protein 1 (KIAA0705), mRNA
8265	17392	26922	2.1	0.0E+00	BE140795.1	EST_HUMAN	RCO-HT0022-090799-002-001 HT0022 Homo sapiens cDNA
8279	18366	23590	1.91	0.0E+00	BE312542.1	EST_HUMAN	601150023F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3503020 5'

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Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8292	18208		1.39	0.0E+00	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C048
8294	18215		5.07	0.0E+00	AI190983.1	EST_HUMAN	qel7b12.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1739231 3'
8304	17411		2.71	0.0E+00	AB011398.1	NT	Homo sapiens gene for AF-6, complete cds
8325	17428		5.01	0.0E+00	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C048
8332	17431		3.24	0.0E+00	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
8351	17445		4.53	0.0E+00	5802873	NT	Homo sapiens antioxidant protein 1 (AOP1), nuclear gene encoding mitochondrial protein, mRNA
8385	18174	23756	1.22	0.0E+00	AF240788.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
8397	18184		3.55	0.0E+00	AL041831.1	EST_HUMAN	DKFZp434K0819.1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434K0819 5'
8423	18334		3.6	0.0E+00	11418318	NT	Homo sapiens G-2 and S-phase expressed 1 (GTSE1), mRNA
8431	17487		4.18	0.0E+00	AL046544.1	EST_HUMAN	DKFZp434G218.1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434G218 5'
8444	18219		1.87	0.0E+00	AI903497.1	EST_HUMAN	IL-BT030-271088-001 BT030 Homo sapiens cDNA
8488	18352		1.73	0.0E+00	N54484.1	EST_HUMAN	yw40e08.s1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:245222 3' similar to SW:POL_BAEVM P10272 POL POLYPROTEIN ;
8504	17543		4.14	0.0E+00	AF106856.1	NT	Homo sapiens adenylosuccinate lyase gene, complete cds
8507	10089	18250	3.7	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
8507	10089	18251	3.7	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
8516	18221		1.76	0.0E+00	10092587	NT	Homo sapiens nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2 (NFATC2), mRNA
8547	8805		3.58	0.0E+00	AF003528.1	NT	Homo sapiens X-linked arylidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
8584	18031	23855	1.9	0.0E+00	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
8646	18155	23754	3.04	0.0E+00	AW590082.1	EST_HUMAN	hg31e08.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2947234 3' similar to contains Alu repetitive element; contains element MER22 repetitive element ;
8677	18183		1.24	0.0E+00	L20483.1	NT	Human gamma-glutamyl transpeptidase mRNA, complete cds
8707	18217		2.42	0.0E+00	AF068757.1	NT	Homo sapiens somatostatin receptor subtype 3 (SSTR3) gene, 5' flanking region and partial cds
8744	17689		5.04	0.0E+00	8835487	NT	Human endogenous retrovirus, complete genome
8785	18208		2.02	0.0E+00	AI204914.1	EST_HUMAN	an0504.x1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1684759 3'
8817	17735		1.78	0.0E+00	AI904646.1	EST_HUMAN	QV-BT085-020399-103 BT085 Homo sapiens cDNA
8828	18208		1.68	0.0E+00	BE439792.1	EST_HUMAN	HTM1-854F HTM1 Homo sapiens cDNA
8839	11162	20364	1.69	0.0E+00	8812457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
8839	11162	20365	1.69	0.0E+00	8812457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
8858	17761	23834	1.41	0.0E+00	AF036365.1	NT	Homo sapiens caveolin-3 (CAV3) mRNA, complete cds

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Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8872	10873	20058	2.95	0.0E+00	H30132.1	EST_HUMAN	yc59e08.r1 Soares breast 3NHBst Homo sapiens cDNA clone IMAGE:182248 5' similar to gb:M64089 GAMMA-GLUTAMYL TRANSPEPTIDASE 5 PRECURSOR (HUMAN);
8872	10873	20057	2.95	0.0E+00	H30132.1	EST_HUMAN	yc59e08.r1 Soares breast 3NHBst Homo sapiens cDNA clone IMAGE:182248 5' similar to gb:M64089 GAMMA-GLUTAMYL TRANSPEPTIDASE 5 PRECURSOR (HUMAN);
8888	17781		26.04	0.0E+00	D50859.1	NT	Human gamma-cytoplasmic actin (ACTG9) pseudogene
8888	17783	23916	5.39	0.0E+00	11418189	NT	Homo sapiens thyroid autoantigen 70kD (Ku antigen) (G22P1), mRNA
8888	17783	23917	5.39	0.0E+00	11418189	NT	Homo sapiens thyroid autoantigen 70kD (Ku antigen) (G22P1), mRNA
8891	17788		1.74	0.0E+00	AB028898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
8909	11262	20478	1.55	0.0E+00	4758488	NT	Homo sapiens GTP binding protein 1 (GTPBP1) mRNA
8945	17822		1.37	0.0E+00	AW664999.1	EST_HUMAN	h88e08.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2878154 3'
8953	17827	23906	1.34	0.0E+00	11430480	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
8957	17830	23908	1.31	0.0E+00	11430480	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
8960	10448	19604	1.62	0.0E+00	8922593	NT	Homo sapiens hypothetical protein FLJ10687 (FLJ10687), mRNA
8987	17858		2.87	0.0E+00	11526291	NT	Homo sapiens G protein-coupled receptor 24 (GPR24), mRNA
9021	12516	21847	3.3	0.0E+00	4885312	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
9032	14093	23186	2.05	0.0E+00	6806918	NT	Homo sapiens CST gene for cerebroside sulfotransferase, exon 1, 2, 3, 4, 5
9038	17881		1.79	0.0E+00	AB028800.1	NT	Homo sapiens cleavage and polyadenylation specific factor 1, 160kD subunit (CPSF1), mRNA
9078	17803	23902	2.37	0.0E+00	9558724	NT	Homo sapiens chromosome 21 segment HS21C048
9103	18377		6.14	0.0E+00	AL183248.2	NT	Homo sapiens chromosome 21 segment HS21C048
9110	9877	18998	2.2	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
9157	10879	19852	1.39	0.0E+00	6912457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
9190	17978	23859	1.41	0.0E+00	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
9198	17883		3.87	0.0E+00	7657020	NT	Homo sapiens DKFZp434P211 protein (DKFZP434P211), mRNA
9217	17898		1.3	0.0E+00	AB028898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
9231	18007	23849	1.35	0.0E+00	8587387	NT	Homo sapiens period (Drosophila) homolog 3 (PER3), mRNA
9257	18025	23853	2.2	0.0E+00	AW025032.1	EST_HUMAN	wu83c07.x1 NC1 CGAP_K143 Homo sapiens cDNA clone IMAGE:2527698 3' similar to TR:Q12844 Q12844 BREAKPOINT CLUSTER REGION PROTEIN; contains TAR1.3 TAR1 repetitive element;
9260	18028		1.77	0.0E+00	AV656287.1	EST_HUMAN	AV656287 GLC Homo sapiens cDNA clone GLCEPG08 3'
9278	10388	19537	3.04	0.0E+00	9968844	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA

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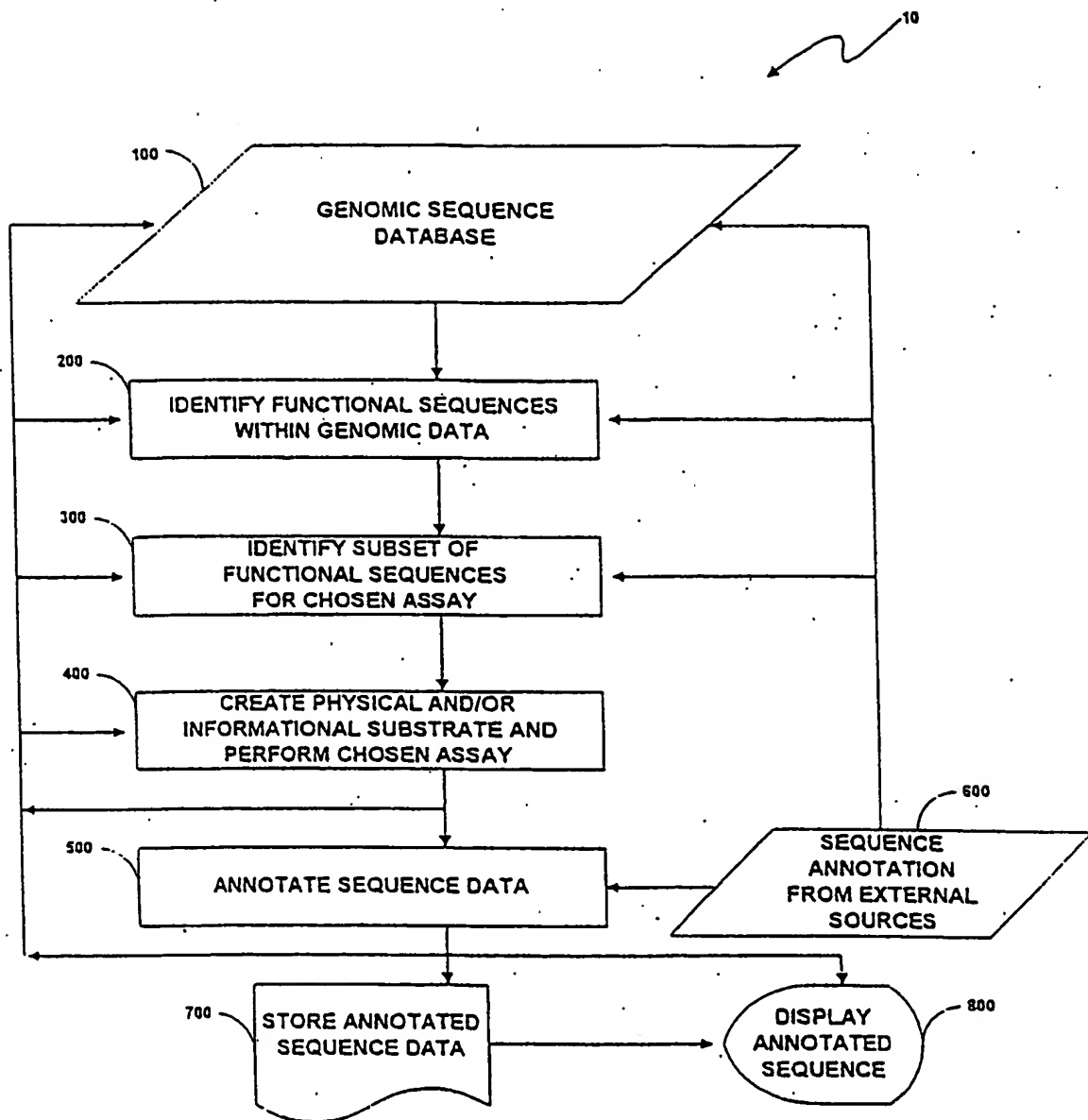


Fig. 1

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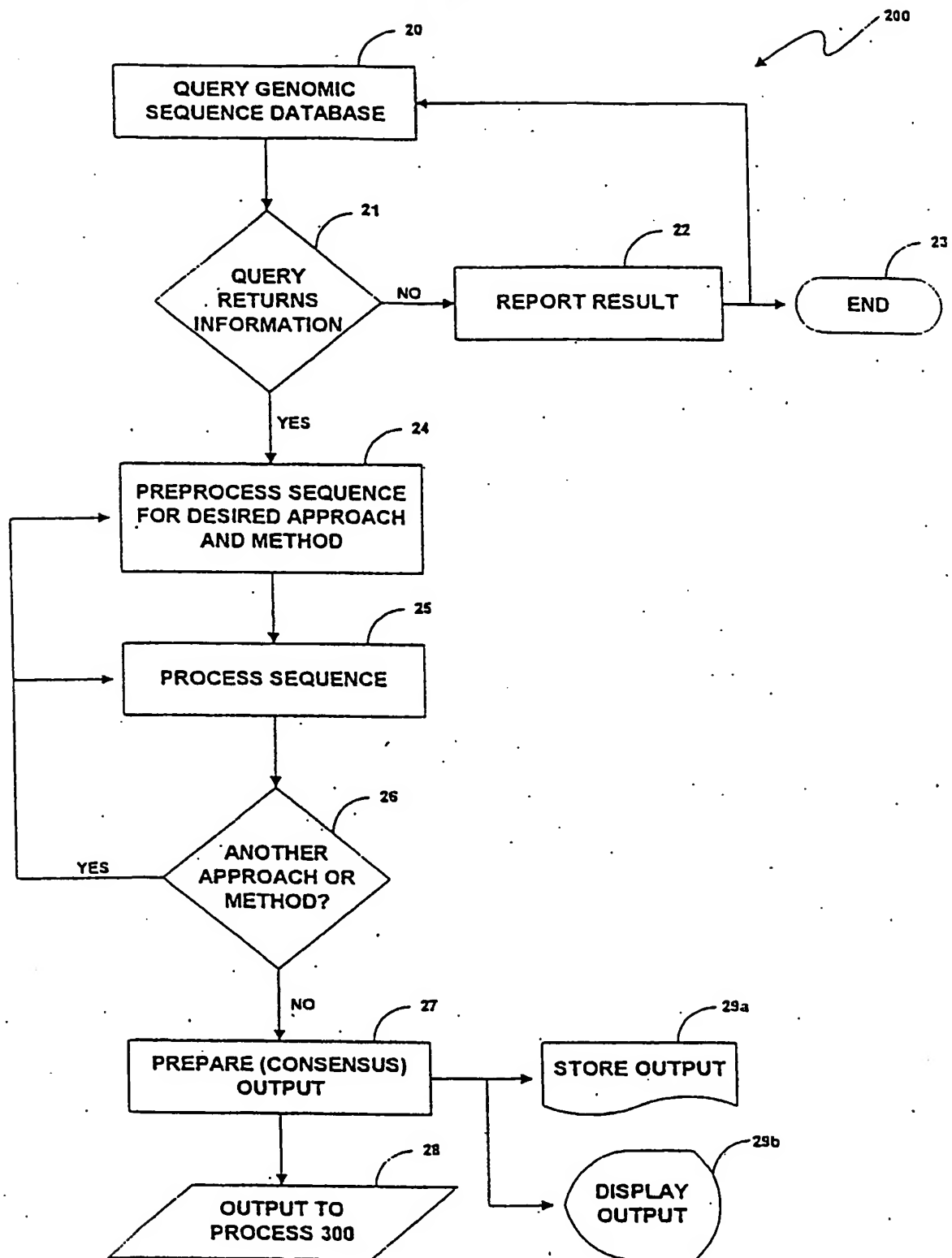


Fig. 2

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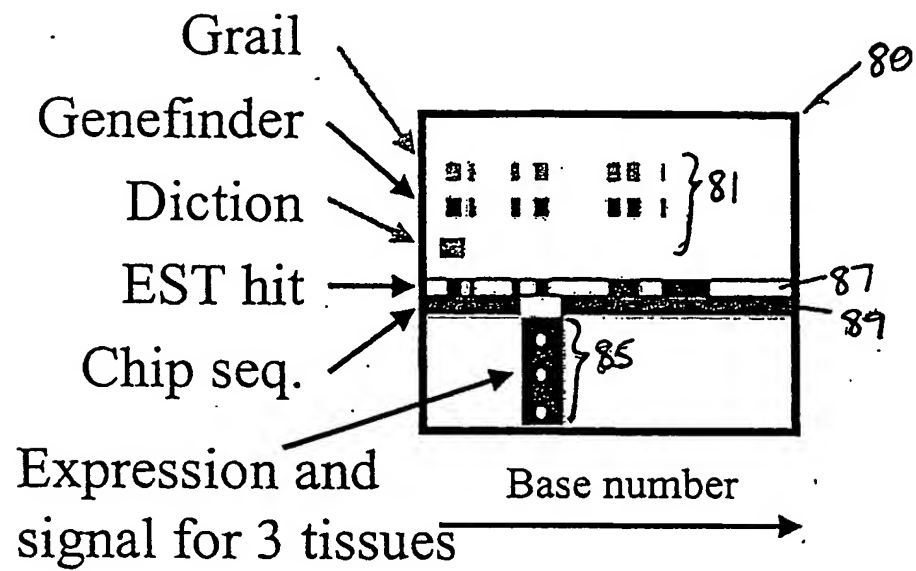


Fig. 4

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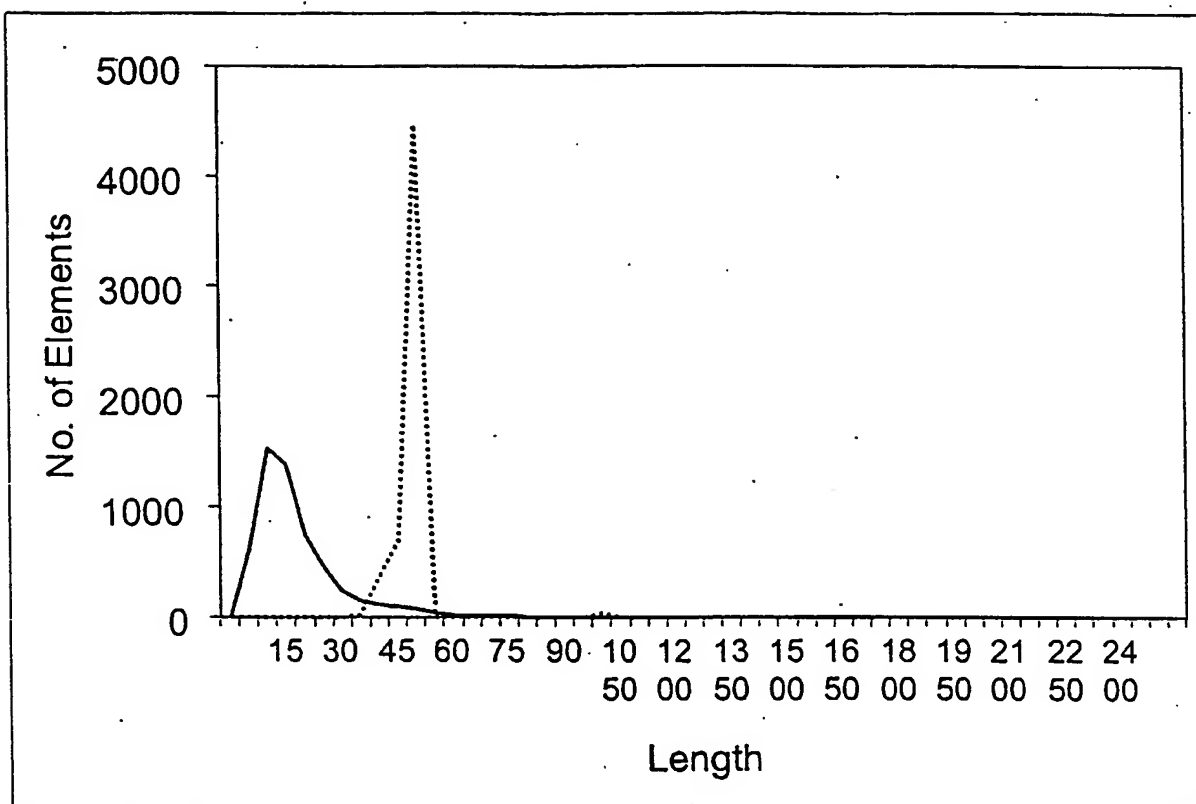


Fig. 5

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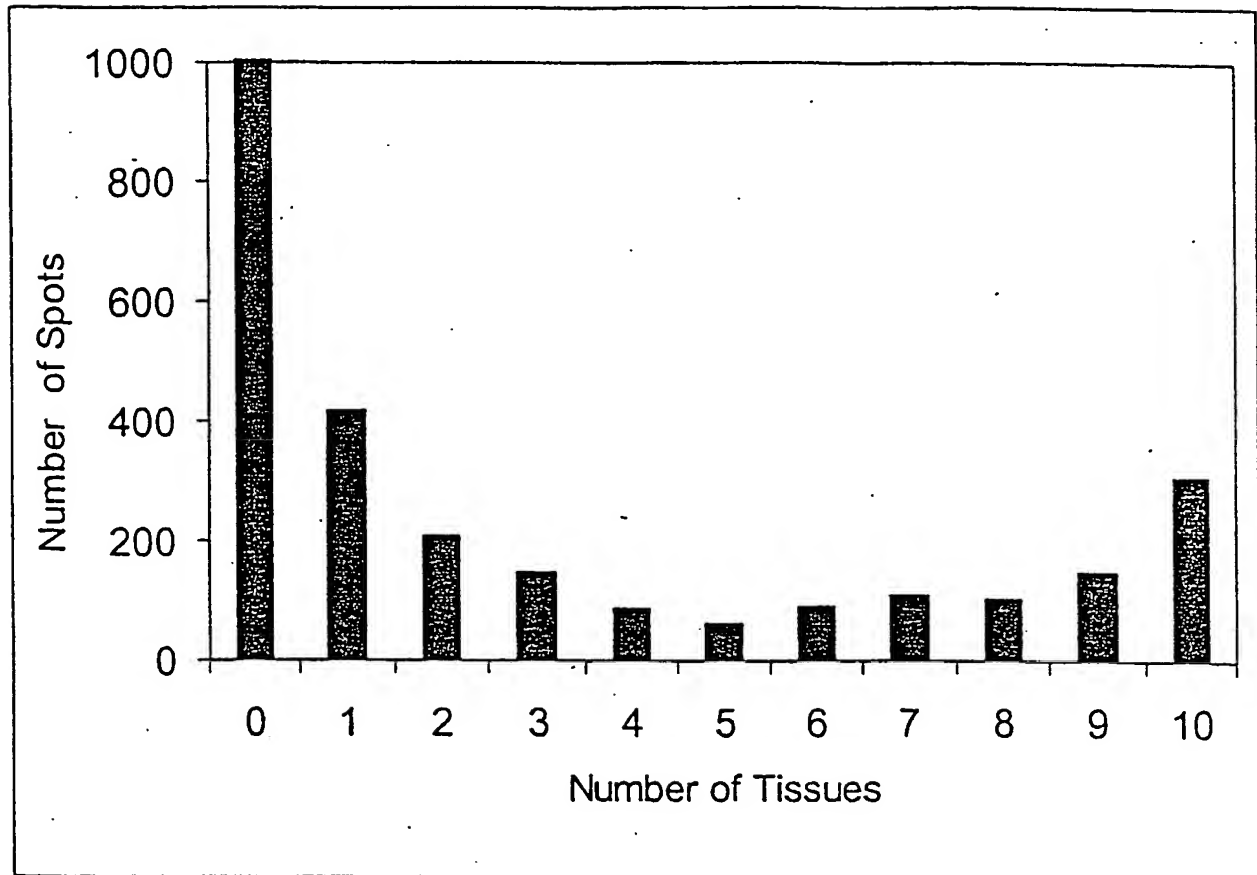


Fig. 6

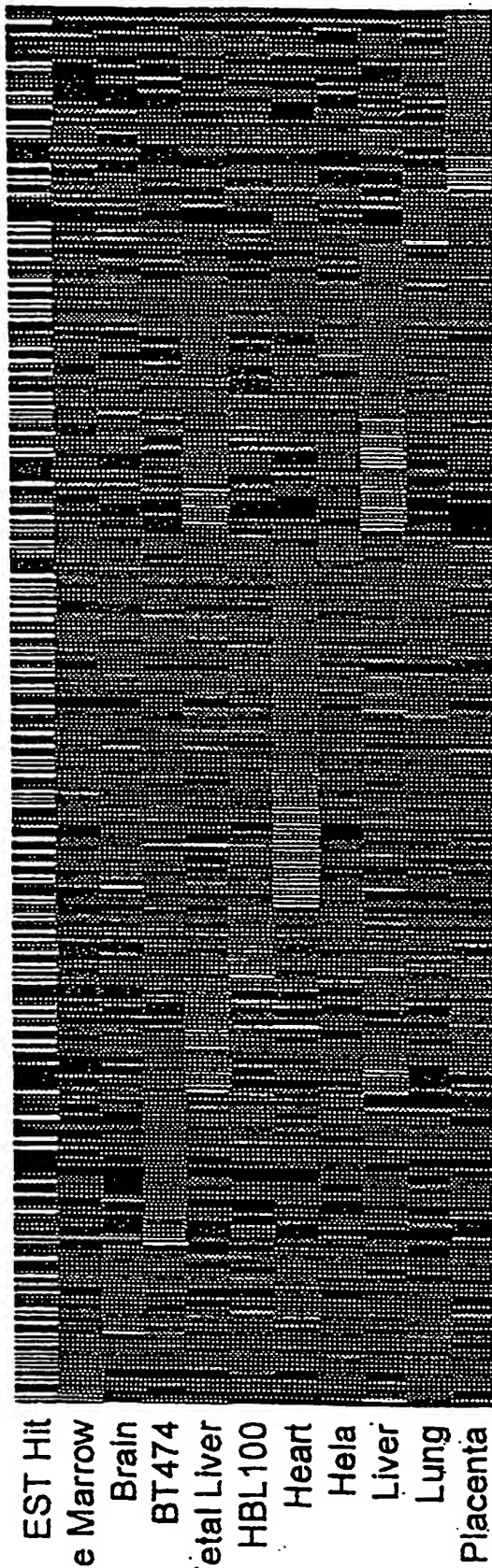


Fig. 7a

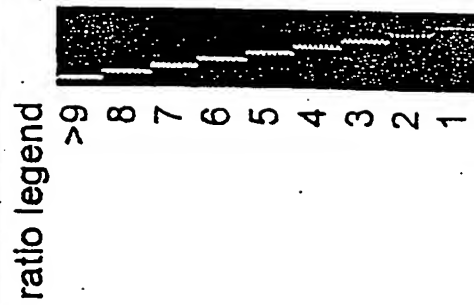


Fig. 7b

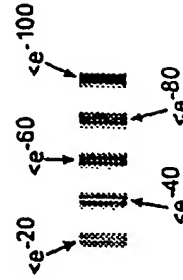


Fig. 7c

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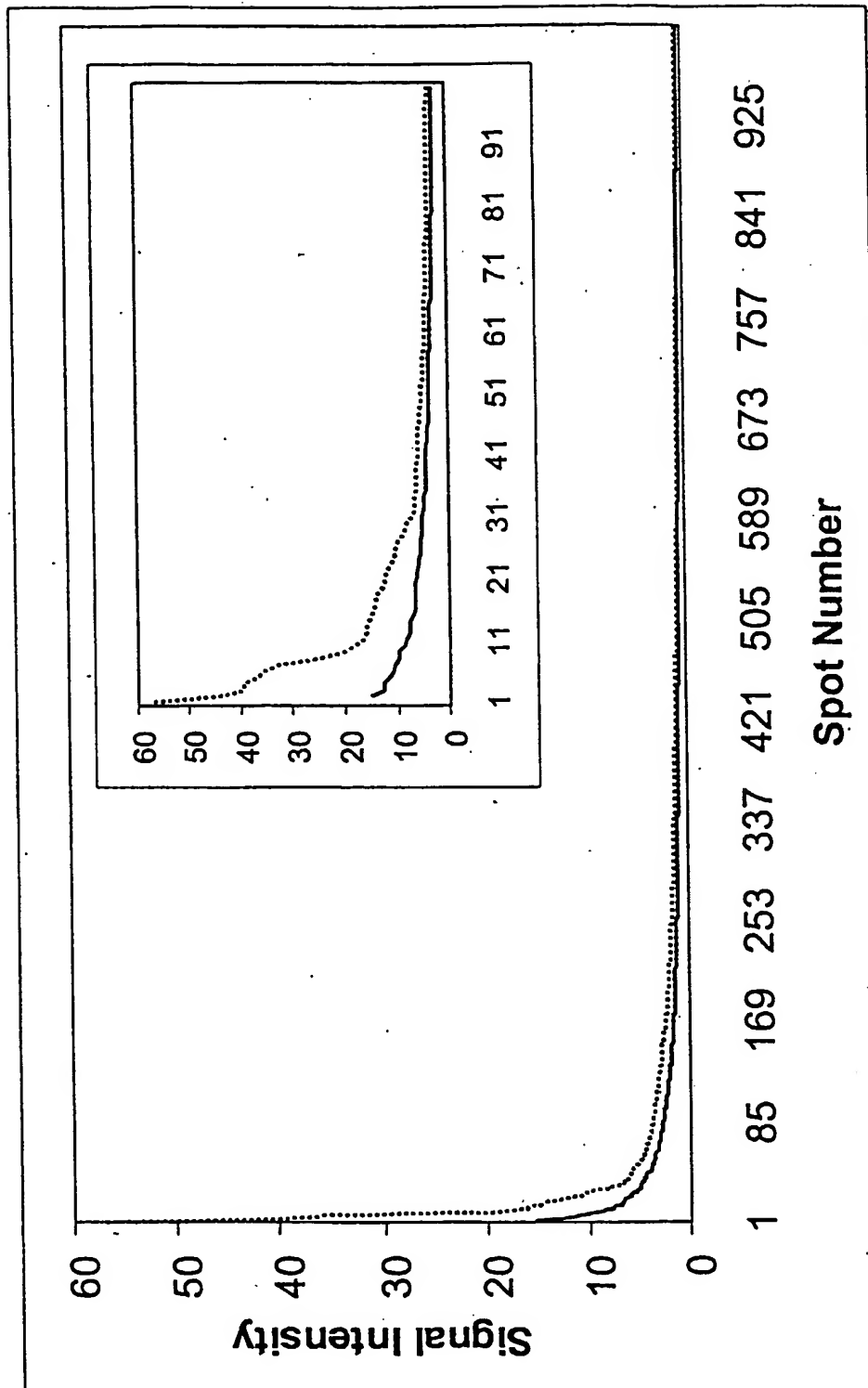


Fig. 8

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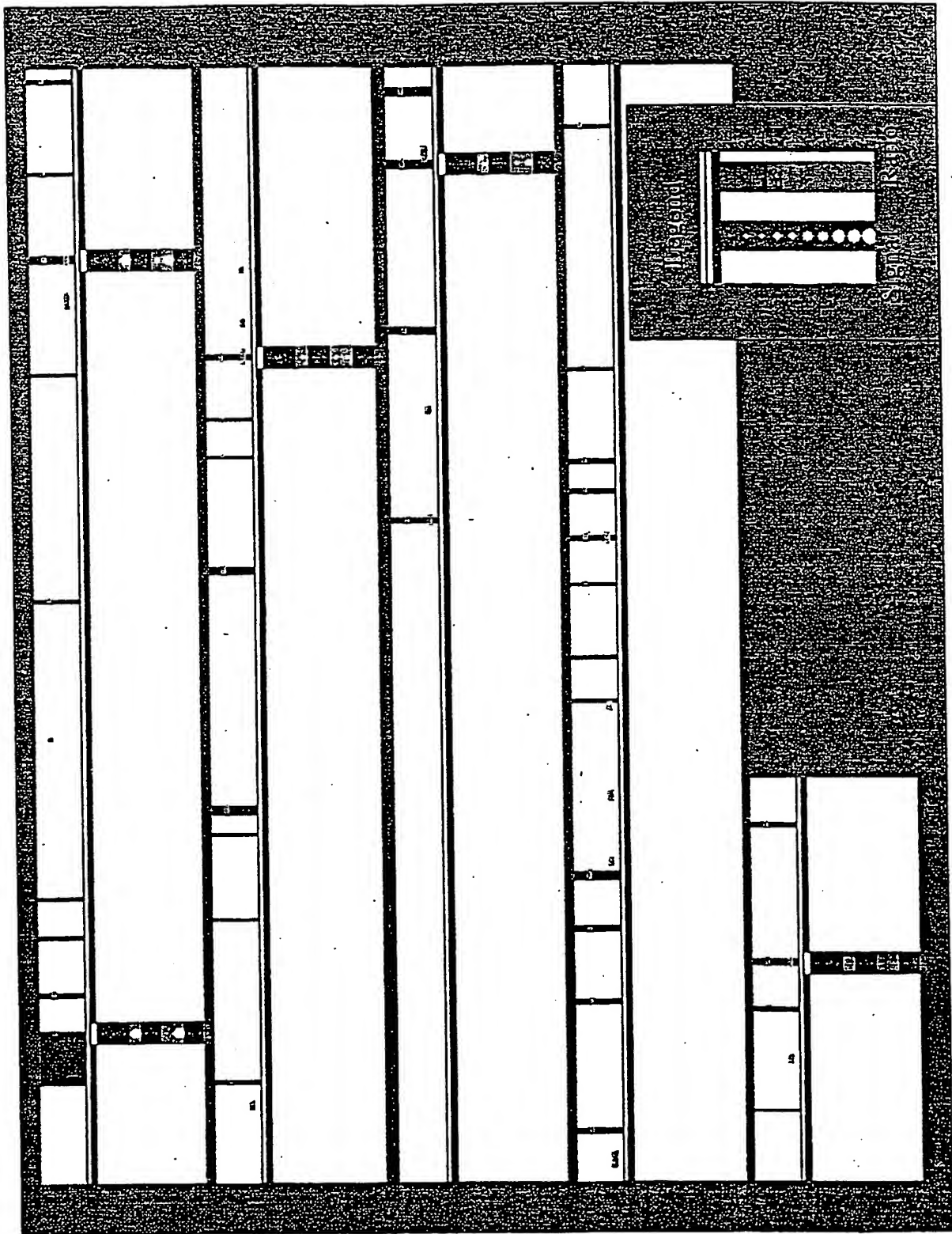
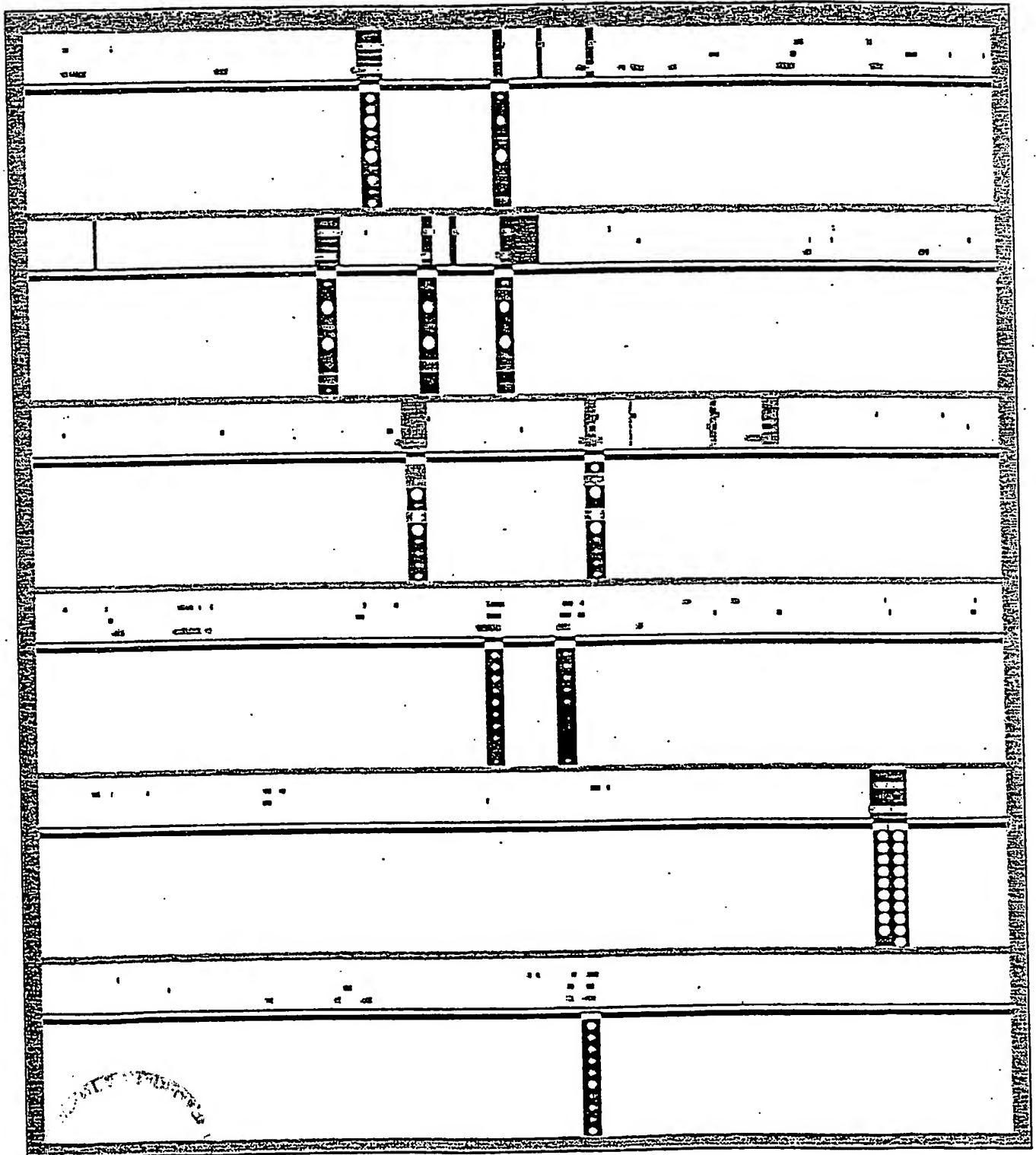


Fig. 9

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Fig. 10



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